

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 8, 2005, 20:45:19 ; Search time 360 Seconds  
(without alignments)  
5820.744 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 4896

Sequence: 1 aatctttatttattcatgtg.....aggcttttttcttaataacc 2709

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO.spool.p/US09774490/runat\_08032005.140757.14830/app\_query.fasta\_1.2887  
-DB=A\_Geneseq\_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09774490 @CNC 1.1.407 @runat\_08032005.140757.14830 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004as:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	4201	85.8	771	2 AAR71380	Human sem
2	4201	85.8	771	4 AAG62726	Amino aci
3	4201	85.8	771	5 AAG96413	Human ova
4	4201	85.8	771	7 ADD08934	Human sem
5	4201	85.8	771	7 ADE25760	Human pro
6	4201	85.8	771	8 ADQ19751	Human sof
7	4197	85.7	770	7 ADN95333	Human BCC
8	4194	85.7	796	2 AAY21264	Human sem
9	2562	52.3	477	2 AAR74175	Human col
10	2245.5	45.9	777	2 AAY27127	Human bra

11	2245.5	45.9	777	3 AAY99427	Human PRO
12	2245.5	45.9	777	4 AAB66176	Protein o
13	2245.5	45.9	777	4 AAU29197	Human PRO
14	2245.5	45.9	777	6 ABU58573	Human PRO
15	2245.5	45.9	777	6 ABU88121	Novel hum
16	2245.5	45.9	777	6 ABU84436	Human sec
17	2245.5	45.9	777	6 ABR66310	Human sec
18	2245.5	45.9	777	6 ABR65700	Human sec
19	2245.5	45.9	777	6 ABU99640	Human PRO
20	2245.5	45.9	777	6 ABU82879	Human PRO
21	2245.5	45.9	777	6 ABU90000	Novel hum
22	2245.5	45.9	777	6 ABR68249	Human sec
23	2245.5	45.9	777	6 ABU96302	Novel hum
24	2245.5	45.9	777	6 ABU92733	Human sec
25	2245.5	45.9	777	6 ABQ08810	Human sec
26	2245.5	45.9	777	6 ABO02862	Human sec
27	2245.5	45.9	777	6 ABR75016	Human sec
28	2245.5	45.9	777	6 ABR94778	Human sec
29	2245.5	45.9	777	6 ABR85751	Human PRO
30	2245.5	45.9	777	6 ABU98911	Novel hum
31	2245.5	45.9	777	6 ABU98126	Human PRO
32	2245.5	45.9	777	6 ABU91832	Novel hum
33	2245.5	45.9	777	6 ABU89525	Human PRO
34	2245.5	45.9	777	6 ABU86366	Human sec
35	2245.5	45.9	777	6 ABU67579	Human sec
36	2245.5	45.9	777	6 ABU80607	Human PRO
37	2245.5	45.9	777	6 ABR99525	Human PRO
38	2245.5	45.9	777	6 ABR98915	Human sec
39	2245.5	45.9	777	6 ABO16438	Human sec
40	2245.5	45.9	777	6 ABR92338	Human sec
41	2245.5	45.9	777	6 ABO18979	Human sec
42	2245.5	45.9	777	6 ABR78400	Human sec
43	2245.5	45.9	777	6 ABU85136	Novel hum
44	2245.5	45.9	777	6 ABO00275	Novel hum
45	2245.5	45.9	777	6 ABO11607	Human sec

## ALIGNMENTS

### RESULT 1

AAR71380  
ID AAR71380 standard; protein; 771 AA.  
XX

AC AAR71380;

XX  
DT 25-MAR-2003 (revised)  
DT 21-NOV-1995 (first entry)  
XX

DE Human semaphorin III protein.

XX  
KW Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium;  
KW variola major virus; smallpox; semaphorin receptor binding activity;  
KW modulation; nerve cell growth; immune response; viral pathogenesis;  
KW neurological disease; neuro-regeneration; oncological infection.

XX Homo sapiens.

XX WO9507706-A1.

XX PD 23-MAR-1995.

XX PF 13-SEP-1994; 94WO-US010151.

XX PR 13-SEP-1993; 93US-00121713.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Goodman CS, Kolodkin AL, Matthes D, Bentley DR, O'Connor T;

XX DR WPI; 1995-131177/17.

XX DR N-PSDB; AAG87442.

XX PT New class of semaphorin peptide(s) and polypeptide(s) - are potent

modulators of nerve cell growth and regeneration.

Example 2; Page 60-63; 101pp; English.

The sequence of the human semaphorin III protein. The proteins encoded by the grasshopper semaphorin I (AA087441), human semaphorin III, vaccinia virus semaphorin IV (AA087443), Drosophila semaphorin I and II (AA087444-5), Tribolium semaphorin I (AA087446) or variola major (smallpox) virus semaphorin IV (AA087447) genes were used to generate a series of peptides (AA0870370-R70418), which retain semaphorin receptor binding activity. The semaphorin derived or semaphorin receptor derived peptides are potent modulators of nerve cell growth, immune responsiveness and viral pathogenesis. They can be used in diagnosis and treatment of neurological disease and neuro-regeneration, immune modulation and diagnosis and treatment of viral and oncological infection and diseases. (Updated on 25 -MAR-2003 to correct PN field.)

Sequence 771 AA;

Alignment Scores:

Pred. No.: 0 Length: 771  
Score: 4201.00 Matches: 771  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 85.80% Indels: 0  
DB: 2 Gaps: 0

US-09-774-490-1 (1-2709) x AAR71380 (1-771)

200 ATGGGCTGGTAACTAGGATTCCTCTCTTTCTGGGAGTATTACTTACAGCAAGACA 259  
1 MetGlyTrpLeuThrArgileValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20  
260 AACTATCAGAAATGGGAGAACAAATGTGCCAAGCTGAAATATCTCTACAAAGAAATGTG 319  
21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLeuLeuSerTyrLysGluMetLeu 40  
320 GAATCCAAATGTGATCACTTTCAATGGCTTGGCCCAAGCTCCAGATTATCATCCTTC 379  
41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
380 CTTTGGATCAGAACCGAGTAGGCTGTATGTTGGAGCAAGATCATATTTTCATTC 439  
61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisilePheSerPhe 80  
440 GACCTGGTTAATATCAGAAATTTCAAAGATTGTGGCCAGTATCTTACACCAAGACA 499  
81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100  
500 GATGAATGCAAGTGGCTGGAAAGACATCCTGAAAGAAATGTGCTAATTTTCATCAAGGTA 559  
101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheileLysVal 120  
560 CTTAAGGCATATAATCAGACTCATTTGTACGCTGTGGAAACGGGGCTTTTCATCCAATT 619  
121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140  
620 TGCACCTACATTTGAATTCGACATCATCTCGAGCAATATTTTAAAGCTGGAGAACTCA 679  
141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
680 CATTTTGAACACGGCTGGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT 739  
161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180  
740 TTAATAGATGGAATATATCTCTGAACTGCAGCTGATTTTATGGGGCGAGACTTTGCT 799  
181 LeuileAspGlyLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
800 ATCTTCGAACTCTGGGACACACCAATCAGACAGAGCAGCATGATTCACAGGTG 859  
201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220

860 CTCAATGATCAAAAGTTTCATTAGTCCACCTCATCTCAGAGAGTGAACAATCTCTGAAGAT 919  
221 LeuAsnAspProLysPheIleSerAlaHisLeuileSerGluSerAspAsnProGluAsp 240  
920 GACAAAGATATCTTTTCTCCGTGAAATGCAATAGATGAGAGACATCTCTGGAAGACT 979  
241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
980 ACTACCGCTAGAAAGTGCAGATATGCAAGATGACTTTTGGAGGCGACAGAAAGTCTGTG 1039  
261 ThrHisAlaArgileGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
1040 AATAAATCGACAAACATCTCCTCAAGCTGCTGTGATTTCTCAGTCCAGGTCCTCAATGCG 1099  
281 AsnLysTrpThrThrPheLeuLysAlaArgLeuileCysSerValProGlyProAsnGly 300  
1100 ATTGACATCTCAATTTTGATGAATCTGAGATGTATCTTAATGAACATTTAAAGATCCTAAA 1159  
301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320  
1160 AATCCAGTTGTATATGGAGTGTTCACGACTTCCAGTAAACATTTTCAAGGGATCAGCCGTG 1219  
321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
1220 TGTATGTATAGCATGAGTGTGAGAAAGGTGTTCCTTGTGTCCATATGCCACAGGAT 1279  
341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360  
1280 GGACCCAACTATCAATGGTGGCTTATCAAGAGAGTCCCTATCCACGCCAGGAACT 1339  
361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
1340 TGTCCACACAAAACATTTGGTGGTTTTCACCTCAAAAGGACCTTCTCTGATGATGTATA 1399  
381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400  
1400 ACCTTTGCAAGAAGTCAATCCAGCCATGATCAATCCAGTGTTCCTATGAACAATCGCCA 1459  
401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
1460 ATAGTATCAAAACGGATGTAATTAATCAATTTACAAATTTGCTAGACCGAGTGGAT 1519  
421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440  
1520 CGAAGAAGTGCAGACATGATGTATGTTTATCGGAACAGATGTTGGGACCGCTCTTAAA 1579  
441 AlaGluAspGlyGlnTyrAspValMetPheileGlyThrAspValGlyThrValLeuLys 460  
1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAAAGAGGTTCCTGCTGGAAGAAATG 1639  
461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480  
1640 ACAGTTTTCGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTCACATTAAGCAGCAACA 1699  
481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500  
1700 CTATATATTGTTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACCGGTGTGATTTTAC 1759  
501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
1760 GGGAAAGCGTGTGAGTGTGCTGCCCGAGACCCCTTACTGTCTGCTGGATGGTCT 1819  
521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
1820 GCATGCTCTCGCTATTTTCCCACTGCAAGAGACCCACAAAGACCAAGATATTAAGAAAT 1879  
541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560  
1880 GGAGACCCACTGACTGCTGTTTACAGCTTACACCTGATTAATCAACATGCGCACGCCCT 1939  
561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580  
1940 GAAGAGAGATCATCTATGGTGTAGAGATAGTACACATTTTGGAAATGCAGTCCGAG 1999



Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240  
 QY 920 GACAAAGTATACCTTTCTTCGTCGAAATGCAATAGATGGAGAACACTCTGGAAGCT 979  
 Db 241 AspLysValTyrPhePhePheGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
 QY 980 ACTCAGCTAGAAATAGGTAGATATGCAAGATGACTTTGGAGGCGCAGAGTCTGGTG 1039  
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
 QY 1040 AATAAATGACAACTTCCTAAAGCTGCTGATTTGCTCAGTCGCCAGGTCCAAATGCG 1099  
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
 QY 1100 ATTGACACTCAATTTGATGAACCTGAGGATGATTCTTAATGAACTTTAAAGATCCTAAA 1159  
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhelYsAspProLys 320  
 QY 1160 AATCCAGTTGTATATGGAGTGTATACGACTTCAGTAAACATTTTCAAGGGATCAGCCGTG 1219  
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePhelYsGlySerAlaVal 340  
 QY 1220 TGTATGTATAGCATGATGATGAGAGGGTTCCTTGGTCCATATGCCACAGGGAT 1279  
 Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360  
 QY 1280 GGACCCAACTATCAATGGTGCTTATCAAGAGAGTCCCTATCCAGCGCCAGAACT 1339  
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
 QY 1340 TGTCCAGCAAAACATTTGGTGGTGTGACTTCAAAAGGACCTTCCTGATGATGTATA 1399  
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400  
 QY 1400 ACCTTTCGAAAGATCATCCAGCCATGTAACAATCCAGTGTTCCTATGAAACAATCCCCA 1459  
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
 QY 1460 ATAGTGATCAAAACCGATGTAATATCAATTTACAAATTTGCTAGACCGAGTGGAT 1519  
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440  
 QY 1520 CGAGAAGATGGACAGTATCATGTTATGTTTATCGGAACAGATGTTGGACCCCTTTTAAA 1579  
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTCTGCTGGAAGAAATG 1639  
 Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480  
 QY 1640 ACAGTTTTCGGAAACCGACTCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699  
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATTGTTTCAACGCTGGGTTGCCAGTCCCTTTACACCGGTGATATTATAC 1759  
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
 QY 1760 GGGAAAGCGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGTCTGGATGTTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
 QY 1820 GCATGTTCTCGTATTTTCCCACTGCAAGAGACCGCAGACGACAGATATAGAAAT 1879  
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATAATCACCATGCGCCAGCCCT 1939  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580  
 QY 1940 GAAGAGAGAAATCATCTATGTTGATGAGAAATAGTAGCAATTTTGGAAATGCAAGTCCGAAG 1999  
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600

QY 2000 TCGCAGAGAGCGCTGGTCTATTGGCAATTCAGAGCGGAAATGAAGACGCAAGAGAG 2059  
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620  
 QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAGTCTCAA 2119  
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
 QY 2120 CAGAGGATTCAGCAATTTACCTCTGCCATCGGTGGAAACATGGTTCATCAAACTCTT 2179  
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660  
 QY 2180 CTTAAGGTAAACCTCGGAAGTCAATTCACACAGAGCATTTTGGAGAACTTCTTCATAAAGAT 2239  
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680  
 QY 2240 GATGATGAGATGGCTCTTAAGACCAAAATATGCTCAATAGCATGACACCTAGCCAGAG 2299  
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
 QY 2300 GTCTGGTACAGAGTTCATCAGCTCATCAACACCCCAATCTCAACACGATGGATGAG 2359  
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
 QY 2360 TTCTGTGAACAAGTTTGGAAAAAGGACCCGAAAAACAACCTCGGCAAGGCCAGGACATACC 2419  
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
 QY 2420 CCAGGAAACAGTAACAAATGGAAGCACTTCAAGAAATATAAGAAAGGTAGAAACAGGAGG 2479  
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGlnAsnLysLysGlyArgAsnArgArg 760  
 QY 2480 ACCACGAAATTTGAGAGGCGCACCCAGGAGTCTC 2512  
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771  
 RESULT 3  
 ID ABG96413 standard; protein; 771 AA.  
 AC ABG96413;  
 DT 11-DEC-2002 (first entry)  
 DE Human ovarian cancer marker M473.  
 KW Human; ovarian cancer; marker; cancer; familial history; brain disorder;  
 KW central nervous system disorder; bacterial meningitis; viral meningitis;  
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;  
 KW brain herniation; inflammation; encephalitis; testicular disorder;  
 KW nontuberculous granulomatous orchitis; connective tissue disorder;  
 KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;  
 KW histological type; carcinogenic; ovarian cancer marker.  
 OS Homo sapiens.  
 PN WO200271928-A2.  
 PD 19-SEP-2002.  
 XX 14-MAR-2002; 2002WO-US007826.  
 XX 14-MAR-2001; 2001US-0276025P.  
 PR 14-MAR-2001; 2001US-0276026P.  
 PR 10-AUG-2001; 2001US-0311732P.  
 PR 19-SEP-2001; 2001US-0323580P.  
 PR 26-SEP-2001; 2001US-0324967P.  
 PR 26-SEP-2001; 2001US-0325102P.  
 PR 26-SEP-2001; 2001US-0325149P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX





Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480  
 QY 1640 ACAGTCTTTCGGAAACCGACTGCTATTTCAGCAATGGAGCTTCCACATAAGCAGCAAA 1699  
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATTGGTTCAACGGCTGGGTTCGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759  
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
 QY 1760 GGGAAAGCGTGTCTGCTAGTGTTCCTCCCGAGACCCCTTACTGCTGGATGGTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
 QY 1820 GCATGTTCTCGTATTTTCCCACTCAAGAGACGACGACGACGACGACGACGACGACGAC 1879  
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCCACTGACTGCTGCTTACAGCTTACACCATGATATACACGATGGCCACAGCCCT 1939  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580  
 QY 1940 GAAGAGAGATCATCTATGCTGTAGAGATAGTAGACATTTTGGATGCGAGTCCGAG 1999  
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
 QY 2000 TCGCAGAGCCCTGCTTATTTGGCAATTCAGAGCGCAATGAGCGCAAAAGAGAG 2059  
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluGluGluGlu 620  
 QY 2060 ATCAGAGTGGATCATCATATCATCAGACAGATCAAGGCTTCTGCTAGTGTACAA 2119  
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
 QY 2120 CAGAAGGATTCAGGCAATTTACTCTGCCATGCGGTGGAAACATGGGTTCATAAACTCTT 2179  
 Db 641 GlnLysAspSerGlyAsnTyrLeuGluHisAlaValGluHisGlyPheIleGlnThrLeu 660  
 QY 2180 CTTAGGTAAACCTGGAGTCTTACACAGAGCATTTTGGAGAACTTCTTCATAAAGAT 2239  
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680  
 QY 2240 GATGATGGAGTGGTCTTAAGACCAAGAAATGTCCAATGATGACACCTAGCCAGAG 2299  
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
 QY 2300 GTCTGTACAGAGCTTCATGAGCTCATCAACCCCACTTCAACAGATGGATGAG 2359  
 Db 701 ValTyrTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
 QY 2360 TTCTGTGAACAAGTTTGGAAAGGCGCAAAACACGCTCGCAAGGCCAGGACATACC 2419  
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
 QY 2420 CCAGGGAACAGTAACAAATGGAGCACTTACAGAAATAAGAAAGCTAGAAACAGGAGG 2479  
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760  
 QY 2480 ACCACGAATTTGAGAGGCGCCAGGAGTGTTC 2512  
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4  
 ADD08934  
 ID ADD08934 standard; protein; 771 AA.  
 XX  
 AC ADD08934;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human semaphorin 3A protein. SEQ ID NO:10.  
 XX

screening; modulator; binding; neuropilin growth factor receptor;  
 vascular endothelial growth factor C;  
 KW vascular endothelial growth factor receptor 3; VEGF-C; VEGFR-3;  
 KW neuropilin; cytosolic; nontropic; neuroprotective; vulnerary;  
 KW vasotropic; cardiac; angiogenic process; nervous system growth;  
 KW nervous system function; cancer; ischaemia; cerebral infarction;  
 KW cerebral bleeding; Alzheimer's disease; myocardial infarction; human.  
 XX Homo sapiens.  
 XX WO2003029814-A2.  
 XX 10-APR-2003.  
 XX 01-OCT-2002; 2002WO-EP011069.  
 XX 01-OCT-2001; 2001US-0326326P.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX (LICN) LICENTIA LTD.  
 XX Alitalo K, Karkkainen M, Karila K;  
 XX WPI; 2003-381660/36.  
 XX N-PSDB; ADD08933.  
 XX Screening for modulators of neuropilin and vascular endothelial growth  
 factor (VEGF)-C or VEGFR-3 interactions, comprises comparing interaction  
 of neuropilin and VEGF-C or VEGFR-3 in the presence and absence of a  
 modulator compound.  
 XX Disclosure; SEQ ID NO 10; 181pp; English.  
 XX The present invention describes a method of screening for modulators of  
 binding between a neuropilin growth factor receptor and a vascular  
 endothelial growth factor (VEGF)-C or VEGFR-3 polypeptide comprising  
 comparing the binding between neuropilin and VEGF-C or VEGFR-3 in the  
 presence and in the absence of a putative modulator compound. Also  
 described: (1) screening for selectivity of a modulator of VEGF-C, VEGFR-  
 3 or neuropilin biological activity; (2) modulating growth, migration or  
 proliferation of cells in a mammalian organism; (3) a bispecific antibody  
 which specifically binds to a neuropilin receptor and a VEGF-C or VEGFR-3  
 polypeptide; (4) modulating neuronal growth or neuronal scarring in a VEGF  
 mammalian organism; and (5) a polypeptide comprising a fragment of a VEGF  
 -C that binds to a neuropilin receptor. The modulators have cytostatic,  
 CC nontropic, neuroprotective, vulnerary, vasotropic and cardiac  
 CC activities. The method is useful in modulating angiogenic processes and  
 CC nervous system growth and function, such as in the treatment of cancer,  
 CC wound, ischaemia, cerebral infarction/bleeding, Alzheimer's disease or  
 CC myocardial infarction. The polypeptide comprising a fragment of a VEGF-C  
 CC that binds to a neuropilin receptor, is useful for manufacturing a  
 CC medicament for the treatment of diseases characterised by aberrant  
 CC growth, migration or proliferation of cells that express a neuropilin  
 CC receptor. The present sequence represents human semaphorin 3A, which is  
 CC used in the exemplification of the present invention.  
 XX Sequence 771 AA;  
 SQ

Alignment Scores:  
 Pred. No.: 0 Length: 771  
 Score: 4201.00 Matches: 771  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 85.80% Indels: 0  
 DB: 7 Gaps: 0

US-09-774-490-1 (1-2709) x ADD08934 (1-771)

QY 200 ATGGGCTGGTAACTAGGATTCGTCTCTTTCTGGGAGTATTACTTACAGCAAGCA 259  
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20  
 QY 260 AACTATCAGATGGGAAGAACATGTGCCAGGCTGAATTTATCTTACAAAGAAATGTTG 319

Db 21 AsnTyrGluAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40  
QY 320 GAATCCAAAGATGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTC 379  
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60  
QY 380 CTTTGGATGAGAAACGGAGTAGCTGTATGTGGAGCAAGGATCACATATTTTCATTC 439  
Db 61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80  
QY 440 GACCTGGTTAAATCAAGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAAGA 499  
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValIleProValSerTyrThrArgArg 100  
QY 500 GATGAATGCAAGTGGCTGGAAAAGACATCCTGAAAGAAATGTCTAAATTTTCATCAAGGTA 559  
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120  
QY 560 CTTAAGGCATATATCAGACTCACTGTAGGCTGTGGAAACGGGGCTTTTCATCCAATT 619  
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140  
QY 620 TGCACCTACATTGAAATTCGACATCATCTCGAGGCAATATTTTAAAGCTGGAGACTCA 679  
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
QY 680 CATTTTGAACACGGCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT 739  
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180  
QY 740 TTAATAGATGGAATATATCTCTGAACTGCACTGATTTTATGGGGCAGACTTTGCT 799  
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
QY 800 ACTTCCGAACTTGGGACACACCACTCAATCAGCAGACAGCATGATTTCCAGGTGG 859  
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220  
QY 860 CTCATATGATCCAAAGTTTATTAGTGCACCTCATCTCAGAGAGTGCACATCTGAAGAT 919  
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluLys 240  
QY 920 GACAAAGTATACTTTTCTCCGTGAAATGCAATAGATGAGAACACTCTCGAAAGCT 979  
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
QY 980 ACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTGGAGGGCAGAAAGTCTGGTG 1039  
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280  
QY 1040 AATAATGACACATCTCCTCAAGCTCGCTGATTTGCTCAGTGCAGGTCCCAATGGC 1099  
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
QY 1100 ATTGACACTCATTTTATGAATGAGGATGTATCTTAATGAACCTTTAAAGATCTTAA 1159  
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320  
QY 1160 AATCCAGTTGTATATGAGTGTATACGACTTCAGTAAACATTTTCAAGGATCAGCCGTG 1219  
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
QY 1220 TGTATGTATAGATGATGTGAGAAGGTGTTCTTGGTCCATATGCCACAGGAT 1279  
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360  
QY 1280 GGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCCTATCCAGGGCCAGGAAT 1339  
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
QY 1340 TGTCCAGCAAAACATTTGGTGGTTTGTACTCTACAAAGGACCTTCCCTGATGTATATA 1399

Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400  
QY 1400 ACCTTTGCAAGAGTCAATCCAGCCATGTACAAATCCAGTGTGTTCCTATGAACTGCCCA 1459  
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
QY 1460 ATAGTGATCAAAACCGATGTAATATCAATTTTACAAAATTTGCTAGACCGAGTGGAT 1519  
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440  
QY 1520 CGAGAAGATGACAGCTATGATGTATTTATCGGAACAGATGTTGGGACCGTCTCTAAA 1579  
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTCTGCTGGAAGAAATG 1639  
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480  
QY 1640 ACAGTTTTTCCGGAACCGACTGCTATTTTCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699  
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
QY 1700 CTATATATTGTTCAACGGCTGGGTGGCCAGCTCCCTTTACCGGTGTGATATTTAC 1759  
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
QY 1760 GGGAAAGCGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGTCTTTGGATGTTCT 1819  
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGACGACGACGACGACGACGACGACGAC 1879  
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560  
QY 1880 GGAGACCCACTGACTCCTGTTTACAGCTTACACCATGATAATACCATGGCCACAGCCCT 1939  
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580  
QY 1940 GAAGAGAGAATCATCTATGGTGTAGAGAAATAGTAGACATTTTGGAAATGCAAGTCCGAG 1999  
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
QY 2000 TCGCAGAGAGCGCTGGTCTATTTGGCAATTCGAGCGGCAATGAAAGCGCAAGAGAGAG 2059  
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620  
QY 2060 ATCAGAGTGATGATCATATCATCAGCAGAGTCAAGCCCTTCTCTAGTACTGTACAA 2119  
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
QY 2120 CAGAAGGATTCAGGCAATTTACCTCTGCCATGGGTGGAACATGGGTTCATACAAACTCT 2179  
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660  
QY 2180 CTTAAGGTAACCTCGAAGTCAATCAGCAGAGCAATTTGGAAGAATCTTCTCATAAAGAT 2239  
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680  
QY 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAG 2299  
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
QY 2300 GTCTGTTACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359  
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
QY 2360 TTCTGTGAACAGTTTGGAAAAGGACCGAAAACACCTGCGGCAAGGCCAGGACATACC 2419  
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
QY 2420 CCAGGGAACAGTAAACAATGGAGCATTCAAGAAAATAAGAAAGTTGAACAGGAGG 2479  
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760

QY 2480 ACCCAGCAATTTGAGAGGCGCCAGGAGTGC 2512  
 DB 761 ThrHisGluPheGluGArgAlaProArgSerVal 771

RESULT 5

AD25760  
 ID ADE25760 standard; protein; 771 AA.

XX ADE25760;

XX 29-JAN-2004 (first entry)

XX Human protein differentially expressed in foam cells #37.

XX Human; differential expression; foam cell; LPS; lipopolysaccharide;  
 KW cardiovascular disease; atherosclerosis.

XX Homo sapiens.

XX US2003194721-A1.

XX 16-OCT-2003.

XX 18-SEP-2002; 2002US-00247671.

XX 19-SEP-2001; 2001US-0323784P.

XX (INCY-) INCYTE GENOMICS INC.

XX Mikita T, Shiffman D, Porter JG, Kaser MR;

PI WPI: 2003-875398/81.

DR N-PSDB; ADE25679.

XX Combination containing several polynucleotide that are differentially  
 PT expressed in foam cells and complements of the polynucleotides, useful  
 PT for diagnosing cardiovascular disease or atherosclerosis.

PS Disclosure; SEQ ID NO 164; 37pp; English.

XX The invention relates to a combination comprising several polynucleotides  
 CC having any one of 127 sequences (S1) such as the sequence of human  
 CC calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4  
 CC hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit  
 CC mRNA, etc., and their complements. The cDNAs are differentially expressed  
 CC in LPS (lipopolysaccharide)-treated foam cells. Also included are  
 CC obtaining an extended or full length gene from a library of nucleic acid  
 CC sequences, an expression vector containing the nucleic acids, a host cell  
 CC containing the vector, a purified polypeptide appearing as ADE25750 and  
 CC ADE25751, producing a protein by culturing the host cell, and a  
 CC composition comprising a purified antibody that specifically binds to the  
 CC proteins. The foam cell-expressed nucleic acids are useful for a high  
 CC throughput detection of differential expression of one or more  
 CC polynucleotides in a sample. The sample is from a subject with  
 CC atherosclerosis and comparison with a standard defines early, mid or late  
 CC stages of the disorder. The foam cell-expressed nucleic acids are useful  
 CC for high throughput screening of a library of molecules or compounds to  
 CC identify a ligand which binds a polynucleotide. The library is chosen  
 CC from DNA molecules, peptides, proteins and RNA molecules. The protein is  
 CC useful for a high throughput screening of library of molecules or  
 CC compounds to identify at least one ligand which specifically binds a  
 CC protein, for purifying a ligand from a sample for making an antibody. The  
 CC foam cell-expressed nucleic acids are useful for diagnosing  
 CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful  
 CC as elements on a microarray which can be used for detecting related  
 CC polynucleotide in a sample, diagnosing cardiovascular disease,  
 CC atherosclerosis. The present sequence represents a protein differentially  
 CC expressed in LPS treated foam cells.

XX Sequence 771 AA;

SQ Alignment Scores:

Pred. No.:	0	Length:	771
Score:	4201.00	Matches:	771
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.80%	Indels:	0
DB:	7	Gaps:	0
US-09-774-490-1 (1-2709) x ADE25760 (1-771)			
QY	200	ATGGGCTGGTTAACTAGGATTGCTCTCTTTCTGGGAGTATTACTTACAGCAGACGA	259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThraAlaGala	20
QY	260	AACTATCAGAATGGGAACAATAAGTCCAAAGGCTGAAATTTATCTCAAAAGAATGTTG	319
DB	21	AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAACAATGTGATCATTCAATGGCTGGCCACACAGCTCCAGTTATCATACCTTC	379
DB	41	GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTTGGATGAGGACGAGTAGGCTGATCTGTGGAGCAAGGATCACATATTTTCATTC	439
DB	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisPheSerPhe	80
QY	440	GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAAGA	499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArg	100
QY	500	GATCAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAATTTTCAAGTA	559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATATACAGACTCAGCTGACCTGTGGAGCGGGCTTTTCATCCAATT	619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProle	140
QY	620	TGCACCTACATTGAAATTTGGACATCATCTCTGAGACACAATATTTTAACTGGAGACTCA	679
DB	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CATTTTGAACCGGCGTGGGAAGAGTCCATATGACCTTAAGCTCTGACAGCATCCCTT	739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThraAlaSerLeu	180
QY	740	TTAATAGATGAGAAATATATCTCTGGAAGTGCAGCTGATTTTATGGGCGAGACTTGTCT	799
DB	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTTCCCAACTCTTTGGGCACACCCACCAATCAGGACAGACAGCATGATTCAGGTGG	859
DB	201	IlePheArgThrLeuGlyHisHisPheIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCCAAAGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT	919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTATATCTTTCTTCCGTAATGCAATAGATGAGAGACACTCTCGAAAAGCT	979
DB	241	AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTAGATAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	280
QY	1040	AATAATGGACACATCTCTCAAGCTGCTGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1099
DB	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320

QY 1160 AATCCAGTTGATATGAGTGTTCAGACTTCAGCTAAACATTTTCAAGGATCAGCCGTG 1219  
 Db 321 AenProValValFyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
 QY 1220 TGTATATAGCATGATGATGAGAGGGTGTCTCTTGGTCCATATCCACAGGAT 1279  
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360  
 QY 1280 GGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGCCGAGAAT 1339  
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
 QY 1340 TGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGAGACCTTCTCTATGATTATA 1399  
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400  
 QY 1400 ACCTTTGCAAGAAGTCCATCCAGCATGTACATCCAGTGTTCCTATGAACAATGCCCA 1459  
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
 QY 1460 ATAGTGATCAAAACGGATGTAATTTATCAAAATTTACAAATTTCTGTAGACCGAGTGGAT 1519  
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440  
 QY 1520 GCAGAAGATGGACAGTATGATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTTAAA 1579  
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
 QY 1580 GTAGTTTCAATTCCTAAAGAGACTGTTGATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639  
 Db 461 ValValSerIleProLysGlnTyrAspLeuGluGluValLeuLeuGluMet 480  
 QY 1640 ACAGTTTTTCGGGAACCGACTGCTATTTCAGCAATGGAGCTTTCCACTAAGCAGCAACAA 1699  
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATTGGTTCAACGGCTGGGTGCCAGCTCCCTTTTACACGGTGTGATATTAC 1759  
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
 QY 1760 GGAAGAGCTGTGCTAGTGTTCCTCGCCGAGACCTTACTGCTGGTGGATGGTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysLysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
 QY 1820 GCATGTTCTCGCTATTTCCTCCACTGCAAGAGACGACAGCAGCAAGATATAAGAAAT 1879  
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCCACTGACTACTGTTACACTTACACATGATGATAATCACCATGGCCACAGCCCT 1939  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580  
 QY 1940 GAAGAGAGATCATCTATGCTAGAGATAGTACACATTTTGGATGCTCCGAG 1999  
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
 QY 2000 TGCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAAATCAAGAGCGAAAGAGAG 2059  
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620  
 QY 2060 ATCAGAGTGGATCATATCATATCAGGACAGATCAAGGCTTCTGCTAGTGTCTACAA 2119  
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
 QY 2120 CAGAGGATTCAGGCAATTTACCTTCCATGGGTGGAGACATGGGTTCATACAACTCTT 2179  
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660  
 QY 2180 CTTAAGGTAACTCGAAGTCAATTGACACAGAGCATTTTGGAGAATCTTCTTCAATAAGAT 2239  
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680  
 QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACTAGCCAGAAG 2299

Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
 QY 2300 GTCTGCTACAGAGACTTTCATGCTCAGCTCATCAACCAACCCCAATCTCAACAGATGGATGAG 2359  
 Db 701 ValTyrTrpArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
 QY 2360 TTCTGTGTAACAATTTGGAAAAAGGAGCCGAAAAACACGTCGCGCAAGGCCAGACATACC 2419  
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
 QY 2420 CCAGGGACACAGTAACAATTTGGAGACCTTACAGAAATTAACAAGGTAGAACACGAGG 2479  
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760  
 QY 2480 ACCCAAGATTTGAGAGGCGACCCAGGAGTGTCT 2512  
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771  
 RESULT 6  
 ADQ19751  
 ID ADQ19751 standard; protein; 771 AA.  
 XX ADQ19751;  
 AC ADQ19751;  
 XX 26-AUG-2004 (first entry)  
 DT Human soft tissue sarcoma-upregulated protein - SEQ ID 2570.  
 DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.  
 KW Homo sapiens.  
 XX WO2004048938-A2.  
 PN 10-JUN-2004.  
 PD 26-NOV-2003; 2003WO-US038193.  
 PF 26-NOV-2002; 2002US-0429739P.  
 PR (PROT-) PROTEIN DESIGN LABS INC.  
 XX A&iz N, Ginsburg WM, Zlotnik A;  
 PI WPI; 2004-441208/41.  
 DR Early detection of soft tissue sarcoma comprises determining expression  
 of a gene in a first soft tissue sample and a normal soft tissue sample  
 and comparing the gene expression, also useful in treating soft tissue  
 sarcoma.  
 XX Example 2; SEQ ID NO 2570; 210pp; English.  
 The invention relates to a novel method for detecting soft tissue sarcoma  
 which comprises obtaining a first soft tissue sample from an individual  
 and a normal soft tissue sample from the same or different individual,  
 determining the expression of a gene in both samples and comparing the  
 expression of the gene in both soft tissue samples, where a higher level  
 of protein expression in the first soft tissue sample indicates the  
 presence of soft tissue sarcoma. The method of the invention has  
 cytostatic applications and may be useful for detecting soft tissue  
 sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 acid sequences may be useful in diagnostic and screening applications.  
 The current sequence is that of a human soft tissue sarcoma-upregulated  
 protein of the invention. The current sequence is not shown within the  
 specification per se but was submitted in CD format by the inventor.  
 SQ Sequence 771 AA;  
 Alignment Scores:  
 Pred. NO.: 0 Length: 771  
 Score: 4201.00 Matches: 771

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.80%	Indels:	0
DB:	8	Gaps:	0
US-09-774-490-1 (1-2709) x ADQ19751 (1-1771)			
QY	200	ATGGGCTGGTTAACTAGGATTCCTCTCTTTCTGGGAGTATTACTTACAGCAAGACA	259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTGAAATATCTCTACAAAGAAATGTTG	319
DB	21	AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCCAAGATGATCACTTCTCAATGGCTGGCCACAGCTCCAGTTATCATACCTTC	379
DB	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTTGGATGAGCAACGGAGTAGGCTGTATGTGGAGCAAGGATCACATATTTTCATTC	439
DB	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGGTTAAATCAAGATTTTCAAAGATTTGTGGCCAGTATCTTACACCAAGACA	499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	100
QY	500	GATGAATCAAGTGGCTGGAAAGACATCTCTGAAAGATGCTTAATTTTCATCAAGGTA	559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATAATCAGACTCACCTGTACGCTGTGGAAACGGGGCTTTTCATCCAAIT	619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TGCACCTACATTGAAATTCGACATCATCTCTGAGGCAATATTTTAAAGCTGGAGAACTCA	679
DB	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CAATTTGAAACGGCGTGGAGAGTCCATATGACCTTAAGCTCTGCACACATCCCTT	739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	180
QY	740	TTAATAGATGGAATATTACTCTGGAACCTGACGCTGATTTTATGGGGGAGACTTTGCT	799
DB	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTCCGAACTCTGGGCACACCAACCAATCAGGACAGACAGCATGATTCAGGTGG	859
DB	201	IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCCAAAGTTCAATAGTCCACCTCATCTCAGAGAGTGACAAATCTCAAGAT	919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTACTTTTCTTCCTGAAAATGCAATAGATCGAGAACACCTCTGAAAAGCT	979
DB	241	AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTPAGATAGGTAGATATGCAAGATGACTTTGGAGGGGACAGAGTCTGGTG	1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal	280
QY	1040	AATAATGACACATCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCTCAATGGC	1099
DB	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTTCATCACTGACAGATGATTTCTCAATGAACCTTTAAAGATCCTAA	1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320
QY	1160	AATCCAGTTGTATATGGATGTTTACGACTTCAGTTAAACATTTTCAAGGATCAGCCGTG	1219

DB	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	340
QY	1220	TGTATGTATAGCATGAGTGTGAGAGGGTGTCTCTTGGTCCATATGCCACAGGAT	1279
DB	341	CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp	360
QY	1280	GGACCCAACTATCAATGGTGCTCTTATCAAGGAGAGTCCCTATCCACGGCCAGGAAT	1339
DB	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
QY	1340	TGTCCCGCAAAACATTTGGTGGTTTGACTCTCAAAGAGACCTTCTCTGATGATGTTATA	1399
DB	381	CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle	400
QY	1400	ACCTTTTGCAAGAAGTCATCCAGCCATGATCAATCCAGTGTTCCTATGAACAATCCGCA	1459
DB	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro	420
QY	1460	ATAGTGATCAAAACGGATGTAATTAACAATTTACAACAATTCGTGTAGACCGAGTGGAT	1519
DB	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
QY	1520	GCAGAGATGACAGTATGATGTTTATCGAACAAGATGTTGGACCGCTCTCTTAAA	1579
DB	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
QY	1580	CTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTTCTCTCGAAGAAATG	1639
DB	461	ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet	480
QY	1640	ACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCCTAAGCAGCAACA	1699
DB	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln	500
QY	1700	CTATATATTTGCTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACCGGTGTGATTTTAC	1759
DB	501	LeuTyrIleGlySerThrAlaGlyValAlaGluLeuProLeuHisArgCysAspIleTyr	520
QY	1760	GGGAAAGCGTGTGCTGAGTGTGGCTCGCCGAGACCCCTTACTGTGCTGGAGTGTCT	1819
DB	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer	540
QY	1820	GCATGTTCTCGTATTTTCCACTGCAAGAGACGCAACAGCAGACAGATATAAGAAT	1879
DB	541	AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn	560
QY	1880	GGAGCCACACTGACTCAGTCTTTCAGACTTACACCATGATTAATCACCTGGCCACAGCCT	1939
DB	561	GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro	580
QY	1940	GAAGAGAAATCATCTATGGTGTAGAGAAATAGTACACATTTTGGAAATGCGATCCGAAG	1999
DB	581	GluGluArgIleIleTyrGlyValGluAsnSerThrPheLeuGluCysSerProLys	600
QY	2000	TGCGAGAGCGCTGCTGCTATTTGGCAATTCAGAGCGCAATGAAGCGCAAAAGAGAG	2059
DB	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu	620
QY	2060	ATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTGTACAA	2119
DB	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln	640
QY	2120	CAGAAGGATTCAGGCAATTTACTCTCTGCCATCGGTGGAAACATGGGTTCATACAACTCTT	2179
DB	641	GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu	660
QY	2180	CTTAAGGTAAACCTCGGAAGTCAATGACACAGAGCAATTTGGAAGAACTTCTTCAAAAGT	2239
DB	661	LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp	680
QY	2240	GATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTACCCAGAGAG	2299
DB	681	AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys	700



QY 2300 GTCTGTACAGAGCTTCATGAGCTCATCAACCCCACTCAACAGATGATGAG 2359  
 |||||  
 Db 701 ValTrpTyArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
 |||||  
 QY 2360 TTCTGTGACAACTTTGGAAAGGACCCGAAACACGTCGCGAAGGCCAGGACATACC 2419  
 |||||  
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
 |||||  
 QY 2420 CCAGGGAACAGTAACAAATGGAAGACACTTACAGAAATAAGAAAGCTAGAAACAGGAGG 2479  
 |||||  
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760  
 |||||  
 QY 2480 ACCACGAATTTGAGAGGACCCAGGAGTGTC 2512  
 |||||  
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771  
 |||||  
 RESULT 7  
 ADN95333  
 ID ADN95333 standard; protein; 770 AA.  
 XX  
 AC ADN95333;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human BEC/LEC-related protein sequence SeqID255.  
 XX  
 KW growth; differentiation; blood endothelial cell; BEC;  
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;  
 KW lymphatic growth agent; VEGF-C; VEGF-D; angiogenic; cytostatic;  
 KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;  
 KW inflammatory disease; cancer metastasis; lymphatic system; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003080640-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 07-MAR-2003; 2003WO-US006900.  
 XX  
 PR 07-MAR-2002; 2002US-0363019P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN) LICENTIA LTD.  
 XX  
 PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;  
 XX  
 DR WPI; 2003-876899/81.  
 DR N-PSDB; ADN95334.  
 XX  
 PS Example 1; SEQ ID NO 255; 176pp; English.  
 XX  
 CC This invention relates to a method of differentially modulating the  
 CC growth or differentiation of blood endothelial cells (BEC) or lymphatic  
 CC endothelial cells (LEC) comprises contacting endothelial cells with a  
 CC composition comprising an agent that differentially modulates blood or  
 CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises  
 CC identifying a human subject with lymphoedema and with a mutation in at  
 CC least one allele of a gene encoding a LEC protein, where the mutation  
 CC correlates with lymphoedema in human subjects, and with the proviso that  
 CC the LEC protein is not VEGFR-3; and administering to the subject a  
 CC composition comprising a lymphatic growth agent selected from VEGF-C or  
 CC VEGF-D polypeptides and polynucleotides. The invention may be useful for  
 CC the development of compounds with an angiogenic, cytostatic,  
 CC vasotropic or antiinflammatory activity or for gene therapy. The method  
 CC is useful in modulating the growth or differentiation of blood  
 CC endothelial cells or lymphatic endothelial cells, in treating hereditary  
 CC lymphoedema, in screening for an endothelial cell disorder or  
 CC predisposition to the disorder or in monitoring the efficacy or toxicity  
 CC of a drug on endothelial cells. The agent is useful in manufacturing a  
 CC medicament for the differential modulation of blood vessel endothelial  
 CC cell or lymphatic vessel endothelial cell growth or differentiation. The

CC lymphatic growth agent may also be used in manufacturing a medicament for  
 CC the treatment of hereditary lymphoedema resulting from a mutation in a  
 CC LEC gene or of other diseases involving the lymphatic vessels, such as  
 CC various inflammatory diseases and cancer metastasis via the lymphatic  
 CC system. The present sequence is that of a human LEC/BEC differentially  
 CC expressed protein which is related to the method of the invention. Note:  
 CC This sequence does not appear in the specification but was obtained by  
 CC the indexer using the source data given in table 14 of the specification.  
 XX  
 SQ Sequence 770 AA;  
 Alignment Scores:  
 Pred. No.: 0 Length: 770  
 Score: 4197.00 Matches: 770  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 85.72% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-774-490-1 (1-2709) x ADN95333 (1-770)  
 QY 200 ATGGGCTGTTAACTAGGATTCTGTCTTTCTGGGAGTATTACTTACAGCAAGCA 359  
 |||||  
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20  
 |||||  
 QY 260 AACTATCAGAAATGGAAGAACAATGTGCCAAGCTGAAATTTATCTTACAAAGAAATGTTG 319  
 |||||  
 Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40  
 |||||  
 QY 320 GAATCCAAATGTGATCATCTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTC 379  
 |||||  
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
 |||||  
 QY 380 CTTTGGGATGAGAACGGAGTAGGTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439  
 |||||  
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysHisIlePheSerPhe 80  
 |||||  
 QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGTGCCAGTATCTTTACACCAAGA 499  
 |||||  
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100  
 |||||  
 QY 500 GATGAATGCAGTGGCTGGAAACACATCTCTGAAGAATGTGCTAATTTTCATCAAGTA 559  
 |||||  
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120  
 |||||  
 QY 560 CTTAAGGCATATAATCAGACTCACCTGTGACGCTGTGGAACGGGGCTTTTCATCAAT 619  
 |||||  
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140  
 |||||  
 QY 620 TGCACCTACATTGAAATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGGAGAACTCA 679  
 |||||  
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
 |||||  
 QY 680 CATTTTAAAACGGCGTGGGAAGATCCATATGACCTTAAGCTGCTGACAGCATCCCTT 739  
 |||||  
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180  
 |||||  
 QY 740 TTAATAGATGGAAGATTTACTCTGAACTGCAGCTGATTATTTATGGGGGAGACTTTGCT 799  
 |||||  
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
 |||||  
 QY 800 APTCTTCCGAACCTTTTGGGCACCCACCAATCAGGACAGACAGCATGATTTCCAGGTGG 859  
 |||||  
 Db 201 IlePheArgThrLeuGlyHisHisIleProIleArgThrGluGlnHisAspSerArgTrp 220  
 |||||  
 QY 860 CTCATATGATCCAAAGTTATATGATGCCACCTCATCTCAGAGAGTGACATCTCTGAAGAT 919  
 |||||  
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240  
 |||||  
 QY 920 GACAAGTATACCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTCGAAAGCT 979  
 |||||  
 Db 241 AspyValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
 |||||



QY 980 ACTCAGCTAGTAATAGGTGATATGATGCTTTGGAGGCGCAGAGTCTGGTG 1039  
 DB 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
 QY 1040 AATAAATGACAACTATCTCTAAAGCTCGTCTGATTTGCTAGTCCAGGTCCTAAATGGC 1099  
 DB 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
 QY 1100 ATTGACACTCATTTGATCACTGAGGAGTGTATTTCTTAATCAATTTAAAGATCCTAAA 1159  
 DB 301 IleAspThrHisPheAspGlnLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320  
 QY 1160 AATCAGCTGTATATGAGTGTATGAGGAGTGTATTTCTTGGTGTCCATATGCCACAGGAT 1219  
 DB 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
 QY 1220 TGTATGTATAGATGATGATGAGAGGGTGTCTTCTTGGTGTCCATATGCCACAGGAT 1279  
 DB 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360  
 QY 1280 GGACCCAACTATCAATGGTGGCTTATCAAGGAAGTCCCTATCCAGCGCCAGGAAT 1339  
 DB 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
 QY 1340 TGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGAGCTTCTCTGATGATGTATA 1399  
 DB 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400  
 QY 1400 ACCTTTGCAAGATGATCCAGCCATGTAATCCAGTGTTCCTATGAACAATCGCCCA 1459  
 DB 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
 QY 1460 ATAGTGATCAAAACGGATTAATATCAATTTACAAATTTGCTAGACCGAGTGGAT 1519  
 DB 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440  
 QY 1520 CGAAGATGAGACATGATGATGATTTATCGGAACAGATGTTGGAGCCGCTCTTAAA 1579  
 DB 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTCTGCTGGAAGAAATG 1639  
 DB 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480  
 QY 1640 ACAGTTTTCGGAACCGACTCTATTTACAGCAATGGAGCTTTCACATAGCAGACAA 1699  
 DB 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATTGGTTCAACGGCTGGGTGCTCCAGCTCCCTTTACACCGGTGTGATTTTAC 1759  
 DB 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
 QY 1760 GGAAGAGCTGTGAGTGTGCTGCTCCGAGACCCCTTACTGTCTTGGATGGTCT 1819  
 DB 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
 QY 1820 GCATGTCTCGCTATTTTCCCACTGCAAGAGACGACAGACGACAGATATAAGAAAT 1879  
 DB 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCCACTGACTGCTTTCAGACTTACACCATGATTAATCACCATGGCCACAGCCCT 1939  
 DB 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580  
 QY 1940 GAAGAGAGATCATATGCTGTAGAGATAGTAGACATTTTGGATGCGATCCGGAAG 1999  
 DB 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
 QY 2000 TCGCAGAGAGCCCTGCTGCTATTTGGCAATTTCCAGAGCGCAATGAAGAGGAAAGAGAG 2059  
 DB 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620  
 QY 2060 ATCAGATGGATGATCATATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGTCTACAA 2119

DB 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
 QY 2120 CAGAAGGATTCAGCAATTACTCTGCCATCGGTGGACATGGGTTTCATACAACTCTT 2179  
 DB 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660  
 QY 2180 CTTAAGGTAAACCTGGAGTCAATGACACAGAGCATTTGGAGAACTTCTTCATAAAGAT 2239  
 DB 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680  
 QY 2240 GATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299  
 DB 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
 QY 2300 GTCTGGTACAGAGACTTCATGACGCTCATCAACACCCCAATCTCAACACAGATGATGAG 2359  
 DB 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
 QY 2360 TTCTGTGAACAAAGTTTGGAAAAGGACCGAAACAAACGTCGCGCAAGCCAGGACATACC 2419  
 DB 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
 QY 2420 CCAGGAAACAGTAAATAATGGAACACATTCAAGAAAATAAGAAAGGTAGAAAACAGGAG 2479  
 DB 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760  
 QY 2480 ACCACAGAAATTTGAGAGGCGACCCAGGAGT 2509  
 DB 761 ThrHisGluPheGluArgAlaProArgSer 770  
 RESULT 8  
 ID AAY21264  
 AC AAY21264;  
 DT 22-JUL-1999 (first entry)  
 DE Human semaphorin III wild type protein fragment 1.  
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.  
 OS Homo sapiens.  
 XX WO9845322-A2.  
 XX 15-OCT-1998.  
 XX 02-APR-1998; 98WO-IB000705.  
 XX 10-APR-1997; 97US-0043163P.  
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 XX (UYRO-) UNIV ROTTERDAM ERASMUS.  
 XX (UYOT-) RIJKSONIV UTRECHT.  
 XX Van Leeuwen FW, Grosveld FG, Burbach JPH;  
 XX WPI; 1998-609901/51.  
 XX N-PSDB; AAX75767.  
 PT Diagnosing disease by detecting frameshift mutations in RNA or  
 PT corresponding protein mutations - used to diagnose cancer and

neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.

Disclosure; Fig 16; 258pp; English.

This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the use of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-M, neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPP-1, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A

Sequence 796 AA;

# Alignment Scores:

Pred. No.:	0	Length:	796
Score:	4194.00	Matches:	773
Percent Similarity:	97.48%	Conservative:	0
Best Local Similarity:	97.48%	Mismatches:	0
Query Match:	85.66%	Indels:	20
DB:	2	Gaps:	1

US-09-774-490-1 (1-2709) x AAY21264 (1-796)

QY	194	TCGAGCATGGCTGGTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGCA	253
DB	4	CysSerMetGlyTrpLeuThrArgileValCysLeuPheTrpGlyValLeuLeuThrAla	23
QY	254	AGAGCAATCTCAGATGGGAGACAAATGGCCAAAGCTGAAATATCTTACAGNA	313
DB	24	ArgAlaAsnTyrglnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrlsGlu	43
QY	314	ATGTTGGAAATCCAAATGTGATCACTTTCAATGGCTGGCCAAAGCTCCAGTATTATCAT	373
DB	44	MetLeuGluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrlsHis	63
QY	374	ACCTCTCTTTGGATGAGGACGAGTAGCTGTATGTTGGAGCAAGGATCACATATT	433
DB	64	ThrPheLeuLeuAspGluGluArgSerArgLeuTyrrValGlyAlaLysAspHisIlePhe	83
QY	434	TCATTGCACTGGTTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACC	493
DB	84	SerPheAspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrlsThr	103
QY	494	AGAAGAGATGAATGCAAGTGGCTGGAAGAGACATCTGAAAGAAATGCTTAATTTTCATC	553
DB	104	ArgArgAspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPhellie	123
QY	554	AAGGTACTTAAGGCATATATATCAGACTCACTTTGTACGCTGTGGAACGGGGCTTTTCAT	613
DB	124	LysValLeuLysAlaTyrrAsnGlnThrHisLeuTyrrAlaCysGlyThrGlyAlaPheHis	143
QY	614	CCAAATTTGCACCTAGATTGAAATTTGACATCATCTCTGAGGACATATTTTAAAGCTGGAG	673
DB	144	ProIleCysThrTyrlleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGlu	163
QY	674	AACTCACTTTTGAAGCGCGTGGGAAGAGTCCCATATGACCTAGCTGTGACAGCA	733
DB	164	AsnSerHisPheGluAsnGlyArgGlyLysSerProTyrrAspProLysLeuLeuThrAla	183
QY	734	TCCCTTTTAATAGATGGAGATTTATATCTCTGGAACCTGCAGCTGATTTTATGGGGCGAGAC	793

DB	184	SerLeuLeuIleAspGlyGluLeuTyrrSerGlyThrAlaAlaAspPheMetGlyArgAsp	203
QY	794	TTTGTCTATCTCCGAACCTCTGGGCACCAACCAATCAGACAGAGCAGCATGATCTCC	853
DB	204	PheAlaIlePheArgThrLeuGlyHisHisProlleArgThrGluGlnHisAspSer	223
QY	854	AGTGGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGCACATCT	913
DB	224	ArgTrpLeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnPro	243
QY	914	GNAAGATGACAAAGTATCTTTTCTCCGTGAAATGCAATAGATGAGAACTCTGCA	973
DB	244	GluAspAspLysValTyrrPhePheArgGluAsnAlaIleAspGlyGluHisSerGly	263
QY	974	AAAGCTACTCAGCTAGATAGGTGATATCAGATATCAGATAGTCTTGGAGGACAGAACT	1033
DB	264	LysAlaThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSer	283
QY	1034	CTGGTGAATAAATGACAAACATCTCTCAAAAGTCTGCTGATTTGCTCAGTGCAGGTCCA	1093
DB	284	LeuValAsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyPro	303
QY	1094	ANTGGCATTGACACTCATTTTGTGATGAACTGACAGGATGATTTCTTAATGACTTAAAGAT	1153
DB	304	AsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAsp	323
QY	1154	CCTAAAAATCCAGTTGATATGGAGTGTTCAGCTTCCTCAGTAACATTTTCAAGGATCA	1213
DB	324	ProLysAsnProValValTyrrGlyValPheThrThrSerSerAsnIlePheLysGlySer	343
QY	1214	GCCGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1273
DB	344	AlaValCysMetTyrrSerMetSerAspValArgValPheLeuGlyProTyrrAlaHis	363
QY	1274	AGGATGAGCAACCACTATCAATGGTGGCTTATCAAGAGAGTCCCTTATCCAGGCCA	1333
DB	364	ArgAspGlyProAsnTyrrGlnTrpValProTyrrGlnGlyArgValProTyrrProArgPro	383
QY	1334	GGAACTGTGCCAGCAAAACATTTGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1393
DB	384	GlyThrCysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAsp	403
QY	1394	GTTTAAACCTTTGCAAGAGTCCATCCAGCATGTACATCCAGTGTTCCT-----	1444
DB	404	ValIleThrPheAlaArgSerHisProAlaMetTyrrAsnProValPheProMetAsnAsn	423
QY	1445	-----ATGAACAAT 1453	
DB	424	ArgProIleValIleLysThrAspValAlaAsnTyrrGlnPheThrGlnIleValMetAsnAsn	443
QY	1454	CGCCCAATAGTGCATCAAAACGGATGTAAATTTATCAATTTTACACAAATTTCTGTAGACCGA	1513
DB	444	ArgProIleValIleLysThrAspValAlaAsnTyrrGlnPheThrGlnIleValValAspArg	463
QY	1514	GTGGATGACAGAGATGAGCAGTATGATGTATGTTTATCGGAACAGATGTGGGACCGTT	1573
DB	464	ValAspAlaGluAspGlyGlnTyrrAspValMetPheIleGlyThrAspValGlyThrVal	483
QY	1574	CTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTATAGAGAGTCTCTGGAA	1633
DB	484	LeuLysValValSerIleProLysGluThrTrpTyrrAspLeuGluGluValLeuLeuGlu	503
QY	1634	GAATGACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATCGAGCTTTCCATAGCAG	1693
DB	504	GluMetThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGln	523
QY	1694	CAACAACTATATATTTGGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTTACACCGGTGTGAT	1753
DB	524	GlnGlnLeuTyrrIleGlySerThrAlaGlyValAlaGlnLeuLeuProLeuHisArgCysAsp	543
QY	1754	ATTTCAGGGAAGCGTGTGCTGAGTGTGCTTCGCCCGGAGACCTTACTGTCTGGTGGAT	1813

Db 544 IleTyrGlyLeuAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAsp 563  
 QY 1814 GTTCTGATGTTCTCGCTATTTTCCACTGCAAGAGACGACAGAGACGACAGATATA 1873  
 Db 564 GlySerAlaCysSerArgTyrPheProThrAlaLysArgGthrArgGlnAspIle 583  
 QY 1874 AGAAATGGAGACCCACTGACTCCTGTTGAGCTTACACCTTACACCATGATGATGACCC 1933  
 Db 584 ArgAsnGlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHis 603  
 QY 1934 ACCCTTGAAGAGAGATCATCTATGTTGAGAGATAGTAGACATTTTGGAAATGCGAGT 1993  
 Db 604 SerProGluGluArgIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSer 623  
 QY 1994 CCGAAGTCCAGAGACGCTGCTGTTATGCAATTCAGAGCGGAAATGAAGAGCGAAA 2053  
 Db 624 ProLysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLys 643  
 QY 2054 GAAGAGATCAGATGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGCTAGT 2113  
 Db 644 GluGluIleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSer 663  
 QY 2114 CTACACAGAGAGATTCAGGAAATACCTCTCCATGCGGTGGAACATGGGTTTATACAA 2173  
 Db 664 LeuGlnGlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGln 683  
 QY 2174 ACTCTTCTTAAGGTAACTGCAAGTCTGATGACAGAGATTTGGAAGAACTTCTTCAT 2233  
 Db 684 ThrLeuLeuLysValThrLeuGluValIleAspThrGluHisGluGluLeuLeuHis 703  
 QY 2234 AAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCATAGCATGACACCTAGC 2293  
 Db 704 LysAspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSer 723  
 QY 2294 GAGAAGTCTGTACAGAGATCTCATGAGCTCATCAACCCCACTCAACAGATG 2353  
 Db 724 GlnLysValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMet 743  
 QY 2354 GATGAGTCTGTGAACAAGTTTGGAAAGGGACCGAAACACACGTCGGCAAGGCGAGGA 2413  
 Db 744 AspGluPheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGly 763  
 QY 2414 CATACCCAGGAGAACAGTAACAAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAAC 2473  
 Db 764 HisThrProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsn 783  
 QY 2474 AGGAGACCCAGCAATTTGAGAGGGGCCACCCAGAGTGT 2512  
 Db 784 ArgArgThrHisGluPheGluArgAlaProArgSerVal 796

RESULT 9  
 AAR74175  
 ID AAR74175 standard; protein; 477 AA.  
 XX AC AAR74175;  
 XX AC AAR74175;  
 DT 01-NOV-1995 (first entry)  
 XX DE Human collapsin.  
 XX KW Collapsin; antibody; therapy.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Binding-site 9..19 /note= "antibody binding site"  
 FT Binding-site 51..65 /note= "antibody binding site"  
 FT FT  
 PN US5416197-A.  
 XX 16-MAY-1995.

XX 15-OCT-1993; 93US-00136922.  
 XX 15-OCT-1993; 93US-00136922.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Luo Y, Raper JA;  
 XX WPI: 1995-193478/25.  
 XX N-PSDB; AAQ92331.  
 XX New antibody to human collapsin - used to inhibit the activity of  
 PT collapsin, to induce neurite out-growth and to treat individuals with  
 PT nerve damage.  
 XX Claim 2; Col 15-18; 11pp; English.  
 XX An antibody capable of specifically binding at least a portion of the  
 CC collapsin protein can be used to purify human collapsin and to inhibit  
 CC the activity of the protein. It can be used to induce neurite outgrowth  
 CC by neuronal cells and to treat individuals suffering from nerve damage  
 XX SQ Sequence 477 AA;  
 Alignment Scores:  
 Pred. No.: 4,896-226 Length: 477  
 Score: 2562.00 Matches: 472  
 Percent Similarity: 99.37% Conservative: 0  
 Best Local Similarity: 99.37% Mismatches: 3  
 Query Match: 52.33% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-774-490-1 (1-2709) x AAR74175 (1-477)  
 QY 899 GAGAGTGACATCTGAAAGATGACAAATATATCTTTCTTCCGTGAAATGCAATAGAT 958  
 Db 2 GluHisAspAsnProGluAspLysValTyrPhePheArgGluAsnAlaIleAsp 21  
 QY 959 GGAGAACACTCTGGAAGAGCTACTCACCTAGAATAGTTCAGATATGCAAGATGACATTT 1018  
 Db 22 GlyGluHisSerGlyLysAlaThrHisAlaArgIleGlyGlnIleCysLysAsnAspPhe 41  
 QY 1019 GGAGGCGACAGAGTCTGCTGAATAAATGGAACAATCTCTCAAGCTCGTCTGATTTGC 1078  
 Db 42 GlyGlyHisArgSerLeuValAsnLysTrpThrPheLeuLysAlaArgLeuIleCys 61  
 QY 1079 TCAGTGCAGAGTCCAAATGGCATTCACACTCATTTTGTAGTAAGTCCAGAGATGATTCCTA 1138  
 Db 62 SerValProGlyProAsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeu 81  
 QY 1139 ATGAACCTTTAAGATCCTAAATAATCCAGTTGTATATGAGTGTGTACGACTTCCAGTAAAC 1198  
 Db 82 MetAsnPheLysAspProLysAsnProValValTyrGlyValPheThrThrSerSerAsn 101  
 QY 1199 ATTTTCAAGGGATCAGCCGTGTGTATGTATAGCATGATGTGTGAGAGGGTGTTCCTT 1258  
 Db 102 IlePheLysGlySerAlaValCysMetTyrSerMetSerAspValArgArgValPheLeu 121  
 QY 1259 GGTCATATGCCACAGGATGGACCCAACTATCATGGTGGCTTATCAAGGAGAGTCC 1318  
 Db 122 GlyProTyrAlaHisArgAspGlyProAsnTyrGlnTrpValProTyrGlnGlyArgVal 141  
 QY 1319 CCCTATCCACGCCAGGAACCTTGCCAGCAAAACATTTGGTGGTGTGTGACTCTCAAAAG 1378  
 Db 142 ProTyrProArgProGlyThrCysProSerLysThrPheGlyGlyPheAspSerThrLys 161  
 QY 1379 GACCTTCTGATGATGTTTATAACCTTTTGCAGAAAGTATCCAGCATGTACAAATCCAGTG 1438  
 Db 162 AspLeuProAspAspValIleThrPheAlaArgSerHisProAlaMetTyrAsnProVal 181  
 QY 1439 TTTCCTATGAACAATCGCCCAATAGTATCAAAACGGATGTAAATATCAATTTACACAA 1498



159 AspLeuGlyValTyLysLeuAspIlellePheLysLeuAspThrArgAsnLeuGluSer 178  
692 GCGCTGGAGAGTCCATATGACCCCTAAGCTGCTGACAGACATCCCTTTTAAATAGATGA 751  
179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198  
752 GAATATATCTCGGAACCTGACCTGATTTATGGGCGAGACTTGGCTATCTTCGGAAT 811  
199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218  
812 CTTGGG-----CACCAACCAATCAGAGCAGACGACGATGATCCAGGTGGCTC 862  
219 LeuGlyProThrHisAspHisIstYrIleArgThrAspIleSerGluHisTyrTrpLeu 238  
863 AATGATCCAAAGTTCATTAGTCCCACTCATCTCAGAGAGTGACAAATCTCGAAGATGAC 922  
239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAspAsp 258  
923 AAGATATATCTTTCTTCGTCGTAATGCAATGATGAGAGACATCTCGGAAGCTACT 982  
259 LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278  
983 CAGCTAGATAGTTCAGATATGCAAGATGATCTTGGAGGCGCAGAGATCTGGTGAAT 1042  
279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298  
1043 AATGACACAACTTCCTCAAGCTGCTGATTTGCTCAGTCCAGGTCCAAATGGCAAT 1102  
299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318  
1103 GACACTCATTTGATGAACCTGAGGATGATTCCTTAATGAATCTTAAAGATCCTAAAT 1162  
319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338  
1163 CAGTTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATG 1222  
339 ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358  
1223 ATGTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1282  
359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378  
1283 CCAACTCATCAATGGTGTCTTCAAGGAGAGTCCCTATCCAGGCGCAGAACTTGT 1342  
379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398  
1343 CCCAGCAAAACATTTGGTGT-----TTGACTCTCAAAAGACCTTCTGATGATGATTA 1399  
399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle 418  
1400 ACCTTTGCAAGAGTATCAGCGCATGATCAATCCAGTGTTCCTATGAACATCGCCCA 1459  
419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438  
1460 ATAGTATCAAAACGGATGATAATTCATTAATTCACAAATTCGTAGACCGAGTGGAT 1519  
439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458  
1520 GCAGAGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1579  
459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478  
1580 GTAGTTTCATTTCTAGGAGACTGCTGATGATGATGATGATGATGATGATGATGATG 1639  
479 ValValSerIleSerLysGlyLysTrp-----AsnMetGluGluValValLeuGluGlu 497  
1640 ACAGTTTTCGGGAACCGATGCTTATTTACAAATGAGCTTTTCCACTAAGACGACAA 1699  
498 GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517  
1700 CTATATATGTTCAACGGCTGGGTGCGGATGCTTCCCTTACACCGGTGATATTAC 1759  
518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537

1760 GGAAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTTGGGATGTTCT 1819  
538 GlyLysAlaCysAlaAspCysLysLeuAlaArgAspProTyrCysAlaIlePheGlyAsn 557  
1820 GCATGTTCTCGCTATTTCCACTGCAAGAGACGCAACAGACGACAGATATAAGNAAT 1879  
558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgArgGlnAspValLysTyr 577  
1880 GGAGACCATGACTCTCTGCTTCCAGCTTACACCATGATAATCACCATGCGCAGACGCT 1939  
578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis----GluThrAla 596  
1940 GAACAGAGATCATCTATGCTAGAGATATAGACACATTTTGGAAATCAGTCCGAAG 1999  
597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616  
2000 TCGCAGAGAGCGTGTCTTATTTGGCAATTCAGAGGCGAAATGAAGAGCGCAAGAGAG 2059  
617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636  
2060 ATCAGAGTGGATGATCATATCATCAGACGACATCAAGCGCTTCTGCTAGTAGTCTACAA 2119  
637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656  
2120 CAGAGGATTCAGGCAATTTACTCTGCGCATGCGGTGGAACATGCGTTCATACAACTCTT 2179  
657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676  
2180 CTTAAGTAAACCTCGGAAGTCAATTCAGACGACGATTTGGAGAACTTCTTCATAAGAT 2239  
677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696  
2240 GATGATGAGATGCTCTTAAGACCAAAATGCTCAATAGCATGACACCTAGCCAGAG 2299  
697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710  
2300 GTCTGGTACAGAGACTTCATCAGCTCATCAACCAACCCCAATCTCAACCATGATGATG 2359  
711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729  
2360 TTCTGTGACAAAGTTTGGAAAGGCGCAAAACAACTCGCAAGGCCAGGACATACC 2419  
730 TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly----- 747  
2420 CCAGGCAACAGTAAACAAATGGAAGCACTTACAAAGAAAATAAGAAAGTAGAAACAGGAG 2479  
748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763  
2480 ACCCAC---GAATTTGAGAGGCGCCAGGAGTGTCT 2512  
764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 11  
AAY99427  
ID AAY99427 standard; protein; 777 AA.  
XX AC AAY99427;  
XX DT 08-AUG-2000 (first entry)  
XX DE Human PRO1491 (UNQ760) amino acid sequence SEQ ID NO:310.  
XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
XX KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.  
XX OS Homo sapiens.  
XX PN WO200012708-A2.  
XX PD 09-MAR-2000.  
XX PF 01-SEP-1999; 99WO-US020111.

XX	01-SEP-1998	98US-0098716P
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PR	08-OCT-1998;	98US-01036788;
PR	08-OCT-1998;	98US-01036799;
PR	08-OCT-1998;	98US-01037111;
PR	14-OCT-1998;	98US-01042579;
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PR	20-OCT-1998;	98US-01050009;
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PR	22-OCT-1998;	98US-01051699;
PR	22-OCT-1998;	98US-01052669;
PR	26-OCT-1998;	98US-01055939;
PR	26-OCT-1998;	98US-01055949;
PR	27-OCT-1998;	98US-01058079;
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PR	27-OCT-1998;	98US-01058829;
PR	27-OCT-1998;	98US-01060629;
PR	28-OCT-1998;	98US-01060239;
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PR	28-OCT-1998;	98US-01060329;
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PR	29-OCT-1998;	98US-01063849;
PR	30-OCT-1998;	98US-01085009;
PR	30-OCT-1998;	98US-01084649;
PR	03-NOV-1998;	98US-01068569;
PR	03-NOV-1998;	98US-01069029;
PR	03-NOV-1998;	98US-01069059;
PR	03-NOV-1998;	98US-01069139;
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PR	03-NOV-1998;	98US-01069349;
PR	10-NOV-1998;	98US-01077839;
PR	17-NOV-1998;	98US-01087759;
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PR	17-NOV-1998;	98US-01088069;
PR	17-NOV-1998;	98US-01088079;
PR	17-NOV-1998;	98US-01088679;
PR	17-NOV-1998;	98US-01089259;
PR	18-NOV-1998;	98US-01088449;
PR	18-NOV-1998;	98US-01088499;
PR	18-NOV-1998;	98US-01088509;
PR	18-NOV-1998;	98US-01088519;
PR	18-NOV-1998;	98US-01088529;
PR	18-NOV-1998;	98US-01088589;
PR	18-NOV-1998;	98US-01089049;

(GETH ) GENENTECH INC.

Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

WPI; 2000-237871/20.  
N-PSDB; AAA37109.

New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.

Claim 12; Fig 176; 773pp; English.

AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAA93340 to AAA93462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding them have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.

[illegible]



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Db      697 HisGluGluGlyGlnVallys-----AspLeuLeuAlaGluSerArg 710
QY      2300 GTCTGTGACAGACTTCATGACGCTCATCAACCCCAATCTCAACACAGATGGATGAG 2359
Db      711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY      2360 TTCTGTGAACAAGTTGGAAAGGACCGAAGAACACACGTCGCGAAGGCGCAGGACATACC 2419
Db      730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY      2420 CCAGGGAACAGTAACAATGGAAGGACACTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db      748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY      2480 ACCCAC---GAATTTGAGAGGGCACCACGAGGTGTC 2512
Db      764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 12
ID      AAB66176
XX      AAB66176 standard; protein; 777 AA.
XX      AAB66176;
XX      02-APR-2001 (first entry)
XX      Protein of the invention #88.
XX      Secreted; transmembrane; gene therapy.
XX      Unidentified.
XX      WO200078961-A1.
XX      28-DEC-2000.
XX      18-FEB-2000; 2000WO-US004342.
XX      23-JUN-1999; 99US-0141037P.
XX      20-JUL-1999; 99US-0144758P.
XX      26-JUL-1999; 99US-0145698P.
XX      01-SEP-1999; 99WO-US020111.
XX      29-OCT-1999; 99US-0162506P.
XX      30-NOV-1999; 99WO-US028313.
XX      02-DEC-1999; 99WO-US028551.
XX      16-DEC-1999; 99WO-US030095.
XX      05-JAN-2000; 2000WO-US000219.
XX      06-JAN-2000; 2000WO-US000376.
XX      (GETH ) GENENTECH INC.
XX      Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
XX      Gao W, Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
XX      Pan J, Paoni NF, Roy WA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX      Williams PM, Wood WI;
XX      WPI; 2001-071395/08.
XX      Secreted and transmembrane proteins and nucleic acids designated PRO,
XX      useful as hybridization probes, in chromosome and gene mapping and gene
XX      therapy.
XX      Claim 1; Fig 176; 787pp; English.
XX      The present invention relates to secreted and transmembrane proteins.
XX      These proteins and the DNA encoding them may be used as hybridization
XX      probes, in chromosome and gene mapping and in the generation of anti-
XX      sense RNA and DNA. They may also be used to generate either
XX      transgenic animals or knockout animals which are in turn useful for
XX      development and screening of therapeutically useful reagents. The nucleic
XX      acids may also be used in gene therapy

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SQ      Sequence 777 AA;
Alignment Scores:
Pred. No.: 7,75e-197 Length: 777
Score: 2245.50 Matches: 413
Percent Similarity: 73.6% Conservative: 141
Best Local Similarity: 54.9% Mismatches: 177
Query Match: 45.8% Indels: 21
DB: 4 Gaps: 9
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QY      275 AAGACAATGTCGCCAAGGCTGAATATATCTTACAAAGAAATTTTGAATCCAAATGTC 334
Db      39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY      335 ATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTTTTGGATGAGAA 394
Db      59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
QY      395 CGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATTTTCAATTCGACCTGGTTAATATC 454
Db      79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY      455 ---AAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACAGAGAGATGAATCCAAG 511
Db      99 AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118
QY      512 TGGGCTGGAAGACATCTGAAAGAATGTGCTAATTTTCATCAAGTACTTAAAGGCATAT 571
Db      119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY      572 AATCAGACTCACTTGTAGCCCTGTGGAACGGGGCTTTTTCATCCAAATTTGCACCTACATTT 631
Db      139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY      632 GAAATTGACATCATCTCGAGGACAATATTTTAAAGTGGAGAACTCACATTTTGAAGAAC 691
Db      159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY      692 GCGCGTGGGAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTATAGATGCA 751
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QY      752 GAAATTATATCTCTGGAACCTCGACATGATTTTATGGGCGGAGACTTTTCTTCCGAAT 811
Db      199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY      812 CTTGGG-----CACCACCACCAATCAGGACAGACGATGATTCAGGTGGCTC 862
Db      219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY      863 AATGATCCAAAGTTTCATTAGTCCGCCCTCATCTCAGAGAGTGACAATCCCTCAAGATGAC 922
Db      239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY      923 AAAGTATATCTTTCTTCGCGTGAATAATGCAATAGATGGAGAACACTCTGGAAGAGCTACT 982
Db      259 LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
QY      983 CACGCTAGATAGGTGAGATATGCAAGAAATGATTTTGGAGGCGCAGAGTCTGTGTAAT 1042
Db      279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
QY      1043 AAATGGACAACATTCCTCAAGCTCGTCTGATTTCTCAGTCCGAGGTCCTCAATGGCATTT 1102
Db      299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY      1103 GACACTCATTTTGTAGTAATCGAGGATGTATTCTTAATGAACCTTTTAAAGATCCTAAAT 1162
Db      319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY      1163 CCAGTTGTATATGGAGTGTTTACGACTTCCAGTAACATTTTCAAGGATCAGCCGCTGTGT 1222

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Db 339 ProValValIyGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358  
 QY 1223 ATGTATAGCATGAGTGTGAGAGGGTTCCTTGGTCCATATCCACAGGGATGGA 1282  
 Db 359 ValTySerMetAlaAspIleAlaValPheAsnGlyProTyAlaHisLysGlySer 378  
 QY 1283 CCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGGCAGAACTCT 1342  
 Db 379 AlaAspHisArgTrpValGlnTyAspGlyArgIleProTyProArgProGlyThrCys 398  
 QY 1343 CCAGCAAAACATTGGTGTGTTTGAACCTTCAAAAGAGACCTTCTGATGATGTATA 1399  
 Db 399 ProSerLysThrTyAspProLeuIleLysSerThrArgAspPheProAspValIle 418  
 QY 1400 ACCTTTGCAAGAGTATCCAGCCATGATCAATCCAGTGTTCCTATGAAACATCCCCA 1459  
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 QY 1520 GCAGAGATGACAGTATGATGTATGTTATCGGAACAGATGTTGGGACCGTCTTAAA 1579  
 Db 459 AlaGluAspGlyGlnTyAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478  
 QY 1580 GTAGTTTCAATTCCTAAGAGACTGCTGATGATTTAGAGAGGTTCTGCTGGAAGATG 1639  
 Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu 497  
 QY 1640 ACAGTTTTCGGAAACCGACTGCTATTTACGAAATGGAGCTTTCACAAAGCAGCAACA 1699  
 Db 498 GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGln 517  
 QY 1700 CTATATATTGTTCAACGGCTGGGTGCCAGTCCCTTTACACCGGTGATATTAC 1759  
 Db 518 LeuTyIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTy 537  
 QY 1760 GGAAAGCTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGCTGGTGGATGGTCT 1819  
 Db 538 GlyLysAlaCysAlaAspCysLysLeuAlaArgAspProTyCysAlaTrpAspGlyAsn 557  
 QY 1820 GCATGTTCTGCTATTTCCCACTGCAAGACAGCAGCAAGACGACGAAATATAAGAAAT 1879  
 Db 558 AlaCysSerArgTyAlaProThrSerLysArgAlaArgGlnAspValLysTy 577  
 QY 1880 GGAGACCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939  
 Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596  
 QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGATAGTAGCACATTTTGGAAATGCAAGTCCGAAG 1999  
 Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616  
 QY 2000 TGCAGAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059  
 Db 617 SerGlnGlnAlaThrIleLysTrpTyIleGlnArgSerGlyAspGluHisArgGluGlu 636  
 QY 2060 ATCAGAGTGTGATCATATCATATCATAGGACATCAAGGCTTCTGCTAGTGTCTACAA 2119  
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 Db 657 LysLysAspSerGlyMetTyTyCysLysAlaGlnGlnHisThrPheIleHisThrIle 676  
 QY 2180 CTTAAGGTAAACCTGGAAGTCTTACACAGAGCAATTTGGAAGAACTTCTTCAATAAGAT 2239  
 Db 677 ValLysLeuThrLeuAsnValIleGluAsnGlnMetGluAsnThrGlnArgAlaGlu 696  
 QY 2240 GATGATGAGATGGCTCTTAAGACCAAGAAATGTCCATAGATGACACCTAGCCAGAG 2299

Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710  
 QY 2300 GTCTGGTACAGAGATTTTCATGAGTCTATCAACCCCAATCTCAACACGATGGATGAG 2359  
 Db 711 LeuArgTyLysAspTyIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729  
 QY 2360 TTCTCTGACAGAGTTTGGAAAGGACCGAAACAAACACGTCGCGAAAGGCCAGCATACC 2419  
 Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747  
 QY 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479  
 Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763  
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 Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775  
 RESULT 13  
 ID AAU29197 standard; protein; 777 AA.  
 AC AAU29197;  
 DT 18-DEC-2001 (first entry)  
 DE Human PRO polypeptide sequence #174.  
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX Homo sapiens.  
 XX WO200168848-A2.  
 XX 20-SEP-2001.  
 XX 28-FEB-2001; 2001WO-US006520.  
 XX 01-MAR-2000; 2000WO-US005601.  
 XX 02-MAR-2000; 2000WO-US005841.  
 XX 03-MAR-2000; 2000US-0187202P.  
 XX 06-MAR-2000; 2000US-0186968P.  
 XX 14-MAR-2000; 2000US-0189320P.  
 XX 14-MAR-2000; 2000US-0189320P.  
 XX 15-MAR-2000; 2000WO-US006884.  
 XX 21-MAR-2000; 2000US-019028P.  
 XX 21-MAR-2000; 2000US-0191007P.  
 XX 21-MAR-2000; 2000US-0191048P.  
 XX 21-MAR-2000; 2000US-0191314P.  
 XX 28-MAR-2000; 2000US-0192655P.  
 XX 29-MAR-2000; 2000US-0193032P.  
 XX 29-MAR-2000; 2000US-0193053P.  
 XX 30-MAR-2000; 2000WO-US008439.  
 XX 04-APR-2000; 2000US-0194449P.  
 XX 04-APR-2000; 2000US-0194647P.  
 XX 11-APR-2000; 2000US-0195975P.  
 XX 11-APR-2000; 2000US-0196000P.  
 XX 11-APR-2000; 2000US-0196187P.  
 XX 11-APR-2000; 2000US-0196690P.  
 XX 18-APR-2000; 2000US-0196820P.  
 XX 18-APR-2000; 2000US-0198121P.  
 XX 18-APR-2000; 2000US-0198585P.  
 XX 25-APR-2000; 2000US-0199397P.  
 XX 25-APR-2000; 2000US-0199550P.  
 XX 03-MAY-2000; 2000US-0201516P.  
 XX 17-MAY-2000; 2000WO-US013705.  
 XX 20-MAY-2000; 2000WO-US014042.  
 XX 30-MAY-2000; 2000WO-US014941.  
 XX 02-JUN-2000; 2000WO-US015264.

PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI; 2001-602746/68.  
 DR N-PSDB; AAS46098.  
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX Claim 11; Fig 348; 774pp; English.  
 XX Sequences AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX Sequence 777 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 7.75e-197 Length: 777  
 Score: 2245.50 Matches: 413  
 Percent Similarity: 73.67% Conservative: 141  
 Best Local Similarity: 54.92% Mismatches: 177  
 Query Match: 45.86% Indels: 21  
 DB: 4 Gaps: 9  
 US-09-774-490-1 (1-2709) x AAU29197 (1-777)  
 QY 275 AAGAACAAAGTGTGCAAGGCTGAAATATCTCAAAAGAAATGTGGAATCCCAATGTG 334  
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 DB 59 IleProPheLeuGlySerSerGluGlyLeuLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78  
 QY 395 CGGAGTAGCTGTATCTGGAGCAAGAGATCATATTTTCATTCGACCTGGTTAATATC 454  
 DB 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98  
 QY 455 ---AAGATTTCAAAGATTGTGCGCCAGTATCTTACACAGAGAGATGAATGCAAG 511  
 DB 99 AsnLysAsnPhelLysIleTyTrpProAlaLysGluArgValGluLeuCysLys 118  
 QY 512 TGGCTGGGAAAGACATCTCGAAAGAAATGTGCTAAATTTTCATCAAGTACTTAAGGCATAT 571  
 DB 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelIleArgValLeuGlnProTyr 138  
 QY 572 AATCAGACTCATTTGACGCTGTGGAAAGGGGGCTTTTCATCCCAATTTGCACCTACATT 631  
 DB

Db 139 AsnLysThrHisIleTyTrpValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158  
 QY 632 GAAATTGGACATCATCTCGAGGACAAATATTTTAAAGCTGGAGAACTCACATTTTGAAC 691  
 Db 159 AspLeuGlyValTyTrpLysGluAspIlePheLysLeuAspThrHisAsnLeuGluSer 178  
 QY 692 GGCCTGGAGAGAGTCCATATACCTTAAGCTGTGACAGCATCCCTTTTAAATAGATGA 751  
 Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198  
 QY 752 GAAATTATCTCTGGAACCTGCAGCTGATTTTATGGGCGAGAGCTTTCCTATCTTCCGAAC 811  
 Db 199 TyrLeuTyTrpSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218  
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 Db 219 LeuGlyProThrHisAspHisIleTyTrpValCysGlyThrAspIleSerGluHisTyTrpLeu 238  
 QY 863 AATGATCCAAAGTTCATTTAGTCCACCTCATCTCAGAGAGTGACAAATCCTGAAGATGAC 922  
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 QY 983 CACGCTAGAATAGTGCAGATATGCAAGATGATTTGGAGGCGCAGAGAGTCTGGTGAAT 1042  
 Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuLeuAsn 298  
 QY 1043 AATGGCAACATCTCTCAAGCTCGTGTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1102  
 Db 299 LysTrpThrThrPheLeuLysAlaArgLeuLysCysSerIleProGlySerAspGlyAla 318  
 QY 1103 GACACTCATTTGATGAAGTGCAGATGATTTCTTAATGAACTTTAAAGATCCTAAAT 1162  
 Db 319 AspThrTyTrpPheAspGluLeuGlnAspIleTyTrpLeuLeuProThrArgAspGluArg 338  
 QY 1163 CCAGTTGTATATGAGTGTTCAGACTTCCAGTAACTTTCAAGGAGTACAGCGGTGTGT 1222  
 Db 339 ProValValTyTrpValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358  
 QY 1223 ATGTATAGATGATGATGTGAGAGGGTGTTCCTTGGTCCATATGCTCCACAGGATGA 1282  
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 Db 399 ProSerLysThrTyTrpAspProLeuLeuLysSerThrArgAspPheProAspAspValIle 418  
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 QY 1640 ACAGTTTTCGGGAACCGCTCTATTTCCAGCAATGAGAGCTTTCCACTGAGGAGCAACA 1699  
 Db 498 GlnIlePheLysHisSerIleLeuLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517

QY	1700	CTATATTGTTCAACGGTGGGGTGGCCAGCTCCCTTTACACCGGTGTGATATTAC	1759	PN	US2003027272-AL.
Db	518	LeuTyrileGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr	537	XX	06-FEB-2003.
QY	1760	GGGAAACGCTGCTAGTGTGCTGCTGCGCCGAGACCTTACTGTCTGGGATGTTCT	1819	XX	21-JUN-2002; 2002US-00176492.
Db	538	GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn	557	XX	18-SEP-1997; 97US-0059263P.
QY	1820	GCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGACAGACGACAGATATAAAGAT	1879	XX	18-SEP-1997; 97US-0059266P.
Db	558	AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr	577	XX	17-OCT-1997; 97US-0062250P.
QY	1880	GGAGACCACTGACTTCACTTCCAGACTTACCATGATAATCACCATGCCACACGCCCT	1939	XX	21-OCT-1997; 97US-0063486P.
Db	578	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596	XX	24-OCT-1997; 97US-0063120P.
QY	1940	GAGAGAGATCATCTATGCTGTAGAGATAGTACACATTTTGGAAATGCCATGCCAAG	1999	XX	28-OCT-1997; 97US-0063540P.
Db	597	AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616	XX	28-OCT-1997; 97US-0063541P.
QY	2000	TCCAGAGAGCGTGTGCTTATTCGCAATCCAGAGCGGAAATCAAGAGCGAAAGAGAG	2059	XX	28-OCT-1997; 97US-0063544P.
Db	617	SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu	636	XX	29-OCT-1997; 97US-0063734P.
QY	2060	ATCAGAGTGATGATCATATCATCAGACAGACATCAAGGCTTCTGCTAGTGTCTACAA	2119	XX	31-OCT-1997; 97US-0063870P.
Db	637	LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln	656	XX	31-OCT-1997; 97US-0064103P.
QY	2120	CAGAAAGATCAGCAATACCTCTGCTGCGGTGGAACATGGGTTCATACAACTCTT	2179	XX	13-NOV-1997; 97US-0065311P.
Db	657	LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle	676	XX	21-NOV-1997; 97US-0066120P.
QY	2180	CTTAAGGTAACTGGAAGTCATTGACACAGACATTTGGAAGAACTTCTTCAATAGAT	2239	XX	24-NOV-1997; 97US-0066466P.
Db	677	ValLysLeuThrLeuAsnValIleGluAsnGluMetGluAsnThrGlnArgAlaGlu	696	XX	24-NOV-1997; 97US-0066772P.
QY	2240	GATGATGGAGATGGCTCTTAAGACAAAGAAATGTCCAATAGCATGACACCTAGCCAGAG	2299	XX	11-DEC-1997; 97US-0069335P.
Db	697	HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg	710	XX	17-DEC-1997; 97US-0069870P.
QY	2300	GCTGCTAGACAGACTTCATGAGCTCATCAACACCCCAATCTCAACAGATGATGAG	2359	XX	18-DEC-1997; 97US-0068017P.
Db	711	LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln	729	XX	11-MAR-1998; 98US-0077632P.
QY	2360	TTCGTGAACAAGTTTGGAAAGGACCGAAACAAACGTCGCAAGCGCAGCATACACC	2419	XX	20-MAR-1998; 98US-0078886P.
Db	730	TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly-----	747	XX	27-MAR-1998; 98US-0079664P.
QY	2420	CCAGGGAACAGTAACAAATGGAAGACATTACAGAAATAAGAAAGGTAGAAACAGGAGG	2479	XX	27-MAR-1998; 98US-0079786P.
Db	748	-----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg	763	XX	31-MAR-1998; 98US-0080107P.
QY	2480	ACCCAC---GAATTTGAGAGGCGCCAGGAGTGTCT	2512	XX	01-APR-1998; 98US-0080327P.
Db	764	HisHisArgAspLeuAspGluLeuProArgAlaVal	775	XX	08-APR-1998; 98US-0081049P.
RESULT 14					
ABU58573					
ID	ABU58573	standard; protein; 777 AA.			
XX	AC	ABU58573;			
XX	DT	15-APR-2003 (first entry)			
XX	DE	Human PRO polypeptide #174.			
KW	KW	Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;			
KW	KW	dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;			
XX	OS	antibody-dependent enzyme mediated prodrug therapy.			
XX	OS	Homo sapiens.			

PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
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GenCore version 5.1.6  
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5: /cgn2\_6/prodata/1/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4201	85.8	771	1	US-08-121-713D-54
2	4201	85.8	771	1	US-08-835-268-54
3	4201	85.8	771	2	US-09-060-692-54
4	4201	85.8	771	3	US-08-833-391-54
5	4201	85.8	771	3	US-09-060-610-54
6	4201	85.8	771	5	PCT-US94-10151A-54
7	3568	72.9	655	4	US-08-556-422A-3
8	2562	52.3	477	1	US-08-136-922-2
9	2030	41.5	775	4	US-09-308-179B-1
10	1834	37.5	875	4	US-09-813-290-2
11	1830	37.4	782	4	US-09-813-290-4
12	982.5	20.1	862	4	US-08-556-422A-2

13	937	19.1	838	4	US-09-854-845-29	Sequence 29, Appl
14	937	19.1	865	4	US-09-854-845-33	Sequence 33, Appl
15	927.5	18.9	843	4	US-09-854-845-27	Sequence 27, Appl
16	927.5	18.9	870	4	US-09-854-845-31	Sequence 31, Appl
17	891	18.2	697	4	US-09-854-845-25	Sequence 25, Appl
18	881.5	18.0	702	4	US-09-854-845-23	Sequence 23, Appl
19	854.5	17.5	739	4	US-09-854-845-45	Sequence 45, Appl
20	854.5	17.5	766	4	US-09-854-845-49	Sequence 49, Appl
21	854.5	17.5	939	4	US-09-520-781-4	Sequence 30, Appl
22	852.5	17.4	630	4	US-09-520-781-30	Sequence 6, Appl
23	845.5	17.3	884	4	US-09-520-781-6	Sequence 43, Appl
24	845	17.3	744	4	US-09-854-845-43	Sequence 43, Appl
25	845	17.3	771	4	US-09-854-845-47	Sequence 47, Appl
26	838.5	17.1	607	4	US-08-556-422A-4	Sequence 4, Appl
27	825.5	16.9	652	4	US-09-578-063-22	Sequence 22, Appl
28	825.5	16.9	730	4	US-09-578-063-21	Sequence 19, Appl
29	825.5	16.9	761	4	US-09-578-063-19	Sequence 8, Appl
30	817	16.7	1070	4	US-09-653-274-8	Sequence 4, Appl
31	817	16.7	1070	4	US-10-461-791-8	Sequence 4, Appl
32	817	16.7	1086	4	US-09-653-274-4	Sequence 13, Appl
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34	816.5	16.7	641	4	US-09-653-274-13	Sequence 13, Appl
35	816.5	16.7	641	4	US-10-461-791-13	Sequence 41, Appl
36	808.5	16.5	598	4	US-09-854-845-41	Sequence 70, Appl
37	802	16.4	760	4	US-09-578-063-70	Sequence 76, Appl
38	802	16.4	760	4	US-09-578-063-76	Sequence 39, Appl
39	799	16.3	603	4	US-09-854-845-39	Sequence 62, Appl
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41	785.5	16.0	724	1	US-08-835-268-62	Sequence 62, Appl
42	785.5	16.0	724	2	US-09-060-692-62	Sequence 62, Appl
43	785.5	16.0	724	3	US-08-833-391-62	Sequence 62, Appl
44	785.5	16.0	724	3	US-09-060-610-62	Sequence 62, Appl
45	785.5	16.0	724	5	PCT-US94-10151A-62	Sequence 62, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-121-713D-54  
; Sequence 54, Application US/08121713D  
; Patent No. 5639856  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey S.  
; APPLICANT: Kolodkin, Alex L.  
; APPLICANT: Matthes, David  
; APPLICANT: Bentley, David R.  
; APPLICANT: O'Connor, Timothy  
; TITLE OF INVENTION: The Semaphorin Gene Family  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/121,713D  
; FILING DATE: 13-SEP-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: B94-002-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)343-4341  
; TELEFAX: (415) 343-4342  
; TELEX:

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 771 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-121-713D-54

Alignment Scores:

Pred. No.: 0 Length: 771  
Score: 4201.00 Matches: 771  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 85.80% Indels: 0  
DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-121-713D-54 (1-771)

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QY 260 AACTATCAGATGGAGAACAAATGTGCCAGGCTGAAATATCTCAAGAAGATGTG 319  
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QY 320 GAATCCCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTC 379  
Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
QY 380 CTTTGGATGAGGAACGGAGTAGGCTGTATGTGGAGCAAGATCAATATTTTCATTC 439  
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QY 500 GATGAATCAAGTGGCTGGAAAGACATCTGGAAGATGTCTAATTTTCATCAAGTA 559  
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QY 980 ACTCAGCTAGATAGGTAGATATGCAAGATGATCTTGGAGGCGACAGATCTGGTG 1039  
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QY 1160 AATCCAGTTGTATATGGAGTGTTCAGGACTTCCAGTAACATTTTCAAGGATCAGCCGTG 1219  
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QY 1220 TGTATGTATAGCATGATGATGAGAGGGTGTTCCTTGGTCCATATGCCCCACAGGAT 1279  
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QY 1340 TGTCCCAGCAAAACATTTTGGTGTTCGACTCTACAAAGGACCTTCTCTGATGATGTTATA 1399  
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QY 2000 TCGCAGAGAGCGCTGCTCTATTGGCAATTCAGAGCGCAATTAAGAGCGGAAAGAGAG 2059  
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QY 2060 ATCAGAGTGGATGATCATATCATGAGACAGATCAAGGCTTCTCTGCTAGTGTCTACAA 2119  
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## RESULT 2

US-08-835-268-54  
; Sequence 54, Application US/08835268  
; Patent No. 5807826  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey S.  
; APPLICANT: Kolodkin, Alex L.  
; APPLICANT: Matthes, David  
; APPLICANT: Bentley, David R.  
; APPLICANT: O'Connor, Timothy  
; TITLE OF INVENTION: The Semaphorin Gene Family  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/835,268  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121,713  
; FILING DATE: 13-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: B94-002-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)343-4341  
; TELEFAX: (415) 343-4342  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 771 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-835-268-54  
Alignment Scores:  
Pred. No.: 0 Length: 771  
Score: 4201.00 Matches: 771  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 85.80% Indels: 0  
DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-835-268-54 (1-771)

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QY 260 AACTATCAGAAATGGGAAGAACAAATGTCCCAAGCGTGAATATTCCTACAAAGAAATGTTG 319  
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QY 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40  
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QY 320 GAATCCAAACAATGTGATCACTTTCAATGGCTTTGGCCAAACAGCTCCAGTTATCATACCTTC 379  
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QY 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
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QY 380 CTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACAATTTTCATTC 439  
Db |||||||  
QY 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80  
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QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGCCAGATATCTTACACCAAGCA 499  
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QY 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100  
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QY 500 GATGAATGCAAGTGGCGCTGGAAAGACATCTCTGAAAGAAATGTGTAATTTTCATCAAGGTA 559  
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QY 560 CTTAAGGCATATAATCAGACTCATTGTACGCTGTGGAACGGGGGCTTTTCATCAATT 619  
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QY 800 ATCTTCCGAACCTCTTGGGACCCACCACCCATCAGACAGACAGCAGCATGATTTCCAGGTG 859  
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QY 860 CTCATATGATCCAAAGTTCATTAGTCCCACTCATCTCAGAGAGTGACAATCCTGAAGAT 919  
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QY 920 GACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTCGGAAAGCT 979  
Db |||||||  
QY 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
|||  
QY 980 ACTCAGCGTAGAATAGGTTCAGATATGCAAGATGACTTTGGAGGGCAGCAGATCTGGTG 1039  
Db |||||||  
QY 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
|||  
QY 1040 AATAAATGGAACAATCTCTCAAGCTCGTCTGATTGCTCAGTCCAGGTCCAATGCG 1099  
Db |||||||  
QY 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
|||  
QY 1100 ATTGACACTCATTTTGTATGATGAACCTGAGGATGTATTCTTAATGAACCTTTAAAGATCCTAA 1159  
|||

Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320  
 QY 1160 AATCCAGTTGTATATGGAGTGTTCAGACTTCCAGTAACATTTTCAAGGGATCAGCCGTG 1219  
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 QY 1400 ACCTTTGCAAGAAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAATCGCCCA 1459  
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 QY 1760 GCGAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTGGGATGTTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
 QY 1820 GCATGTTCTCGTATTTTCCCACTGCAAGAGACGACAGACGACAGATATAAGAAAT 1879  
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCACTACTACTGTTTACAGCTTACACCATGATTAATCACCATGGCCACAGCCCT 1939  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580  
 QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGATAGTAGACATTTTGGATGCGAGTCCGAG 1999  
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
 QY 2000 TCCGAGAGACGCTGCTTATTTGGCAATTCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059  
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620  
 QY 2060 ATCAGATGGATCATATCATCATCAGACAGATCAAGGCTTCTGCTAGTAGTCTACAA 2119  
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
 QY 2120 CAGAGGATTCAGGCAATTAATCTGCTGCGTGGAACTGGGTTCATACAACTCTT 2179  
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660  
 QY 2180 CTTAAGGTAACTCGAAGTCAATTCACAGAGCATTTTCGAAAGAACTTCTTCATAAAGAT 2239

Db 661 LeuLysValThrLeuGluValIleAspThrGluHisIleuGluLeuLeuHisLysAsp 680  
 QY 2240 CATCATGAGATGCTCTTAAGACCAAGAAATGTCCAAATAGCATGACACCTAGCCAGAG 2299  
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
 QY 2300 GTCTGGTACAGACTTTCATGCTCAGCTCATCAACACACCCCAATCTCAACACAGTGGATGAG 2359  
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
 QY 2360 TTCTGTGACCAAGTTTGGAAAAGGACCGAAAACAACTCGCGCAAGGCCAGGACATACC 2419  
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
 QY 2420 CCAGGGAACAGTAACTGAAGGACCTTACAGAAATAAAGAAAGGTAGAAAACAGAGAGG 2479  
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnAsnLysLysGlyArgAsnArgArg 760  
 QY 2480 ACCACCAAGTTTGAAGGCGCCAGGAGTGTCT 2512  
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 3  
 US-09-060-692-54  
 ; Sequence 54, Application US/09060692  
 ; Patent No. 5935865  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodman, Corey S.  
 ; APPLICANT: Kolodkin, Alex L.  
 ; APPLICANT: Matthes, David  
 ; APPLICANT: Bentley, David R.  
 ; APPLICANT: O'Connor, Timothy  
 ; TITLE OF INVENTION: The Semaphorin Gene Family  
 ; NUMBER OF SEQUENCES: 100  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
 ; STREET: 268 Bush Street, Suite 3200  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/060,692  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/121,713  
 ; FILING DATE: 13-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Oeman, Richard A.  
 ; REGISTRATION NUMBER: 36,627  
 ; REFERENCE/DOCKET NUMBER: B94-002-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415)343-4341  
 ; TELEFAX: (415) 343-4342  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 54:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 771 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-060-692-54

Alignment Scores:  
 Pred. No.: 0 Length: 771  
 Score: 4201.00 Matches: 771  
 Percent Similarity: 100.00% Conservative: 0



Best Local Similarity: 100.00%		Mismatches: 0
Query Match: 85.80%		Indels: 0
DB: 2		Gaps: 0
US-09-774-490-1 (1-2709) x US-09-060-692-54 (1-771)		
QY	200	ATGGGCTGTTAACTAGGATTTGCTCTCTTTCTGGGAGTATTACTTACAGCAAGAGCA 259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY	260	AACTATCAGAAATGGGAAGCAATGTCGAAGCTGAAATTCCTACAAAGAAATGTTG 319
DB	21	AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY	320	GAATCCAAATATGATCACTTTCAATGGCTGGCCAAAGCTCCAGTTCATATCATCTTC 379
DB	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY	380	CTTTTGGATCAGAAACGAGTAGGCTGTATGTTGGAGCAAGGATCAATATTTTCATTC 439
DB	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY	440	GACCTGTTAAATCAAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAGCA 499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY	500	GATGAATCAAGTGGCTCGAAAGACATCCCTGAAGAATGTGCTAATTTTCATCAAGTA 559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY	560	CTTAAGGCATATAATCAGACTCACTTGTACGCTGTGGAACGGGGCTTTTCATCAAT 619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY	620	TGCACCTACTAATGAATTCGACATCATCTGAGGCAATATTTTAACTGGAGACTCA 679
DB	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY	680	CATTTTGAACCGCGCTGGGAAGAGTCCATATGACCCTAAGCTGTGACAGCATCCCTT 739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY	740	TTAATAGATGGAATTTACTCTGGAACCTGACGCTGATTTTATGGGGCAGACTTTGCT 799
DB	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY	800	ATCTCCGAACTCTGGGCACACACCAATCAGGACAGACAGAGCATGATTCAGGTGG 859
DB	201	IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY	860	CTCAATGATCCAAAGTTCTATTAGTCCACCTCATCTCAGAGAGTGACATCTCAAGAT 919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY	920	GACAAAGTATCTTTTCTCCGTGAAAATGCAATAGATGGAGAACACTCTGAAAAGCT 979
DB	241	AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY	980	ACTCAGCTAGAAATAGTCAATATGCAAGTACTTTGGAGGGCAGCAAGATCTGGTG 1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY	1040	AATAATGACAACTTCCTCAAAGCTCGCTGATTTGCTCAGTGCAGGTCCTCAATGGC 1099
DB	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY	1100	ATTGACACTCATTTTCATCACTGAGGATGTATTCCTAATGAACCTTTAAAGATCTTAA 1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY	1160	AATCCAGTTGTATGAGGTGTTTACGACTTCAGTAAACATTTTCAAGGATCAGCCGTG 1219
DB	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340

QY	1220	TGTATGTATAGCATGATGATCTGAGAAGGGTGTCTCTTGGTCCATATATCCACAGGGAT 1279
DB	341	CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY	1280	GGACCAACTATCAATGGGTGCTTATCAAGAAGAGTCCCTTCCAGCCGACGAACT 1339
DB	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY	1340	TCGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCTCTCATGATGTATATA 1399
DB	381	CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY	1400	ACCTTTGCAAGAAGTCAATCCAGCCATGTACAAATCCAGTGTTCCTATGAACATCCCCA 1459
DB	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY	1460	ATAGTATCAAAAACGAGTGTAAATATCAATTTACAAATTTGTCGTAGACCGAGTGGAT 1519
DB	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY	1520	GCAGAAGATGAGCAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGTCTTAAA 1579
DB	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY	1580	GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTTAGAAGAGGTTCTCTGGAAGAAATG 1639
DB	461	ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
QY	1640	ACAGTTTTCGGGAACCGACTCTCTATTTCCAGCAATGGAGCTTTCACCTAAGCAGCAACAA 1699
DB	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
QY	1700	CTATATATTGGTTCACCGCTGGGTGCCAGCTCCCTTTACACGGGTGATATTTAC 1759
DB	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY	1760	GGGAAGAGCTGTGCTGAGTGTGTGCTCGCCCGAGAGCCCTTACTGTCTTGGGATGCTTCT 1819
DB	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY	1820	GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGACAGATATAAGAAAT 1879
DB	541	AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
QY	1880	GGAGACCACTGACTCTGTTACAGCTTACACCTACCATGATTAATCAACATGCCACGCCCT 1939
DB	561	GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY	1940	GAAGAGAGATCATCTATGTTGTTAGAGATAGTAGCACATTTTGGAAATCGAGTCGGAAG 1999
DB	581	GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY	2000	TCGACAGAGACGCTGCTCTATTGGCAATTCAGAGCGCAAAATCAAGAGCAAAAGAGAG 2059
DB	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY	2060	ATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGCTACTACAA 2119
DB	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY	2120	CAGAAGGATTTCAGGCAATTACCTCTGCCATCGGTGGAAATCGGGTTTCATAAACTCTT 2179
DB	641	GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY	2180	CTTAAGGTAACCTCGAAGTCAATTCACACAGAGCAATTCGAAAGAACTTCTTCATAAGAT 2239
DB	661	LeuLysValThrLeuGluValIleAspThrGluHisLeuLeuGluGluLeuHisLysAsp 680
QY	2240	GATGATGAGATGGCTCTNAGACCAAGAAATGTCCAATAGCATGACACTGACCCAGAG 2299
DB	681	AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700

QY 2300 GTCTGCTACAGAGCTTCATGTCAGCTCATCAACACCCCAATCTCAACACGATGATGAG 2359  
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
 QY 2360 TTCTGTGAACAGATTGGAAAAGGACCGAAACCAACCTCGCAAGGCCAGGACATACC 2419  
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
 QY 2420 CCAGGACAGTAACAATGGAGCAGCTTACAGAAATAGAAAGGTAGAAACAGGAGG 2479  
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760  
 QY 2480 ACCACAGATTGGAGGAGCCACCCAGGAGTGC 2512  
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4  
 US-08-833-391-54  
 ; Sequence 54, Application US/08833391  
 ; Patent No. 6013781  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodman, Corey S.  
 ; APPLICANT: Kolodkin, Alex L.  
 ; APPLICANT: Matthes, David  
 ; APPLICANT: Bentley, David R.  
 ; APPLICANT: O'Connor, Timothy  
 ; TITLE OF INVENTION: The Semaphorin Gene Family  
 ; NUMBER OF SEQUENCES: 100  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
 ; STREET: 268 Bush Street, Suite 3200  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/833,391  
 ; FILING DATE:  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/121,713  
 ; FILING DATE: 13-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Osman, Richard A.  
 ; REGISTRATION NUMBER: 36,627  
 ; REFERENCE/DOCKET NUMBER: B94-002-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 343-4341  
 ; TELEFAX: (415) 343-4342  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 54:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 771 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-833-391-54

Alignment Scores:  
 Pred. No.: 0  
 Score: 4201.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 85.80%  
 Indels: 0  
 Gaps: 3  
 Length: 771  
 Matches: 771  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-833-391-54 (1-771)

QY 200 ATGGCTGTTTAACTAGGATTGTCTGCTTTCTGGGAGTATTACTTACAGCAAGACA 259  
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20  
 QY 260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGGCTGAAATTTATCTCAAGAAATGTTG 319  
 Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40  
 QY 320 GAATCCAACATGTGATCATTCTCAATGGCTTGCCACACAGCTCCAGTTATCATACCTTC 379  
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
 QY 380 CTTTGTGATGAGGAACGAGTAGGTGTATCTGTGGAGCAAAAGGATCAATATTTTCATTC 439  
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80  
 QY 440 GACCTGGTTAATATCAAGGATTTTCAAAGATTGTGTGGCCAGTATCTTACACCAAGA 499  
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100  
 QY 500 GATGAATGCAAGTGGCTGGAAAGACATCTGAAAGAAATGTCTAAATTTTCATCAAGGTA 559  
 Db 101 AspGluCysLysTrpAlaGlyLysAspLysLeuLysGluCysAlaAsnPheLysVal 120  
 QY 560 CTTAAGGCATATAATCAGACTCATTGTACGCTGTGGAACGGGGCTTTTCATCCAATT 619  
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140  
 QY 620 TGCACCTACATGAAATTTGGACATCATCTCGAGGACAAATATTTTAAAGCTGGAGAACTCA 679  
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
 QY 680 CATTTTGAACACGGCTGGGAAGAGTCCATATGACCTCACTTAAGCTGCTCACAGCATCCCTT 739  
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180  
 QY 740 TTAATAGATGAGAAATATATCTCTGGAACTGCAGCTGATTTTATGGGCGAGACTTTGCT 799  
 Db 181 LeuLeuAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
 QY 800 ATCTTCCGAATCTTTGGGACACACACCCATCAGGACAGAGCAGCATGATTCAGGTTGG 859  
 Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220  
 QY 860 CTCATGATCCAAAGTTTCATTAGTCCACCTCATCTCAGAGAGTGACAAATCCTCAAGAT 919  
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240  
 QY 920 GACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGGAAAAGCT 979  
 Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
 QY 980 ACTACGCTAGATAGGTTCAGATATGCAAGAAATGACTTTTGGAGGCGCAGAAAGTCTGGTG 1039  
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
 QY 1040 AATAAATGGACAATCTCTCAAAGCTCGTCTGATTTCCTCAGTCCAGGTCCTCAATGCG 1099  
 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
 QY 1100 ATTGACACTCATTTTGTGAATGAGCTGAGGATGTATTCTTAATGAATCTTAAAGATCCTAAA 1159  
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320  
 QY 1160 AATCCAGTTGATATGAGAGTGTTCAGACTTCCAGTAATCTTTCAAGGGATCAGCCGTG 1219  
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
 QY 1220 TGATGTATAGCATGAGTGTGAGAAGGTTGTTCTTGGTCCATATGCCCCACAGGAGT 1279  
 Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360  
 QY 1280 GGACCCAACTATCAATGGGTGCTTTATCAAGGAAGAGTCCCTCTATCCAGCGCCAGAACT 1339

Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
QY 1340 TGTCCAGCAAAACATTTGGTGGTTCCTCACTCAAAAGGACCTTCCCTGATGATGTATA 1399  
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400  
QY 1400 ACCTTTCGCAAGAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAATCGCCCA 1459  
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
QY 1460 ATAGTGATCAAAACGGATGTAATTCATTTACAAATTCGTAGACCGAGTGGAT 1519  
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440  
QY 1520 CGAGAAGATGACAGTATGATGTTATTCGGAACAGATGTTGGGACCGCTTCTTAAA 1579  
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
QY 1580 STAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639  
Db 461 ValValSerIleProLysGluThrTyrAspLeuGluValLeuLeuGluMet 480  
QY 1640 ACAGTTTTCGGAACCGACTCTATTTCCAGCAATGGAGCTTTCACCTAAGCAGCAACA 1699  
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
QY 1700 CTATATATTGGTTCACGCGCTGGGTTGCCAGCTCCCTTTACACCGGTGCTATTTAC 1759  
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
QY 1760 GCGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCCCTTACTGTGCTTGGGATGTTCT 1819  
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTTPAspGlySer 540  
QY 1820 GCAATGTTCTCGCTATTTCCCACTGCAAGAGACGCAAGACGACAGATATAAGAAAT 1879  
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560  
QY 1880 GGAGACCCACTGACCTGCTCAGCTTACACCTTACACCATGATTAATCACCATGGCCACAGCCT 1939  
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580  
QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGATAGTACATTTTGGATGCACTCGAG 1999  
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
QY 2000 TCGCAGAGACGCTGCTGCTATTGGCAATTCAGAGCGCAATGAAGAGCGAAAGAGAG 2059  
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620  
QY 2060 ATCAGATGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGTAGTCTACAA 2119  
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
QY 2120 CAGAAGGATTTCAGGCAATTCCTGCTCCATCGGTGGACATGGGTTTCATACAACTCTT 2179  
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660  
QY 2180 CTTAAGGTAACCTCGAAGTCAATTCACACAGACGATTTGGAAGAACTTCTTCATAAGAT 2239  
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680  
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCATAGCATGACACCTAGCCAGAG 2299  
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
QY 2300 GTCGTGACAGAGATTCATGATGAGCTCATCAACCCCACTCAACACGATGATGAG 2359  
Db 701 ValTTPtyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
QY 2360 TTCTGTGAACAAGTTTGGAAAGGGAACCGAAACCAACGTCGGCAAGGCCAGGACATACC 2419

Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACCTTCAAGAAATAAGAAAGGTAGAAACAGGAGG 2479  
Db 741 ProGlyAsnSerAsnLysTyrLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760  
QY 2480 ACCACGAAATTTGAGAGGCGCCACGAGGAGTGTCT 2512  
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 5  
US-09-060-610-54  
; Sequence 54, Application US/09060610  
; Patent No. 6344544  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey S.  
; APPLICANT: Kolodkin, Alex L.  
; APPLICANT: Matthes, David R.  
; APPLICANT: Bentley, David R.  
; APPLICANT: O'Connor, Timothy  
; TITLE OF INVENTION: The Semaphorin Gene Family  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/060,610  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/835,268  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: B94-002-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)343-4341  
; TELEFAX: (415) 343-4342  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 771 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-060-610-54

Alignment Scores:  
Pred. No.: 0 Length: 771  
Score: 4201.00 Matches: 771  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 85.80% Indels: 0  
DB: 3 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-060-610-54 (1-771)

QY 200 ATGGCTGTTAACTAGGATTCGTCTTTCTGGGAGTATTACTTACAGCAAGCA 259  
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20  
QY 260 AACTATCAGAATGGGAAGCAATGTCCAGGCTGAAATTATCTTACAAAGAAATGTTG 319

Db 21 AsnTyrGlnAsnGlyLeuAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40  
 QY 320 GAATCCAAATGTCATCATCTTCAATGGCTGGCCAAAGCTCCAGTATCATACCTTC 379  
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
 QY 380 CTTTGGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGATCATATTTTCATTC 439  
 Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80  
 QY 440 GACCTGGTTATATCATCAAGATTTTCAAGATGTTGGCCAGTATCTTACACAGAAGA 499  
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100  
 QY 500 GATGAATCCAGTGGCTGGAAAGACATCTCTGAAGATGCTGAATTTTCATCAAGTGA 559  
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120  
 QY 560 CTTAAGGCATATAATCAGACTCAGCTTGTACGCTGTGGAACGGGGCTTTTCATCCAATT 619  
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140  
 QY 620 TGCACCTCATGGAATTTGACATCATCTCTGAGGACAATATTTTAAAGCTGAGAACTCA 679  
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
 QY 680 CATTTTGAAGCGCGCTGGGAAGAGTCCATATGACCTTAAGCTCTCAGACGATCCCTT 739  
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180  
 QY 740 TTAATAGATGGAATTTATCTCTGGAATCGAGCTGATTTTATGGGGCGAGACTTTGCT 799  
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
 QY 800 ATCTTCCGAACTCTTGGGCACACACACCAATCAGACAGACGATGATTCAGGTGG 859  
 Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220  
 QY 860 CTCATATGATCCAAAGTTCATTTAGTCCACCTCATCTCAGAGAGTGAACATCTCAAGAT 919  
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240  
 QY 920 GACAAAGTATCTTTTCTCGTGAAATGCAATAGATGGAGAACACTCTGGAAAGCT 979  
 Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
 QY 980 ACTCAGCTAGATAGTATGATGCAAGATGATCTTGGAGGGCAGAGATCTGCTG 1039  
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
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 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
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 QY 1160 AATCAGTGTGTATGAGTGTATGAGTCTCCAGTAACTTTCAAGGGATCAGCGGTG 1219  
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
 QY 1220 TGTATGTATAGCATGATGATGAGAGGGTGTCTTGGTCCATATGCCCCACAGGGAT 1279  
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 QY 1280 GGACCCCACTCATCAATGGTGGCTTATCAAGGAAGATGCCCTATCCAGCGCCAGGAAT 1339  
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
 QY 1340 TGTCCCGCAAAACATTTGGTGGTGTGCTCTCAAGAGGACTCTCTGATGATGTTATA 1399  
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400

QY 1400 ACCTTTGCAAGAGTCAATCCAGCCATGTACCAATCCAGTGTCTTCTATGAACAATGCCCA 1459  
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
 QY 1460 ATAGTGATCAAAACGGATGTAATTTCAATTTTACAAATTTCTGTTAGACCGAGTGGAT 1519  
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440  
 QY 1520 GCAGAGATGACAGTATGATGTTATCGGAACAGATGTTGGACCGTCTCTTAAA 1579  
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
 QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTCTCTGGAAGAAATG 1639  
 Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluGluMet 480  
 QY 1640 ACAGTTTTCGGGAAACCGACTGCTATTTTACAGATGGAGCTTTCACATAGCAGCAACA 1699  
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATTGCTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGTGTGATATTTAC 1759  
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
 QY 1760 GGGAAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCCCTTACTGTGTCTTGGGATGGTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
 QY 1820 GCATGTTCTCGTATTTTCCCACTGCAAGAGACGCAACAGCAGCAAGATATAAGAAAT 1879  
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCACTGACTCAGTGTTCAGACTTACACATGATTAATCACATGGCCACAGCCCT 1939  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580  
 QY 1940 GAAAGAGAAATCATCTGCTGTAGAGAAATAGTAGCACATTTTGGAAATGACAGTCCGAAG 1999  
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
 QY 2000 TCGCAGAGAGCGTGTCTTATTTGGCAATTCAGAGCGCAATTAAGAGCGCAAGAAAGAG 2059  
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620  
 QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTCTACAA 2119  
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
 QY 2120 CAGAAGGATTCAGGCAATTTACCTCTGCCATCGGTGGAAACATGGGTTTCATACAACTCTT 2179  
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660  
 QY 2180 CTTAAGGTAAACCTCGGAAGTCAATTCACACAGAGCAATTTGGAAGAATCTTCTTCATAAGAT 2239  
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680  
 QY 2240 GATGATGAGATGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAGAG 2299  
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
 QY 2300 GTCTGGTACAGAGACTTTCATGAGCTCATCAACCAACCCCAATCTCTCAACACGATGGATGAG 2359  
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
 QY 2360 TTCTGTGAACAAATTTGGAAGGACCGAAAAACACGTCGGCAAGGCCAGGACATACC 2419  
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
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QY 2480 ACCAGCAATTGAGAGGAGCACCAGGAGTGC 2512  
 Db 761 ThrHisGluPheGluAlaProArgSerVal 771

RESULT 6  
 PCT-US94-10151A-54  
 ; Sequence 54, Application PC/TUS9410151A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: The Semaphorin Gene Family  
 ; NUMBER OF SEQUENCES: 66  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLEHR HOEBACH TEST ALBRITTON & HERBERT  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/10151A  
 ; FILING DATE: 13-SEP-1994  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Osman, Richard A.  
 ; REGISTRATION NUMBER: 36,627  
 ; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299 FHT UR  
 ; INFORMATION FOR SEQ ID NO: 54:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 771 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US94-10151A-54

Alignment Scores:  
 Pred. No.: 0 Length: 771  
 Score: 4201.00 Matches: 771  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 85.80% Indels: 0  
 DB: 5 Gaps: 0

US-09-774-490-1 (1-2709) x PCT-US94-10151A-54 (1-771)

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QY 320 GAATCCAAATGTGATCTCTTCAATGGCTTGGCCCAAGCTCCAGTTCATCATCTTC 379  
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60

QY 380 CTTTGGATGAGAAACGGAGTAGGCTGTATGTTGGAGCAAGATCACATATTTTCATTC 439  
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80

QY 440 GACCTGTTAATATCAAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGCA 499  
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QY 500 GATGAATGCAAGTGGCTGGAAAAAGACATCTCTGAAAGAAATGCTTAATTTTCATCAAGTA 559  
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QY 560 CTTAAAGGCATATAATCAGACTCAGCTGTGTACGCTGTGGAAACGGGGCTTTTCATCCAAAT 619  
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140

QY 620 TGCACCTACATTGAAATTGGACATCATCTCTGAGCAATATTTTAAAGCTGGAGAACTCA 679  
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160

QY 680 CATTTTAAAAACGGCGGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTT 739  
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180

QY 740 TTAATAGATGGAGAATTATCTCTGAACTGCAGCTGATTTTATGGGCGAGACTTTGCT 799  
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QY 800 ATCTTCCGAACCTCTTTGGGCACCACCACCAATCAGGACAGACAGCATGATTCAGGTGG 859  
 Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220

QY 860 CTCATGATCCAAAGTTCAATTAGTCCACCTCATCTCAGAGAGTGACAACTCTGAAGAT 919  
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QY 920 GACAAAGTATATCTTTTCTCGTGAATGCAATGCAATAGATGGAGAACACCTCTGAAAAGCT 979  
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QY 980 ACTCAGCTTAGAATAGGTGAGATATGCAAGAAATGACTTTTGGAGGGCACAAGATCTGGTG 1039  
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QY 1040 AATAAATGGACAAATTCCTCAAGCTGCTGATTTGCTCAGTGCCAGGTCAAATGGC 1099  
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300

QY 1100 ATTGACACTCATTTTGTGAACTGAGGATGATTCCTTAATCAACTTTAAAGATCCTAAA 1159  
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320

QY 1160 AATCCAGTTGTATATGGAGTGTTTACGACTTCAGTAAATTTTCAAGGGATCAGCCGTG 1219  
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QY 1220 TGTATGTATAGCATGATGATGAGAGGGTGTCTTGGTCCATATGCCACACAGGAT 1279  
 Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360

QY 1280 GGACCCAACTATCAATGGGTGCTTTTCAAGCAAGAGTCCCTATCCAGGCCAGCAACT 1339  
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380

QY 1340 TGCTCCAGCAAAACATTTTGGTGGTGTGACTCTACAAAGACCTCTCTCATGATGTATA 1399  
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400

QY 1400 ACCTTTGCAAGAGTATCCAGCCATGTACAAATCCAGTGTTCCTTATGAACAATCCCCCA 1459  
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420

QY 1460 ATAGTGTCAAAACCGATGTAATTTATCAATTTTACAAATTTGCTAGACCGAGTGGAT 1519  
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440

QY 1520 GCAGAGAGTGGACAGTATGATGTTATGTTTATCGGAACAGATGTTGGGACCGCTCTTAAA 1579  
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460

QY 1580 GTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTAGAAGAGGTTCTCTGGAAGAAATG 1639

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; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556.422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-556-422A-3

461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
1640 ACAGTTTTTCGGAAACCGACTCTATTTCAGCAATGGAGCTTTCACATAAGCAGCAACA 1699
481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
1700 CTATATATTGGTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
1760 GGAAGAGCGTGTGAGTGGTTGCTCGCCGAGACCCCTTACTGTGCTGGATGGTCT 1819
521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
1820 GCATGCTCTCGTATTTCCTCACTCAAGAGACGACACAGACGACACAGATATAAGAAAT 1879
541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
1880 GGAGACCCACTGACTCAGCTGTTTCAGACTTACACCATGATAATCACCATGGCCACGCCCT 1939
561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
1940 GAAGAGAGAAATCATCTATCGGTAGAGAAATAGTAGACATTTTGGAAATGCAGTCCGAAG 1999
581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
2000 TGCAGAGAGCCCTGGTCTATTGGCAATTCAGAGCGCGAAATGAGAGCGGAAAGAGAG 2059
601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
2060 ATCAGAGTGGATGATCATATCATATCAGACAGATCAAGGCTTCTGCTAGTGTCTACAA 2119
621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
2120 CAGAAGGATTCAGGCAATTAATCTCTGCCAATGGGTGGAAACATGGGTTCATACAACTCTT 2179
641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
2180 CTTTAGGTACCTGCAAGCTATTGACAGAGCAATTCGGAAGACTTCTTCATAAGAT 2239
661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
2240 GATGATGAGAGTGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACTAGCCAGAGAG 2299
681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
2300 GTCTGTGACAGACTTCATGCACTCATCAACCCCAATCTCAACGATGGATGAG 2359
701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
2360 TTCTGTGAACAGTTTGGAAAGGACCGAAACACACGTCGGCAAGGCGCAGACATACC 2419
721 PheCysGluGlnValTrpLysArgAspArgGlySerGlnArgGlnArgProGlyHisThr 740
2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAAATAAGAAAGGTAGAAACAGGAGG 2479
741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
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761 ThrHisGluPheGluArgAlaProArgSerVal 771

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RESULT 7
US-08-556-422A-3
; Sequence 3, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSELOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.

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; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556.422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-556-422A-3

Alignment Scores:
Pred. No.: 0 Length: 655
Score: 3568.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.88% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-556-422A-3 (1-655)

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DB 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAATATGATCATCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTC 379
DB 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGTGATGAGGAACGAGTAGGCTGTATGTTGGACAAAGGATCACATATTTTCATTC 439
DB 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGA 499
DB 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCATCAAGTA 559
DB 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCAGCTTGTACGCTGTGGAAACGGGGCTTTTTCATCAAT 619
DB 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGAAATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGGAGAACTCA 679
DB 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTCTGACAGCATCCCTTT 739
DB 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGAAATATATCTCTGAACTGCAGCTGATTTTATCGGGCGAGACTTTGCT 799
DB 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTCTTTGGGCACCCACCAATCAGGACAGACAGACAGCATGATTTCCAGGTG 859
DB 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTCAATTAAGTCCCACTCATCTCAGAGAGTGCACATCTAGAGAT 919
DB 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAGTATATCTTTTCTTCGTCGAAATGCAATAGATGGAGAACACACTCTCGAAAAGCT 979
DB 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260

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QY 980 ACTACGCTAGATAGTGCAGATATGCAAGATGACTTTGGAGGGCAGAGAAGTCTGGNG 1039  
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 QY 1040 AATAAATGACAACTTCCTCAAGCTCTCTGATTGCTCAGTGCAGGTCCAAATGCG 1099  
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 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320  
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 Db 341 CysMetTySerMetSerAspValArgValPheLeuGlyProTyzAlaHisArgAsp 360  
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 Db 361 GlyProAsnTyzGlnTrpValProTyzGlnGlyArgValProTyzProArgProGlyThr 380  
 QY 1340 TGTCCAGCAAAACATTTGGTGGTTTGTACTACAAAGGACCTTCCTGATGATGTATA 1399  
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400  
 QY 1400 ACCTTTGCAAGAGTCATCCGCCATGTACATCCAGTGTTCCTATGAACATCGCCA 1459  
 Db 401 ThrPheAlaArgSerHisProAlaMetTyzAsnProValPheProMetAsnAsnArgPro 420  
 QY 1460 ATAGTGATCAAAACGGATTAATATCAATTTACACAATTTGTGTAGACCGAGTGGAT 1519  
 Db 421 IleValIleLysThrAspValAsnTyzGlnPheThrGlnIleValValAspArgValAsp 440  
 QY 1520 GCAAGATGACAGATGATGTATGTTTATCGGAACAGATGTTGGGACCGTTCCTAAA 1579  
 Db 441 AlaGluAspGlyGlnTyzAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
 QY 1580 GTAGTTTCATTTCTTAAGGAGCTGGTATGATTTAGAGAGGTTCCTGCGAAGATG 1639  
 Db 461 ValValSerIleProLysGlnThrTrpTyzAspLeuGluValLeuLeuGluMet 480  
 QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699  
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATTTGTTCAACGGCTCGGGTTCGCCAGTCCCTTTACACCGGTGTGATATTAC 1759  
 Db 501 LeuTyzIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyz 520  
 QY 1760 GGGAAAGCGTGTCTGAGTGTTCCTCGCCGAGACCCCTTACTGTCTGGATGGTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyzCysAlaTrpAspGlySer 540  
 QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGACAGACGCAAGATATAAGAAAT 1879  
 Db 541 AlaCysSerArgTyzPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCCCACTGACTGTTTACAGCTTTACACCATGATAATCACCATGGCCACAGCCCT 1939  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisPheAsnHisPheGlyHisSerPro 580  
 QY 1940 GAAGAGAGATCATCTATGCTGTAGAGAAATAGTACCATTTTGGAAATGCAAGTCCGAG 1999  
 Db 581 GluGluArgIleIleTyrglyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
 QY 2000 TCGCAGAGACCGTGTCTATTGGCAATTCAGAGCGCAATTAAGAGCGAAAGAGAG 2059  
 Db 601 SerGlnArgAlaLeuValTyzTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620

QY 2060 ATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTACAA 2119  
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuArgSerLeuGln 640  
 QY 2120 CAGAAGGATTCAGGCAATTTACCTGCTCCATGCGGTGGAACATGGG 2164  
 Db 641 GlnLysAspSerGlyAsnTyzLeuCysHisAlaValGluHisGly 655

RESULT 8  
 US-08-136-922-2  
 ; Sequence 2, Application US/08136922  
 ; Patent No. 5416197  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Raper, Jonathan A.  
 ; APPLICANT: Luo, Yuling  
 ; TITLE OF INVENTION: Compositions Which Regulate Neural  
 ; TITLE OF INVENTION: Regeneration and Methods of Making and Using the Same  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
 ; ADDRESS: No. 5416197ris  
 ; STREET: One Liberty Place  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/136,922  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Deluca, Mark  
 ; REGISTRATION NUMBER: 33,229  
 ; REFERENCE/DOCKET NUMBER: UPN-1428  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-568-3100  
 ; TELEFAX: 215-568-3439  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 477 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-136-922-2

Alignment Scores:  
 Pred. No.: 3,46e-246 Length: 477  
 Score: 2562.00 Matches: 472  
 Percent Similarity: 99.37% Conservative: 0  
 Best Local Similarity: 99.37% Mismatches: 3  
 Query Match: 52.33% Indels: 0  
 DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-136-922-2 (1-477)

QY 899 GAGAGTGAATCTCGAAGATGACAAAGTATATCTTTCTCCGCGAATAATGCAATAGAT 958  
 Db 2 GluHisAspAsnProGluAspLysValTyzPhePheArgGluAsnAlaIleAsp 21  
 QY 959 GGAGAACACTCTGGAAAGCTACTCACCTAGAATAGCTCAGATGCAAGATGACTTT 1018  
 Db 22 GlyGluHisSerGlyLysAlaThrHisAlaArgIleGlyGlnIleCysLysAsnAspPhe 41  
 QY 1019 GGAGGGCAGACAGAGTCTGTGAATAAATGGACAACATTCCTCAAGCTCGTCTGATTTGC 1078  
 Db 42 GlyGlyHisArgSerLeuValAsnLysTrpThrThrPheLeuLysAlaArgLeuLysCys 61  
 QY 1079 TCAGTGCCAGGTCCAAATGGCACTCATTTTGTGTAAGTGCAGGATGATTTCTTA 1138





Db 147 ValGlyHisSerGluGluProLeuPheHisLeuGluSerHisArgSerGluArgGly 166  
 QY 695 CGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAAATAGATGAGAGAA 754  
 Db 167 ArgGlyArgCysProPheAspProAsnSerSerPheValSerThrLeuValGlyAsnGlu 186  
 QY 755 TTATACTCTGGAACTGCACTGATTTTATGATGGCGAGACTTGTCTATCTTCGAACTCTT 814  
 Db 187 LeuPheAlaGlyLeuTyrSerAspTyrTrpGlyArgAspSerAlaIlePheArgSerMet 206  
 QY 815 GGCACACACCCCAATCAGGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAG 874  
 Db 207 GlyLeuGlyHisIleArgThrGluHisAspAspGluArgLeuLeuGlyGluProLys 226  
 QY 875 TTCATTAGTGGCCACCTCATCTCAGAGAGTGACAACTCCTCAAGATGACAAAGTATATCTTT 934  
 Db 227 PheValGlySerTyrMetIleProAspAsnGluAspArgAspAsnLysMetTyrPhe 246  
 QY 935 TTCTCCGTGGAATGCAATAGATGGAGAACACTCTGGAAAGCTACTCAGCGTAGAATA 994  
 Db 247 PhePheThrGluLysAlaLeuGluAlaGluAsnAsnAlaHisThrIleTyrThrArgVal 266  
 QY 995 GGTCAATATGCAAGATGACATTTGGAGGCGACAGAGCTGGTGAATAAATGGCAACA 1054  
 Db 267 GlyArgLeuCysValAsnAspMetGlyGlyGlnArgIleLeuValAsnLysTrpSerThr 286  
 QY 1055 TTCTCAAAAGCTGCTGATTTGCTCAGTGCCAGGTCCAAATGGCATTCACACTCATTTT 1114  
 Db 287 PheLeuLysAlaArgLeuValCysSerValProGlyMetAsnGlyIleAspThrTyrPhe 306  
 QY 1115 GATGAAGTCCAGGATGATTTCTTAATGAATTTAAAGATCCCTAAATCCAGTTGATAT 1174  
 Db 307 AspGluLeuGluAspValPheLeuLeuProThrArgAspProLysAsnProValIlePhe 326  
 QY 1175 GGAGTCTTACGATCCAGTAACATTTCAAGGATCAGCGGTGATGATATGATACGATG 1234  
 Db 327 GlyLeuPheAsnThrThrSerAsnIlePheArgGlyHisAlaValCysValTyrHisMet 346  
 QY 1235 AGTGATGTGAGAGGGGTTCCTTGGTCCATATGCCACAGAGGATGGACCAACTATCAA 1294  
 Db 347 SerSerIleArgGluAlaPheAsnGlyProTyrAlaHisLysGluGlyProGluTyrHis 366  
 QY 1295 TGGGTGCTTATCAAGGAAGTCCCTATCCACGCCAGGAACTTGTCCCGCAAGAAACA 1354  
 Db 367 TrpSerLeuTyrGluGlyValProTyrProArgProGlySerCysAlaSerLysVal 386  
 QY 1355 TTGTGGTGT---TTTGACTCTACAAGGACCTTCTGATGATGATTAACCTTTGCAAGA 1411  
 Db 387 AsnGlyGlyLysTyrGlyThrThrLysAspTyrProAspAspAlaIleArgPheAlaArg 406  
 QY 1412 AGTCATCCAGCATGTACAAATCCAGTGTTCCTATGAACAATGCCCAATAGTATCAA 1471  
 Db 407 MetHisProLeuMetTyrGlnProIleLysProValHisLysLysProIleLeuValLys 426  
 QY 1472 ACGGATGTAATTAATCAATTTTACACAAATTTGCTAGACCGAGTGGATGAGAGATGGA 1531  
 Db 427 ThrAspGlyLysTyrAsnLeuArgGlnLeuAlaValAspArgValGluAlaGluAspGly 446  
 QY 1532 CAGTATGATGTATGTTTATCGAAACAGATGTTGGACCGCTTCTTAAAGTAGTTTCAATT 1591  
 Db 447 GlnTyrAspValLeuPheIleGlyThrAspThrGlyIleValLeuLysValIleThrIle 466  
 QY 1592 CCTAAGGAGACTGGTATGATTTAGAGAGGTTCTGCTGGAAGAATGACAGTTTTCGG 1651  
 Db 467 TyrAsnGlnGluThrGluTrpMetGluGluValIleLeuGluGluLeuGlnIlePheLys 486  
 QY 1652 GAACGACTGCTATTTTACCAATAGGAGCTTTCACCTAAGCAGCAACATATATATTTGT 1711  
 Db 487 AspProAlaProIleSerMetGluIleSerSerLysArgGlnGlnLeuTyrIleGly 506  
 QY 1712 TCAACGGCTGGGTTCGCCAGCTCCCTTTACACCGGTGTGATATTTACGGGAAGCGTGT 1771  
 Db 507 SerAlaSerAlaValAlaGlnValArgPheHisCysAspMetTyrGlySerAlaCys 526

QY 1772 GCTGAGTGTGCTCGCCGAGACCCCTTACTGCTGCTTGGATGGTTCGATGTTCTCC 1831  
 Db 527 AlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyIleSerCysSerArg 546  
 QY 1832 TATTTTCCCACCT-----CCAAAGAGACCCACAGACGACAGATATAGAATGGA 1882  
 Db 547 TyrTyrProThrGlyAlaHisAlaLysArgArgPheArgGlnAspValArgHisGly 566  
 QY 1883 GACCCACTGACTCACTGTTTCAGACTTACACCATGATTAATCACCATGGCCACGCCCTGAA 1942  
 Db 567 AsnAlaAlaGlnGlnCysPheGlyGlnGlnPheValGlyAspAlaLeuAspArgThrGlu 586  
 QY 1943 GAGAGAAATCATCTATGTTAGAGAAATAGTACACATTTTGGAAATGCAAGTCCG 2002  
 Db 587 GluArgLeuAlaTyrGlyIleGluSerAsnSerThrLeuLeuGluCysThrProArgSer 606  
 QY 2003 CAGAGAGCGCTGCTATTTGGCAATTCAGAGCGGCAATGAAGAGGCGAAAGAGATC 2062  
 Db 607 LeuGlnAlaLysValIleTrpPheValGlnLysGlyArgAspValArgLysGluGluVal 626  
 QY 2063 AGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTCTACACAG 2122  
 Db 627 LysThrAspAspArgValValLysMetAspLeuGlyLeuLeuPheLeuArgValArgLys 646  
 QY 2123 AAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGACATCGGTTCATACAACTCTTCT 2182  
 Db 647 SerAspAlaGlyThrTyrPheCysGlnThrValGluHisAsnPheValHisThrValArg 666  
 QY 2183 AAGGTAACCTCGAAGTCAATTCACAGAGCATTTTGGAAAGAACTTCTTCATAAAGATGAT 2242  
 Db 667 LysIleThrLeuGluValValGluHisLysValGluGlyMetPheHisLysAspHis 686  
 QY 2243 GATGAGATGGCTCTTAAGACCAAAAGAAATGTCC-----AATAGCATGACACCT 2290  
 Db 687 GluGluGlu-----ArgHisHisLysMetProCysProProLeuSerGlyMetSerGln 704  
 QY 2291 AGCCAGAAAGTCTGTTAGACAGACTTCATGACAGTTCATCAACCCCACTTCACACAG 2350  
 Db 705 GlyThrLysProTyrTrpLysGluPheLeuGlnLeuIleGlyTyrSerAsnPheGlnArg 724  
 QY 2351 ATGGATAGTCTCTGAACAATTTGGAAAGGGACCGGAAACAAACAGCTCGGAAAGGCCA 2410  
 Db 725 ValGluGluTyrCysGluLysValTrpCysThrAspLysLysArgLysLysLeuLysMet 744  
 QY 2411 GCACATACCCAGGAAACAGTAACAAATGGAAGCACTTACAGAGAAATAGAAGGTAGA 2470  
 Db 745 -----SerProSerLysTrpLysTyrAlaAsnProGlnGluLys---Arg 758  
 QY 2471 AACAGGAGGACCCAGCAATTTGAGAGGCGCCACCCAGG 2506  
 Db 759 LeuArgSerLysAlaGluHisPheArgLeuProArg 770

RESULT 10

US-09-813-290-2  
 ; Sequence 2, Application US/09813290  
 ; Patent No. 6815538  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Wilganowski, Nathaniel L.  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Hilbun, Erin  
 ; APPLICANT: Wang, Xiaoming  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Scoville, John  
 ; TITLE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encodi  
 ; FILE REFERENCE: LEX-0151-USA  
 ; CURRENT APPLICATION NUMBER: US/09/813,290  
 ; CURRENT FILING DATE: 2001-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/190,638  
 ; PRIOR FILING DATE: 2000-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/191,188  
 ; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: US 60/193,639  
 ; PRIOR FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 875  
 ; TYPE: PR1  
 ; ORGANISM: homo sapiens  
 ; US-09-813-290-2

Alignment Scores:  
 Pred. No.: 1.66e-173 Length: 875  
 Score: 1834.00 Matches: 379  
 Percent Similarity: 62.24% Conservative: 150  
 Best Local Similarity: 44.59% Mismatches: 261  
 Query Match: 37.46% Indels: 60  
 DB: 4 Gaps: 16

US-09-774-490-1 (1-2709) x US-09-813-290-2 (1-875)

QY	87	CTCGCTGTTCTCCCATGTCAGCCAGTCT---ATTTCAGATTGTTGAACCTTCTCTGG	143
DB	43	LeuSerSerAlaProLeuProAlaGlnAspTrpValGluProLeuProTyrIleTrp	62
QY	144	CGG-----CACAAATACA	155
DB	63	ProGlyGlySerArgAlaAsnTyrAsnArgProAlaGlyProGluGlyGlySerAla	82
QY	156	GGAAGAGACTTAAGCAGCAAGGACCTACA---GGCTGTCAGCATGGCTGGTTAA	212
DB	83	GlyArgGlnArgCysProGlnPheProSerMetAlaProSerAlaTrpAla-Ile--	101
QY	213	CTAGGATGTCGTCTTTCTGGGAGATTACTTACCAAGAGCAAACTATCAGAATG	272
DB	102	-----Cys- TrpLeuLeuGlyGlyLeuLeuHisGlySerSerGlyProSerP	119
QY	273	GGAAGAACAAATGCGCAAGCTGAAATATCTCAAGAGAAATGTTGGAATCCAAATG	332
DB	119	roGlyProSerValProArgLeuArgLeuSerTyrArgAspLeuLeuSerAlaAsnArgS	139
QY	333	TGATCATCTTAAATGGCTGGCCACAGCTCCAGTTATCATACCTTCCTTTGGATGAGG	392
DB	139	erAlaIlePheLeuGlyProGlnGlySerLeuAsnLeuGlnAlaMetTyrLeuAspGluT	159
QY	393	AACGGAGTAGGCTGATGTTGGAGCAAGAGTACATATTTTCATTCGACCTGGTTAATA	452
DB	159	yrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSerLeuArgLeuAspGlnA	179
QY	453	TC---AAGGATTTTCAAAAGATTGTGGCCAGTATCTTTACACCAAGAGAGATGAATGCA	509
DB	179	laTrpProAspProArgGluValLeuTrpProGlnProGlyGlnArgGluGlyCysv	199
QY	510	AGTGGCTGGAAGACATCTCGAAGAGATGCTTAATTTTCATCAAGGTACTTAAGCAT	569
DB	199	alArgIlyGlyArgAspProLeuThrGluCysAlaAsnPheValArgValLeuGlnProH	219
QY	570	ATAATCAGACTCACTTGTACGCTGGAACCGGGCTTTTCATCCAAATTTGCACCTACA	629
DB	219	isAsnThrHisLeuLeuAlaCysGlyThrGlyAlaPheGlnProThrCysAlaLeuI	239
QY	630	TTGAAATTCGACATCATCTCGAGGACAATATTTTAAAGCTGGAGAACTCACATTTGAAA	689
DB	239	leThrValGlyHisArgGlyGlu---HisValLeuHisLeuGluProGlySerValGluS	258
QY	690	AGCGCGTGGGAAGAGTCCATAGCCTTAAGCTGCTGACAGATCCCTTTTAATAGATG	749
DB	258	erGlyArgGlyArgCysProHisGluProSerArgProPheAlaSerThrPheIleAspG	278
QY	750	GAGAATTATCTGGAACCTGACAGCTGATTTTATGGGGGAGACTTTTGTCTATCTCCGAA	809
DB	278	lyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArgGluAlaMetIlePheArgS	298
QY	810	CTCTTGGGCACCAACCAATCAGGACAGCAGCATGATTCCAGGTGGCTCAATGATC	869

DB	298	erGlyGlyProArgProAlaLeuArgSerAspSer---AspGlnSerLeuLeuHisAspP	317
QY	870	CAAAGTTCATTAGTCCACCTCATCTCAGAGAGTGACAATCCTCAAGATGACAAAGTAT	929
DB	317	roArgPheValMetAlaAlaArgIleProGluAsnSerAspGlnAsnAspIlyValT	337
QY	930	ACTTTTCTTCGCTGAAAT-----GCAATAGATGGAGAACACTCTCGAAAAAGCTACTC	983
DB	337	yrPhePhePheSerGluThrValProSerProAspGly---GlySerAsnHisValThrV	356
QY	984	ACGCTAGAAATAGTTCAGATATGCAAGATAGTCTTTGGAGGGCAGCAAGAGTCTGGTAATA	1043
DB	356	alSerArgValGlyArgValCysValAsnAspAlaGlyGlyGlnArgValLeuValAsnL	376
QY	1044	AATGGACAACATCTCTCAAGCTCGTCTGATTGCTCAGTGCAGGTCCAAATGCAATG	1103
DB	376	ysTrpSerThrPheLeuLysAlaArgLeuValCysSerValProGlyGlyAlaG	396
QY	1104	ACACTCATTTGATGAACCTGCAGGATGATTCTTAATGAACCTTTAAAGATCCTAAATATC	1163
DB	396	luThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpProLysAlaGlyLysSerL	416
QY	1164	CAGTTGATATGAGTGTATTAGACTTCCAGCTTCCAGTAACATTTTCAAGGGATCAGCCGTGTA	1223
DB	416	euGluValTyrAlaLeuPheSerThrValSerAlaValPheGlnGlyPheAlaValCysv	436
QY	1284	CCAACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTATCCAGCGCCAGCAACTTGT	1343
DB	456	roGlnHisGlnTrpGlyProTyrGlyLysValProPheProArgProGlyValCysP	476
QY	1344	CCAGCAAAACATTTGGT-----GGTTTGAATCTTACAAAGACCTTCTCTGATG	1391
DB	476	roSerLysMetThrAlaGlnProGlyArgProPheGlySerThrLysAspTyrProAspG	496
QY	1392	ATGTTTAACTTTCGAAGAGTCAATCCAGCATGTACAATCCAGTGTTCCTATGAACA	1451
DB	496	luValLeuGlnPheAlaAlaGlnHisProLeuMetPheTrpProValArgProArgHisG	516
QY	1452	ATCGCCCAATAGTATCAAAACCGGATGTAATAATTAATCAATTTACACAAATTTGCTAGACC	1511
DB	516	lyArgProValLeuValLysThrHisLeuAlaGlnGlnLeuHisGlnIleValValAspA	536
QY	1512	GAGTGGATGCAAGATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG	1571
DB	536	rgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGlyThrAspSerGlySerV	556
QY	1572	TTCTTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATGATGATGATGATGATGATG	1631
DB	556	alLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluProGluGluValValLeuG	576
QY	1632	AAGAAATGACAGTCTTTTCGGGAACCGGACTGCTATTTTTCAGCAATGAGGCTTTCCATAGC	1691
DB	576	luGluLeuGlnValPheLysValProThrProIleThrGluMetGluIleSerValLysA	596
QY	1692	AGCAACATATATATGTTTCAACGGCTGGGTTGGCCAGCTCCCTTTTACACCGGTGTG	1751
DB	596	rgLmMetLeuTyrValGlySerArgLeuGlyValAlaGlnLeuArgLeuHisGlnCysG	616
QY	1752	ATATTTTACGGGAACCGGTGTGCTGATGTTGGCTCGCCGAGACCTTACTGCTGCTGGG	1811
DB	616	luThrTyrGlyThrAlaCysAlaGluCysLeuAlaArgAspProTyrCysAlaTrpA	636
QY	1812	ATGTTTCTGCATGTTCTCGCTATTTTCCACT---GCAAGAGACGCAACAGACGCAAG	1868
DB	636	spGlyAlaSerCysThrHisTyrArgProSerLeuGlyLysArgArgPheArgGlnA	656
QY	1869	ATATGAAGAAATGAGACCACTGACTCTGTTTACAGCTTACCATGATATCATCATG	1928

656 sp1leArgHisGlyAsnProAlaLeuGlnCysLeu-----G 668

1929 GCCACAGCCCTGAAGAGAGA-----ATCATCTATGGTGTAG 1964

668 l yGlnSerGlnGluGluAlaValGlyLeuValAlaAlaThrMetValTy rGlyThrG 688

1965 AGAATAGTACACATTTTGGATGCGAGTCCGAGAGCGAGAGCGCTGCTATTGGC 2024

688 l uHisAsnSerThrPheLeuGluCysLeuProLysSerProGlnAlaAlaValArgTrpL 708

2025 AATTCCAGAGCGCAAAATGAAGAGCGAAACAGACAGATCAGAGTGGATCATATCATCA 2084

708 e uLeuGlnArgProGlyAspGluGlyProAspGlnValIlyThrAspGluArgValLeuH 728

2085 GGACAGATCAAGGCCTTCTCTACGTAGTCTACACAGAGAGGATTACGGCAATTACCTCT 2144

728 i sThrGluArgGlyLeuLeuPheArgArgLeuSerArgPheAspAlaGlyThrTy rThrC 748

2145 GCATCGCGTGGAAACATGGTTCATCAAACTCTTCTTAAGGTAAACCTGGAGTCAATGG 2204

748 y sThrThrLeuGluHisGlyPheSerGlnThrValValArgLeuAlaLeuValValIleV 768

2205 ACACAGAGCATTTGGAGAACTCTTCATAAAGATGATGAGAGATGGCTCTAAGACCA 2264

768 a llaSerGlnLeuAspAsnLeuPheProGluProLysProGluGluProProAlaA 788

2265 AAGAAATGTCCAATAGCATCACCTAGCCAGAGGTCTGGTACAGAGACTTCATGCACG 2324

788 r gGlyGlyLeuAlaSerThrProPro-----LysAlaTrpTy rLysAspIleLeuGlnL 806

2325 TCATCAACACCCCAATCTCAACAGCATGATGAGTTCGTGAACAAGTTTGGAAAGGG 2384

806 e uilleGlyPheAlaAsnLeuProArgValAspGluTy rCysGluArgValTy rCysArgG 826

2385 ACCGAAACAA-----CGTCGGCAAGGCCAGACATACCCCAAGGA 2426

826 l yThrThrGluCysSerGlyCysPheArgSerArgSerArgGlyLysGlnAlaArgGlyL 846

2427 ACAGTAAACAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAACAGAGAGACCCACG 2486

846 y sSer-----TrpAlaGlyLeuGluLeuGlyLysMetLysSerArgValHisAlaG 864

2487 AATTGAGAGGGCACCAGGAGTGC 2512

864 l uHisAsnArgThrProArgGluVal 872

RESULT 11

US-09-813-290-4

Sequence 4, Application US/09813290

Patent No. 6815538

GENERAL INFORMATION:

APPLICANT: Walke, D. Wade

APPLICANT: Wilganski, Nathaniel L.

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Hilbun, Erin

APPLICANT: Wang, Xiaoming

APPLICANT: Donoho, Gregory

APPLICANT: Scoville, John

TITLE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encod

FILE REFERENCE: LEX-0151-USA

CURRENT APPLICATION NUMBER: US/09/813,290

CURRENT FILING DATE: 2001-03-20

PRIOR APPLICATION NUMBER: US 60/190,638

PRIOR FILING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 60/191,188

PRIOR FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: US 60/193,639

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 782

TYPE: PRT

QY 1109 CATTTTGATGAATCGAGGATGTTTCTTAATGAACCTTTAAAGATCCTAAATAATCCAGTT 1168  
 Db 305 HisPheAspGlnLeuGluAspValPheLeuLeuTyrProLysAlaGlyLysSerLeuGlu 324  
 QY 1169 GTATATGAGGATTTACAGCTTCCAGTACATTTTCAAGGGATACGCGTGTGTATGAT 1228  
 Db 325 ValTyrAlaLeuPheSerThrValSerAlaValPheGlnGlyPheAlaValCysValTyr 344  
 QY 1229 AGCATGAGTGTGAGAGGGTGTCTTGTGTCATATGCCACAGGGATGGCCCAAC 1288  
 Db 345 HisMetAlaAspIleTyrGluValPheAsnGlyProPheAlaHisArgAspGlyProGln 364  
 QY 1289 TATCAATGGCTCCCTTATCAAGAGAGAGTCCCTATCCAGGCCAGGAACCTGTCCACG 1348  
 Db 365 HisGlnTyrGlyProTyrGlyLysValProPheProArgProGlyValCysProSer 384  
 QY 1349 AAAACATTTGGT-----GGTTTGTACTTACAAAGAGCCTTCCCTGATGATGT 1396  
 Db 385 LysMetThrAlaGlnProGlyArgProPheGlySerThrLysAspTyrProAspGluVal 404  
 QY 1397 ATAACTTTGCAAGAGTCATCCGCCATGATCAATCCAGTGTTCCTATGAAACATCGC 1456  
 Db 405 LeuGlnPheAlaArgAlaHisProLeuMetPheTyrProValArgProArgHisGlyArg 424  
 QY 1457 CCAATAGTGCATCAAAACGATGATAATTTACAAATTTGTCTAGACCGAGTG 1516  
 Db 425 ProValLeuValLysThrHisLeuAlaGlnGlnLeuHisGlnIleValValAspArgVal 444  
 QY 1517 GATGAGAGATGGACGATGATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTT 1576  
 Db 445 GluAlaGluAspGlyThrTyrAspValIlePheLeuGlyThrAspSerGlySerValLeu 464  
 QY 1577 AAAGTAGTTTCAATTCCTTAAGAGACTGGTATGATTAGAGAGGTCTGCTGGAAGA 1636  
 Db 465 LysValIleAlaLeuGlnAlaGlyLysSerAlaGluProGluGluValValLeuGlu 484  
 QY 1637 ATGACAGATTTTCGGGAACCGACTGCTATTTCAGCAATGGAGCTTTCCACTAAGCAGCA 1696  
 Db 485 LeuGlnValPheLysValProThrProIleThrGluMetGluIleSerValLysArgGln 504  
 QY 1697 CAATATATATGTTTCAACGGCTGGGTGCGAGCTCCCTTTTACACGGTGTGATTT 1756  
 Db 505 MetLeuTyrValGlySerArgLeuGlyValAlaGlnLeuArgLeuHisGlnCysGluThr 524  
 QY 1757 TACGGGAACGCTGTCTGAGTGTGCTCGCCGCGAGACCTTACTGTCTTGGATGCT 1816  
 Db 525 TyrGlyThrAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaIleAspGly 544  
 QY 1817 TCTGATGTTCTCGCTATTATTTCCCACT---GCAAGAGACGCAAGACGACAGATATA 1873  
 Db 545 AlaSerCysThrHisTyrArgProSerLeuGlyLysArgPheArgGlnAspIle 564  
 QY 1874 AGAATGGAGACCCACTGACTGACTGCTTCCAGACTTACCATGATTAATCACCATGCCAC 1933  
 Db 565 ArgHisGlyAsnProAlaLeuGlnCysLeu-----GlyGln 576  
 QY 1934 AGCCCTGAGAGAGA-----ATCATCTGCTGTAGAGAT 1969  
 Db 577 SerGlnGluGluGluAlaValGlyLeuValAlaLaThrMetValTyrGlyThrGluHis 596  
 QY 1970 AGTAGACATTTTGGATGTCAGTCCGAAGTCGACAGAGCGCTGTCTATTGGCAATTC 2029  
 Db 597 AsnSerThrPheLeuGluCysLeuProLysSerProGlnAlaAlaValArgTrpLeuLeu 616  
 QY 2030 CAGAGCGGAATGAAGAGCGAAAGAGATCAGAGTGTGATGATCATCATCATCAGGACA 2089  
 Db 617 GlnArgProGlyAspGluGlyProAspGlnValLysThrAspGluArgValLeuHisThr 636  
 QY 2090 GATCAAGGCTTCTGCTAGTGTCTTACCAAGAGGATTCAGGCAATACCTCTGCCAT 2149  
 Db 637 GluArgGlyLeuLeuPheArgArgLeuSerArgPheAspAlaGlyThrTyrThrCysThr 656  
 QY 2150 GCGGTGGAACATGGGTTCATCAAACTCTTCTTAAGGTAAACCCCTGGAAGTCATTGACACA 2209

Db 657 ThrLeuGluHisGlyPheSerGlnThrValValArgLeuAlaLeuValValIleValAla 676  
 QY 2210 GAGCATTTGGGAAGAACTTCTTCATAAAGATGATGATGGAGTGGCTCTCAAGCAAGAA 2269  
 Db 677 SerGlnLeuAspAsnLeuPheProGluProLysProGluGluProProAlaArgGly 696  
 QY 2270 ATGTCCAATAGCATGACACCTAGCCAGAAAGTCTGGTACAGAGACTTCATGCGAGCTCATC 2329  
 Db 697 GlyLeuAlaSerThrProPro-----LysAlaTyrTyrLysAspIleLeuGlnLeuIle 714  
 QY 2330 AACCAACCCCAATCTCAACACGATGATGATGTTCTGTGAACAAGTTTGGAAAGGCCGCA 2389  
 Db 715 GlyPheAlaAsnLeuProArgValAspGluTyrCysGluArgValTyrCysArgGlyThr 734  
 QY 2390 AAACAA-----CGTCGCAAGGCCAGGCAGCATACCCAGGGACAGT 2431  
 Db 735 ThrGluCysSerGlyCysPheArgSerArgSerArgGlyLysGlnAlaArgGlyLysSer 754  
 QY 2432 AACAAATGGAAGCACTTACAAAGAAATAAGAAAGGTAGAAACAGGAGGACCCAGCAATTT 2491  
 Db 755 -----TrpAlaGlyLeuGluLeuGlyLysLysMetLysSerArgValHisAlaGluHis 772  
 QY 2492 GAGAGGCCACCCAGGAGTGTCT 2512  
 Db 773 AsnArgThrProArgGluVal 779  
 RESULT 12  
 US-08-556-422A-2  
 ; Sequence 2, Application US/08556422A  
 ; Patent No. 6576754  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HALL, Kathryn T.  
 ; APPLICANT: FREEMAN, Gordon J.  
 ; APPLICANT: SCHULTZE, Joachim L.  
 ; APPLICANT: BOUSSIOTIS, Vassiliki  
 ; APPLICANT: NADLER, Lee M.  
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES  
 ; FILE REFERENCE: DFN-005CPA2  
 ; CURRENT APPLICATION NUMBER: US/08/556,422A  
 ; CURRENT FILING DATE: 1995-11-09  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 862  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-08-556-422A-2  
 Alignment Scores:  
 Pred. No.: 1,15e-88 Length: 862  
 Score: 982.50 Matches: 246  
 Percent Similarity: 51.42% Conservative: 115  
 Best Local Similarity: 35.04% Mismatches: 218  
 Query Match: 20.07% Indels: 123  
 DB: 4 Gaps: 26  
 US-09-774-490-1 (1-2709) x US-08-556-422A-2 (1-862)  
 QY 284 GTGCCAAGGTGAATATTCCTACAAAGATTTGGATCCCAACAATGTGATCACTTTC 343  
 Db 27 IleProArgIleThrTrpGluHisArgGluVal-----HisLeuValGlnPhe 42  
 QY 344 RATGCTTGGCCCAACAGCTCCAGTTATCATCTTCTTTCGATGAGAACGGAGTAGG 403  
 Db 43 HisGlu---ProAspIleTyrAsnTyrSerAlaLeuLeuLeuSerGluAspLysAspThr 61  
 QY 404 CTGTATGTTGGCAAGAGATCACAATATTTTCAGCTGTGTTAATCAAGGATTTT 463  
 Db 62 LeuTyrIleGlyAlaArgGluAlaValPheAlaValAsnAlaLeuAsnIleSerGluLys 81  
 QY 464 CAA---AGATTGTGTGGCCAGTATCTTACACCACCAAGAGATGAATGCAAGTGGGTGA 520

Db 82 GlnHisGluValTyrTrpLysValSerGluAspLysLysAlaLysCysAlaGluLysGly 101  
 QY 521 AAAGACATCTGAAAGATGTGCTAATTTTCATCAAGGTACTTAAAGCATATATCAAGACT 580  
 Db 102 LysSerLysGlnThrGluCysLeuAsnTyrIleAsgValLeuGlnProLeuSerAlaThr 121  
 QY 581 CACTGTAGCCCTGGAGAGGGGGCTTTTCATCCAAATTTGCACCTACATGGAATGGA 640  
 Db 122 SerLeuTyrValCysGlyThrAsnAlaPheGlnProAlaCysAspHisLeuAsnLeu--- 140  
 QY 641 CATCATCTCGAGACAATATTTTAAGCTGGAGAACTCACATTTGAAAAACGGCGTGG 700  
 Db 141 -----ThrSerPheLysPheLeuGlyLysAsn---GluAspGlyLysGly 154  
 QY 701 AAGAGTCCATATGACCTAAGCTGTCAGACAGCATCCCTTTTAAATAGATGAGAATATATAC 760  
 Db 155 ArgCysProPheAspProAlaHisSerTyrThrSerValMetValAspGlyGluLeuTyr 174  
 QY 761 TCTGGAACCTGCAGCTGATTTATGGGCGAGACTTTGGCTATCTTCGAACTCTTGGGCAC 820  
 Db 175 SerGlyThrSerTyrAsnPheLeuGlySerGluProIleIleSerArgAsn---SerSer 193  
 QY 821 CACCACCCATCAGGACAGCAGCATGATTCAGGTGCTCAATGATCCAAAGTTCAAT 880  
 Db 194 HisSerProLeuArgThrGlu---TyrAlaIleProTrpLeuAsnGluProSerPheVal 212  
 QY 881 AGTGCCCACTCATCTCAGAGACT---GACAACTCTT-----GAAGATGACAAAGTATAC 931  
 Db 213 PheAlaAspValIleArgLysSerProAspSerProAspGlyGluAspArgValTyr 232  
 QY 932 TTTTCTTCCTCGTAAATGCAATAGATGGAGAACACTCTGGAAGAACTACTCAGCTAGA 991  
 Db 233 PhePhePheThrGluValSerValGluTyrGluPheValPheArgValLeuIleProArg 252  
 QY 992 ATAGGTACATATGCAAGATGACTTTGGAGGCGACAGAGCTGTGTGATTAATGCGACA 1051  
 Db 253 IleAlaArgValCysLysGlyAspGlnGlyLeuArgThrLeuLysLysLysTrpThr 272  
 QY 1052 ACATTCCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAATGGCATTCACACTCAT 1111  
 Db 273 SerPheLeuLysAlaArgLeuIleCysSerArgProAspSerGlyLeuVal----- 289  
 QY 1112 TTGTATGAATCAGGATGTATTCCTAATGAATCTTAAAGATCTTAAAGATCCGAGTTGPA 1171  
 Db 290 PheAsnValLeuArgAspValPheValLeuArgSerProGlyLeuLysValProValPhe 309  
 QY 1172 TATGAGTGTTCAGACTCCAGTACATTTTCAAGGATCAGCGTGTGTATGTATAGC 1231  
 Db 310 TyrAlaLeuPheThrProGlnLeuAsnAsnValGlyLeuSerAlaValCysAlaTyrAsn 329  
 QY 1232 ATGAGTGTGTGAGAGGGTGTTCCTT---GGTCCATATGCCACAGG-----GAT 1279  
 Db 330 LeuSerThrAlaGluValPheSerHisGlyLysTyrMetGlnSerThrThrValGlu 349  
 QY 1280 GGACCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGCGCAGGAAT 1339  
 Db 350 GlnSerHisThrLysTrpValArgTyrAsnGlyProValProLysProArgProGlyAla 369  
 QY 1340 TGT-----CCAGCAAAACATTTGGTGGTGTGTGACTCTACAAAGAGCTTCTGTATGAT 1393  
 Db 370 CysIleAspSerGluAlaArgAlaAlaAsnTyrThrSerSerLeuAsnLeuProAspLys 389  
 QY 1394 GTTATACTTTGCAAGAGTATCCAGCATCTCAATCCAGTGTTCCTATGACAAT 1453  
 Db 390 ThrLeuGlnPheValLysAspHisProLeuMetAspSerValThrProIleAspAsn 409  
 QY 1454 CGCCCAATATGATCAAAACGGATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1513  
 Db 410 ArgProArgLeuIleLysLysAspValAsnTyr-----ThrGlnIleValValAspArg 427  
 QY 1514 GTGGATGCAAGATCGACAG---TATGATGTATCTTTATTCGGAACAGATGTGGGACC 1570  
 Db 428 ThrGlnAlaLeuAspGlySerValTyrAspValMetPheValSerThrAspArgGlyAla 447

QY 1571 GTTCTTAAGTAGTATTTCAATTCCTAAGGAGACTTGGTATGATTTAGACAGGTT----- 1624  
 Db 448 LeuHisLysAlaIleSer-----LeuGluHisAlaValHis 459  
 QY 1625 CTGCTGGAGAAATCAGACTTTTTCGGGAACCGACTGCTGCTATTTACAGCAATGAGCTTCC 1684  
 Db 460 IleIleGluGluThrGlnLeuPheGluAspPheGluProValGlnThrLeuLeuLeuSer 479  
 QY 1685 ACTAAGCAG-----CAACAACATATATTTGCTTCAACCGCTGGGGTTCGCCAGCTCCCT 1738  
 Db 480 SerLysLysGlyAsnArgPheValTyrAlaGlySerAsnSerGlyValValGlnAlaPro 499  
 QY 1739 TTACACCGGTGTGATTTTACCGGAAAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1798  
 Db 500 LeuAlaPheCysGlyLysHisGly---ThrCysGluAspCysValLeuAlaArgAspPro 518  
 QY 1799 TACTCTGCTTGG-----TACTCTGCTTGG-----TACTCTGCTTGG----- 1810  
 Db 519 TyrCysAlaTrpSerProProThrAlaThrCysValAlaLeuHisGlnThrGluSerPro 538  
 QY 1811 -----GATGGTTCCTGCAATTTTCTGCTATTTCTGCTATTTTCTGCTATTTTCTCC 1840  
 Db 539 SerArgGlyLeuIleGlnLumMetSerGlyAspAlaSerValCys-----Pro 554  
 QY 1841 ACTGCAAGAGAGCGCAAGACGACAGCAAGATATAGAAATGGAGACCACCTACTCTGT 1900  
 Db 555 AspLysSerLysGlySerTyrArgGln-----TACTCTGCTTGG----- 563  
 QY 1901 TCAGACTTACCATCATGATTAATCACCATGCCACAGCCCTGAAGAGAGAAATCATCTATGT 1960  
 Db 564 -----HisPhePheLysHisGlyGlyThrAlaGlu----- 573  
 QY 1961 GTAGAGAATAGTAGCACATTTTGAATGCACTTTCGAACTCCGAGTCCGAGAGCGCTGTAT 2020  
 Db 574 -----LeuLysCysSerGlnLysSerAsnLeuAlaArgValPhe 586  
 QY 2021 TGGCAATTCAGAGCGGAAATGAAGCGGAAAGAGAGATCAGAGTGGATGATCATATC 2080  
 Db 587 TrpLysPheGln-----AsnGlyValLeuLysAlaGlu-----SerProLysTyrGly 602  
 QY 2081 ATCAGACAGATCAAGCGCTTCTGCTAGTATCTTCAACAGAGAGATTCAGCAATTAC 2140  
 Db 603 LeuMetGlyArgLysAsnLeuLeuIlePheAsnLeuSerGluGlyAspSerGlyValTyr 622  
 QY 2141 CTCTCCATCGGTGCAACATGGTTCATACAACTCTTCTTAAAGTA----- 2188  
 Db 623 GlnCysLeuSerGluGluArgValLysAsnLysThrValPheGlnValValAlaLysHis 642  
 QY 2189 -----ACCTGGAAGTCAATTGAC 2206  
 Db 643 ValLeuGluValLysValValProLysProValValAlaProThrLeuSerValValGln 662  
 QY 2207 ACAGAG 2212  
 Db 663 ThrGlu 664

RESULT 13

US-09-854-845-29  
 ; Sequence 29, Application US/09854845  
 ; Patent No. 6750054  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Wang, Xiaoming  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Enco  
 ; FILE REFERENCE: LEX-0177-USA  
 ; CURRENT APPLICATION NUMBER: US/09/854,845  
 ; CURRENT FILING DATE: 2001-05-14  
 ; PRIOR APPLICATION NUMBER: US 60/205,274  
 ; PRIOR FILING DATE: 2000-05-18  
 ; PRIOR APPLICATION NUMBER: US 60/208,893



279	Il	Leu	Gln	lys	lys	Trp	Thr	Ser	Phe	Leu	Leu	Ala	Arg	Leu	Leu	Cys	His	Leu	Pro	---	297
1091	CC	AAAT	GGC	ATT	GAC	ACT	CAT	TTT	TGT	ATG	AAC	TGC	GAG	GAT	GAT	TTC	TAA	TGA	ACT	TTAA	1150
298	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	
1151	GAT	CCT	TAA	AAAT	CC	AGT	TGT	TAT	ATG	GAG	TGT	TAC	GACT	TTC	CA	GT	-----	-----	-----	-----	1204
312	Thr	Ser	Ser	Arg	Thr	His	Phe	Tyr	Ala	Ala	Phe	Thr	Leu	Ser	Thr	Gln	Trp	Leu	Thr	Leu	331
1205	AAG	GGAT	TC	AGC	CGT	GTG	TAT	GAT	CAT	CAG	TAG	TGT	GAG	AGG	TGT	TCC	TGT	TGT	CCCA	1264	
332	Glu	Ala	Ser	Ala	Leu	Cys	Arg	Tyr	Asp	Leu	Ala	Glu	Leu	Leu	Leu	Ala	Phe	Ala	Gly	Pro	351
1265	TAT	GCC	CA	CAG	GAT	GC	CA	CT	AT	CA	TG	TGGT	GC	CT	TAT	CA	AG	AG	AG	AG	1324
352	Tyr	Met	Glu	Tyr	Gln	Asp	Gly	Ser	Arg	Tyr	Glp	Gly	Arg	Tyr	Glu	Gly	Val	Pro	Glu	371	
1325	CC	AGC	CG	CA	AG	AA	CT	TGT	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	1378	
372	Pro	Arg	Pro	Gly	Ser	Cys	Thr	Asp	Ser	Leu	Arg	Ser	Gln	Gly	Tyr	Asn	Ser	Ser	Gln	391	
1379	GAC	TTT	CCT	GAT	CA	TGT	TAT	AAC	TTT	GCA	AG	AT	CAT	CC	AGC	CA	TGT	TAC	AT	1438	
392	Asp	Leu	Pro	Ser	Leu	Val	Leu	Asp	Phe	Val	Leu	His	Pro	Leu	Met	Ala	Arg	Pro	Val	411	
1439	TTT	CCT	AT	GAA	CA	AT	CGC	CA	AT	AG	TAT	GAT	CA	AA	AC	CG	AT	GAT	CA	AA	1498
412	Val	Pro	Thr	Arg	Gly	Arg	Pro	Leu	Leu	Leu	Leu	Leu	Arg	Asn	Leu	Arg	Tyr	-----	-----	429	
1499	ATT	GTC	TGT	AG	AC	GAG	TGA	TC	GAG	AAG	AT	GGA	-----	-----	-----	-----	-----	-----	-----	1555	
430	Leu	Thr	Gly	Thr	Pro	Val	Thr	Pro	Ala	Gly	Pro	Thr	Tyr	Asp	Leu	Leu	Phe	Leu	Gly	449	
1556	AC	AG	AT	GTT	GGG	AC	CGT	CTT	TAA	AG	TAG	TTT	CA	AT	TCC	TAA	AG	GAG	ACT	1615	
450	Thr	Ala	Asp	Gly	Trp	Leu	His	Ala	Val	Val	Leu	Gly	Ser	Gly	Met	His	-----	-----	-----	466	
1616	GA	AG	GTT	CTC	TG	GA	GA	AA	TG	AC	AGT	TTT	TCC	GG	AA	CC	GAT	GCT	AT	1675	
467	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	483	
1676	GAC	TTT	TCC	ACT	AAG	CA	CA	CA	ACT	TAT	TAT	TGGT	TCA	AC	CGC	TGT	GGG	TGT	CCCA	1735	
484	Val	Leu	Ser	Leu	Leu	Gln	His	Ser	Leu	Tyr	Val	Gly	Ala	Pro	Ser	Gly	Val	Leu	Gln	503	
1736	CC	TTT	AC	CGG	TGT	CA	TAT	TAT	TAC	GGA	AA	CGT	GTG	CT	GAG	TGT	CCCT	CGC	CCG	1795	
504	Pro	Leu	Ser	Ser	Cys	Ser	Arg	Tyr	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	522	
1796	CC	TAT	CT	GCT	TGG	AT	GGT	TCT	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	1849	
523	Pro	Tyr	Cys	Gly	Trp	Asp	Pro	Gly	Thr	His	Ala	Cys	Ala	Ala	Ala	Thr	Thr	Leu	Ala	Asn	542
1850	AG	AC	GCA	CAC	AG	AC	GA	TAT	A	AG	AA	TGG	AG	AC	CA	CT	GA	CT	TGT	1909	
543	Arg	Thr	Ala	Leu	Leu	Gln	Asp	Leu	Glu	Arg	Gly	Asn	-----	-----</							



QY 2138 TACCTCTGCATCGCGTGAACATCGGTTTCATACAACTCTTCTT 2182  
 Db 630 TyrGlyCysTyrAlaGluGlnAenGly---LeuArgThrLeuLeu 643

## RESULT 14

US-09-854-845-33  
 ; Sequence 33, Application US/09854845  
 ; Patent No. 6750054  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Wang, Xiaoming  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod  
 ; FILE REFERENCE: LEX-0177-USA  
 ; CURRENT APPLICATION NUMBER: US/09/854,845  
 ; CURRENT FILING DATE: 2001-05-14  
 ; PRIOR APPLICATION NUMBER: US 60/205,274  
 ; PRIOR FILING DATE: 2000-05-18  
 ; PRIOR APPLICATION NUMBER: US 60/208,893  
 ; PRIOR FILING DATE: 2000-06-02  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 33  
 ; LENGTH: 865  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 ; US-09-854-845-33

## Alignment Scores:

Pred. No.: 3,94e-84 Length: 865  
 Score: 937.00 Matches: 228  
 Percent Similarity: 50.23% Conservative: 101  
 Best Local Similarity: 34.81% Mismatches: 258  
 Query Match: 19.14% Indels: 68  
 DB: 4 Gaps: 21

US-09-774-490-1 (1-2709) x US-09-854-845-33 (1-865)

QY 287 CCAAGCTGAATTCCTACAAAGAAATGTTGGATCCAAACATGTGATCATCTTCAAT 346  
 Db 34 ProArgMetThrIleProTyrGluGluLeuSerGlyThrArgHis-----PheLys 50  
 QY 347 GCGTTGGCCACACGCTCCAGTTATCATCTCTCTTTGGATGAGGACCGAGTAGTGCTG 406  
 Db 51 GlyGlnAla-----GlnAsnTyrSerThrLeuLeuGluGluAlaSerAlaArgLeu 68  
 QY 407 TATGTGGAGAAAGATCACATATTTTCATTCGACCTGGTTTAATATCAAGAT----- 460  
 Db 69 LeuValGlyAlaArgGlyAlaLeuPheSerLeuSerAlaAsnAspIleGlyAspGlyAla 88  
 QY 461 TTTCAAAGATTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAGTGGGCTGGA 520  
 Db 89 HisLysGluIleHisTrpGluAlaSerProGluMetGlnSerLysCysHisGlnLysGly 108  
 QY 521 AAAGACATCTCAAGAAATGCTGCTAATTTTCATCAAGGTACTTAAGCATATAATCAGACT 580  
 Db 109 LysAsnAsnGlnThrGluCysPheAsnHisValArgPheLeuGlnArgLeuAsnSerThr 128  
 QY 581 CACTTGTAGCCCTGTGGAAACGGGGCTTTTCATCCAAATTTGACCTACATTTGAAATTTGGA 640  
 Db 129 HisLeuTyrAlaCysGlyThrHisAlaPheGlnProLeuCysAlaAlaIleAspAla--- 147  
 QY 641 CATCATCTCTGAGACAAATATTTTAAAGCTGGAGAACTCATATTTGAAACCGCGCTGGG 700  
 Db 148 -----GluAlaPheThrLeuProThrSer---PheGluGluGlyLysGlu 161  
 QY 701 AAGAGTCCATATGACCTTAAGCTGCTGACGAGCATCCCTTTTAAATAGATCGAGATATATAC 760  
 Db 162 LysCysProTyrAspProAlaArgGlyPheThrGlyLeuIleIleAspGlyGlyLeuTyr 181  
 QY 761 TCTGGAACTGCAGCTGATTTTATGGGGCGGAGACTTTTGCTATCTTCGAACTCTTGGGCAC 820

Db 182 ThrAlaThrArgTyrGluPhe-----ArgSerIleProAspIleArgSerArgHis 199  
 QY 821 CACCACCAATCAGGACAGAGCATGATTCAGGTGGCTCAATGATCCAAAGTTTCATT 880  
 Db 200 ProHisSerLeuArgThrGluGluThrProMetHisTrpLeuAsnAspAlaGluPheVal 219  
 QY 881 AGTGCCCACTCATCTCAGAGAGTGCACATCTCT-----GAAGATGACAAAGATATAC 931  
 Db 220 PheSerValLeuValArgGluSerLysAlaSerAlaValGlyAspAspLysValTyr 239  
 QY 932 TTTTCTCTCCGTGAAATGCAATAGATGAGAGAACTCTGGAAAAGCTACTCAC----- 985  
 Db 240 TyrPhePheThrGluArgAlaThrGlu---GluGlySerGlySerPheThrGlnSerArg 258  
 QY 986 -----GCTAGAATAGTCAGATATCAAGAATGACTTTGGAGGGCAGACA 1030  
 Db 259 SerSerHisArgValAlaAlaArgValAlaCysLysGlyAspLeuGlyGlyLys 278  
 QY 1031 AGTCTGGTGAATAATGACAACTCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGT 1090  
 Db 279 IleLeuGlnLysLysTrpThrSerPheLeuLysAlaArgLeuIleCysHisIlePro--- 297  
 QY 1091 CCAATGCGCATTTGACACTCATTTTCATGAACCTGACAGGATGATTCCTTAATGAACTTTAA 1150  
 Db 298 -----LeuTyrGluThrLeuArgGlyValCysSerLeuAspAlaGlu 311  
 QY 1151 GATCCTAAAAATCCAGTTGTATATGAGTGTTCAGACTTCCAGT-----AACATTTTC 1204  
 Db 312 ThrSerSerArgThrHisPheTyrAlaAlaPheThrLeuSerThrGlnTrpLysThrLeu 331  
 QY 1205 AAGGATCAGCGTGTGTATGATAGCATGATGATGAGAGGGTGTCTCTGCTCA 1264  
 Db 332 GluAlaSerAlaIleCysArgTyrAspLeuAlaGluIleGlnAlaValPheAlaGlyPro 351  
 QY 1265 TATGCCACAGGGTGGACCAACTATCAATGGGTGCCTTATCAAGGAGAGTCCCTAT 1324  
 Db 352 TyrMetGluTyrGlnAspGlySerArgArgTrpGlyArgTyrGluGlyValProGlu 371  
 QY 1325 CCACGGCAGAACTTGT-----CCACGAAACATTTGGTGGTTTGGACTCTCAAAAG 1378  
 Db 372 ProArgProGlySerCysIleThrAspSerLeuArgSerGlnGlyTyrAsnSerSerGln 391  
 QY 1379 GACCTTCCTGATGATGTTTATACTTCGAAAGATCATCCAGCCATGATACATCAGTG 1438  
 Db 392 AspLeuProSerLeuValLeuAspPheValLysLeuHisProLeuMetAlaArgProVal 411  
 QY 1439 TTTCTATGAACATCGCCCAATAGTATGATCAAAACGGATGATAATATCAATTTACAA 1498  
 Db 412 ValProThrArgGlyArgProLeuLeuLysArgAsnIleArgTyr-----ThrHis 429  
 QY 1499 ATTGTCGTAGACCGAGTGCATGCAAGATGGA---CAGTATGATGTTTATGTTTATCGA 1555  
 Db 430 LeuThrGlyThrProValThrThrProAlaGlyProThrTyrAspLeuLeuPheLeuGly 449  
 QY 1556 ACAGATGTTGGACCGCTTCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGTTTA 1615  
 Db 450 ThrAlaAspGlyTyrIleHisLysAlaValValLeuGlySerGlyMethHis----- 466  
 QY 1616 GAAGAGTTCCTCGGAAGAAATGACAGTTTTTCGGGACCGAGCTGCTATTATTCAGCAATG 1675  
 Db 467 -----IleIleGluGluThrGlnValPheArgGluSerGlnSerValGluAsnLeu 483  
 QY 1676 GAGCTTTCCACTAAGCAGCACAACATATATTTGTTCAACGGCTGGGGTTCGCCAGCTC 1735  
 Db 484 ValIleSerLeuLeuGlnHisSerLeuTyrValGlyAlaProSerGlyValIleGlnLeu 503  
 QY 1736 CTTTATACCGGTGTGATATTTACGGGAAAGCGTGTGCTGAGTGTGCTCCCGGAGAC 1795  
 Db 504 ProLeuSerSerCysSerArgTyr---ArgSerCysTyrAspCysIleLeuAlaArgAsp 522  
 QY 1796 CTTTACTGTGCTGGATGGTGTCT-----GCATGTTCTCGCTATTTTCCCACTCGCAAG 1849

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Db      523 ProTyrCysGlyTyrAspProGlyThrHisAlaCysAlaAlaThrThrThrIleAlaAsn 542
Qy      1850 AGACGCACAGCAGCAAGATATAAGAAATGAGAGCCCACTGACTCAGCTGTTTCAGACTTA 1909
Db      543 ArgThrAlaLeuIleGlnAspIleGluArgGlyAsn-----ArgGlyCys 557
Qy      1910 CACCATGATAATCACCATGGCCACAGCCCTGAAGAGAGATCATCTATGGTGTAGAGAAT 1969
Db      558 GluSerSerArgAspThrGlyProProProProLeuLeuYsThrArgSerValLeuArgGly 577
Qy      1970 AGTAGACACATTTTGAATGACGAGTCGAAGTCGAGAGCCCTGCTATTTGG-----2023
Db      578 AspAspValLeuLeuProCysAspGlnProSerAsnLeuAlaArgAlaLeuTrpLeuLeu 597
Qy      2024 -----CAATTCAGAGCGGAATGAAGAGCGCAAGAGAGATCAGAGTGGATGATCAT 2077
Db      598 AenGlySerMetGlyLeuSerAspGlyGlnGlyGlyTyrArgValGlyValAsp-----615
Qy      2078 ATCATCAGGACAGATCAAGCCCTCTGCTACGCTAGTCTACACAGAGAGGATTCAGGCAAT 2137
Db      616 -----GlyLeuLeuValThrAspAlaGlnProGluHisSerGlyAsn 629
Qy      2138 TACCTCTGCATCGCGTGAACATGGTTCATACAACTCTTCTT 2182
Db      630 TyrGlyCysTyrAlaGluGluAsnGly---LeuArgThrLeuLeu 643

RESULT 15
US-09-854-845-27
; Sequence 27, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 843
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-27

Alignment Scores:
Pred. No.:      3,44e-83      Length:      843
Score:          927.50      Matches:      230
Percent Similarity: 50.15%      Conservative: 101
Best Local Similarity: 34.85%      Mismatches: 256
Query Match:      18.94%      Indels:      73
DB:              4          Gaps:      23

US-09-774-490-1 (1-2709) x US-09-854-845-27 (1-843)
Qy      287 CCAAGGCTGAATTTATCTTACAAAGAAATGTTGGAATCCAAACATGTGATCATCTTTCAAT 346
Db      34 ProArgMetThrIleProTyrGluGluLeuSerGlyThrArgHis-----Phelys 50
Qy      347 GCCTGGCCCAACAGCTCCAGTATCATACCTCTTTTGGATGAGAGACGAGTAGGCTG 406
Db      51 GlyGlnAla-----GlnAsnTyrSerThrLeuLeuGluGluAlaSerAlaArgLeu 68
Qy      407 TATGTTGAGCAAGGATCACATATTTTCATTCGACCTGGTAAATATCAAGAT-----460
Db      69 LeuValGlyAlaArgGlyAlaLeuPheSerLeuSerAlaAsnAspIleGlyAspGlyAla 88

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Qy      461 TTTCAAAGATTGTGTGCCAGTATCTTTACACCAAGAGAGATGAATGCAAGTGGCTGGA 520
Db      89 HisLysGluIleHisIleTrpGluAlaSerProGluMetGlnSerLysCysHisGlnLysGly 108
Qy      521 AAAGACATCTCGAAGAATGTCTAAATTTTCATCAAGGTACTTAAGGCATATATCAGACT 580
Db      109 LysAsnAenGlnThrGluCysPheAsnHisValArgPheLeuGlnArgLeuAsnSerThr 128
Qy      581 CACTTGTACGCTGTGGAACGGGGCTTTTCATCCAAATTTGCACCTACATGCAAAATGGA 640
Db      129 HisLeuTyrAlaCysGlyThrHisAlaPheGlnProLeuCysAlaAlaIleAspAla---147
Qy      641 CATCATCTCTGAGGACAAATATTTTAAAGCTGAGAACTCACATTTTGAACACGGCGTGG 700
Db      148 -----GluAlaPheThrLeuProThrSer---PheGluGluGlyLysGlu 161
Qy      701 AAGAGTCCATATGACCCTAAGCTGCTGACAGATCCCTTTTAATAGATGGAGAATTATAC 760
Db      162 LysCysProTyrAspProAlaArgGlyPheThrGlyLeuIleIleAspGlyGlyLeuTyr 181
Qy      761 TCTGAACTGCGAGCTGATTTTATGGGGCGAGACTTTTGCTATCTTCCGAACCTCTTGGGCA 820
Db      182 ThrAlaThrArgTyrGluPhe-----ArgSerIleProAspIleArgSerArgHis 199
Qy      821 CACCACCAATCAGACAGACAGACATGATCCAGGTGGCTCAATGATCCAAAGTTCAAT 880
Db      200 ProHisSerLeuArgThrGluGluThrProMetHisTrpLeuAsnAspAlaGluPheVal 219
Qy      881 AGTGCCCACTCATCTCAGAGAGTGCACAAATCCT-----GAAGATGCAAAAGTATAC 931
Db      220 PheSerValLeuValArgGluSerLysAlaSerAlaValGlyAspAspLysValTyr 239
Qy      932 TTTTCTTTCGTGAAATGCAATAGATGGAGAACACTCTCGAAAAGCTACTCAC-----985
Db      240 TyrPhePheThrGluArgAlaThrGlu---GluGlySerGlySerPheThrGlnSerArg 258
Qy      986 -----GCTAGAATAGTTCAGATATGCAAGAATGATCTTCTTAAATGAACCTTAA 1150
Db      259 SerSerHisArgValAlaArgValAlaArgValCysLysGlyAspLeuGlyLysLys 278
Qy      1031 AGTGTGTGATTAATGAGACACATCTCTCAAGCTCGTCTGATTTGCTGAGTGGCAGGT 1090
Db      279 IleLeuGlnLysLysTrpThrSerPheLeuLysAlaArgLeuIleCysHisIlePro---297
Qy      1091 CCAATGCGCATTCACACTCATTTTGAACCTGAGAGATGATATCTTCTTAAATGAACCTTAA 1150
Db      298 -----LeuTyrGluThrLeuArgGlyValCysSerLeuAspAlaGlu 311
Qy      1151 GATCTTAAATCCAGTTGTATATGAGAGTGTTCAGACTTCCAGT-----AACATTTTC 1204
Db      312 ThrSerSerArgThrHisPheTyrAlaAlaPheThrLeuSerThrGlnTrpLysThrLeu 331
Qy      1205 AAGGATCAGCGGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1264
Db      332 GluAlaSerAlaIleCysArgTyrAspLeuAlaGluIleGlnAlaValPheAlaGlyPro 351
Qy      1265 TATGCCACAGGAGTGGACCAACTATCAATGGGTGCTTATCAAGGAGAGTCCCTAT 1324
Db      352 TyrMetGluTyrGlnAspGlySerArgArgTrpGlyArgTyrGluGlyValProGlu 371
Qy      1325 CACGGCCAGCAACTTGT-----CCAGCAAAACATTTGGTGGTGGTGGTGGTGGTGGTGGT 1378
Db      372 ProArgProGlySerCysIleThrAspSerLeuArgSerGlnGlyTyrAsnSerSerGln 391
Qy      1379 GACCTTCCTGATGATTTATAACCTTTCGAGAGTTCATCCAGCCATGATCAATCCAGTG 1438
Db      392 AspLeuProSerLeuValLeuAspPheValLysLeuHisProLeuMetAlaArgProVal 411
Qy      1439 TTTCTATCAACAACTAGTTCATCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1498
Db      412 ValProThrArgGlyArgProLeuLeuLysArgAsnIleArgTyr-----ThrHis 429
Qy      1499 ATTGCTGAGACCGAGTGGATGCAAGATGGA---CAGTATGATGTTATGTTTTCGGA 1555

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Db      430 LeuThrGlyThrProValThrThrProAlaGlyProThrTyrAspLeuLeuPheLeuGly 449
QY      1556 ACAGATGTTGGGACCGCTTCTTAAAGTAGTTTCAATTCTTAAGGAGACTTGGTATGATTTA 1615
Db      450 ThrAlaAspGlyTrpIleHisIysAlaValValLeuGlySerGlyMethHis----- 466
QY      1616 GAAGAGGTTCTGCTGAAGAAATGACAGATTTTCGGGAACCGACTGCTATTTTCAGCAATG 1675
Db      467 -----IleIleGluThrGlnValPheArgGluSerGlnSerValGluAsnLeu 483
QY      1676 GAGCTTTCACCTAAGCAGCAACAATATATATATGTTTCAACGGCTGGGGTGGCCAGCTC 1735
Db      484 ValIleSerLeuLeuGlnHisSerLeuTyrValGlyAlaProSerGlyValIleGlnLeu 503
QY      1736 CCTTTACACCGGTGTCATATTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGAC 1795
Db      504 ProLeuSerSerCysSerArgTyr---ArgSerCysTyrAspCysIleLeuAlaArgAsp 522
QY      1796 CCTTACTGTGCTGGGATGGTTCT-----GCATGTTCTCGCTATTTTCCCACTGCCAAG 1849
Db      523 ProTyrCysGlyTrpAspProGlyThrHisAlaCysAlaAlaAlaThrThrIleAlaAsn 542
QY      1850 AGA-----CGCACAGACGA---CAAGATATAAGAAATGAGACCCACTGACT 1894
Db      543 ArgSerGlnGlySerArgThrAlaLeuIleGlnAspIleGluArgGlyAsn----- 559
QY      1895 CACTGTTTCAGACTTACACCATGATATACCATGGCCACAGCCCTGAAGAGAGAAATCATC 1954
Db      560 -----ArgGlyCysGluSerSerArgAspThrGlyProProProLeuIysThrArg 577
QY      1955 TATGGTGTAGAGAATAGTAGACATTTTGGAAATGCAGTCCGAAGTCGCAGAGAGCGCTG 2014
Db      578 SerValLeuArgGlyAspAspValLeuLeuProCysAspGlnProSerAsnLeuAlaArg 597
QY      2015 GTCTATTGG-----CAATTCAGAGCGGAAATGAAGAGCGGAAAAGAGAGATC 2062
Db      598 AlaLeuTrpLeuLeuAsnGlySerMetGlyLeuSerAspGlyGlnGlyGlyTyrArgVal 617
QY      2063 AGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGCTAGTCTACAACAG 2122
Db      618 GlyValAsp-----GlyLeuLeuValThrAspAlaGlnPro 629
QY      2123 AAGGATTTCAGCAATTACCTCTGCCATGCGGTGGACATGGGTTTCATACAAACTCTTCTT 2182
Db      630 GluHisSerGlyAsnTyrGlyCysTyrAlaGluGluAsnGly---LeuArgThrLeuLeu 648
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Search completed: March 8, 2005, 21:42:01  
Job time : 151 secs



GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 8, 2005, 20:46:14 ; Search time 92.5 Seconds  
(without alignments)  
5635.702 Million cell updates/sec

Title: US-09-774-490-1  
Perfect score: 4896  
Sequence: 1 aatcttttatttcatcgatg.....aggcttttttctctaataacc 2709

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+n2p.model -DEV=xlp  
-O=/cgn2\_1/USPTO\_spool\_p/US09774490/runat\_08032005\_140758\_14848/app\_query.fasta\_1.2887  
-DB=PIR\_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LCOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09774490 @CNC 1 1 138 @runat\_08032005\_140758\_14848 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4201	85.8	771	2	D49423 semaphorin III pre
2	3989.5	81.5	772	2	I48747 semaphorin D - mou
3	3784.5	77.3	772	2	A49069 collapsin - chicke
4	3478.5	71.0	666	2	I58169 semaphorin III - m
5	2118	43.3	749	2	G01856 semaphorin V - hum
6	2059.5	42.1	748	2	I48744 semaphorin A - mou
7	1952	39.9	753	2	G02173 semaphorin III fam
8	1850.5	37.8	751	2	I48748 semaphorin E - mou
9	966	19.7	834	2	S66498 M-sema F protein p
10	857.5	17.5	782	2	I48746 semaphorin C - mou
11	828	16.9	1011	2	JC8059 semaphorin 6D-1 -
12	802	16.4	760	2	I48745 semaphorin B - mou
13	785.5	16.0	724	2	C49423 semaphorin II prec
14	766.5	15.7	730	2	JH0798 fasciclin IV precu

15	731.5	14.9	656	2	B49423 semaphorin I - fru
16	730	14.9	1074	2	JC5928 semaphorin F precu
17	699.5	14.3	712	2	T27165 hypothetical prote
18	684.5	14.0	711	2	A49423 semaphorin I precu
19	534	10.9	653	2	T03102 semaphorin homolog
20	327	6.7	676	2	T33853 hypothetical prote
21	197	4.0	1894	2	JC4980 plexin 1 precursor
22	188.5	3.9	1945	2	TJ3937 plexin A - fruit f
23	186	3.8	1872	2	JC4976 plexin 3 precursor
24	184	3.8	441	2	S29921 hypothetical prote
25	180	3.7	403	2	E42521 A39r protein - vac
26	172	3.5	1884	2	JC4975 plexin 2 precursor
27	170	3.5	1905	2	I51553 Plexin - African c
28	167	3.4	2051	2	TJ3164 plexin B - fruit f
29	154.5	3.2	1568	2	T09074 semaphorin recepto
30	134.5	2.7	1806	2	T23298 hypothetical prote
31	127.5	2.6	295	2	JQ1775 sail9r protein - v
32	123	2.5	573	1	CSBYT catalase [EC 1.11.
33	120	2.5	904	2	S3896 DNA mismatch repai
34	119	2.4	1104	1	A36866 microbial collagen
35	118.5	2.4	1291	2	T09273 probable tail-host
36	118.5	2.4	1654	2	A12067 two-component sens
37	118	2.4	1379	1	S01254 hepatocyte growth
38	117.5	2.4	1029	2	H86179 hypothetical prote
39	115	2.3	3381	2	T42389 versican precursor
40	114.5	2.3	993	2	A36873 protein-tyrosine k
41	114	2.3	692	1	S57592 probable phosphoe
42	113	2.3	1276	2	T09204 probable tail-host
43	112.5	2.3	248	2	A46652 glucosamine-6-phos
44	112	2.3	4273	2	C59679 polyketide synthas
45	111.5	2.3	6642	2	T29757 protein UNC-89 - C

#### ALIGNMENTS

##### RESULT 1

D49423  
Semaphorin III precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: D49423  
R:Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.  
Cell 75, 1389-1399, 1993  
A:Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone  
A:Reference number: A49423; MUID:94094332; PMID:8269517  
A:Accession: D49423  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-771 <KOL>  
A:Cross-References: UNIPROT:Q14563; GB:L26081; NID:G799328; PIDN:AAA65938.1; PID:G43656  
C:Genetics:  
A:Gene: GDB:SEMA1  
A:Cross-References: GDB:283448  
C:Superfamily: semaphorin

Alignment Scores:  
Pred. No.: 1.39e-309 Length: 771  
Score: 4201.00 Matches: 771  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 85.80% Indels: 0  
DB: 2 Gaps: 0

US-09-774-490-1 (1-2709) x D49423 (1-771)

QY : 200 ATGGCTGGTTAACTAGGATTCGTCTTTCTGGGAGTATTACTTACAGCAGCA 259  
Db : 1 MetGlyTrpLeuThrArgileValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20  
QY : 260 AACTATCATGATGGGAGCAATCTGCCAGCTGGAATTCCTACAAAGAAATGTTG 319  
Db : 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40

320 GAATCCAAACATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATCTTC 379  
Db  
41 GluSerAsnAsnValileThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
380 CTTTGGATGAGAACGAGTAGGTGATGTTGGAGCAAGCATCACTATTTTCATTC 439  
Db  
61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80  
440 GACCTGGTTAAATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGA 499  
Db  
81 AspLeuValAsnIleLysAspPheGlnIlylleValTrpProValSerTyrThrArg 100  
500 GATGAATGCAAGTGGCTGCAAAAGACATCTCTCAAGATGCTTAATTCATCAAGTA 559  
Db  
101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120  
560 CTTAAGGCATATAATCAGACTCATCTGTAGCGCTGTGNAACGGGGCTTTTCATCAATT 619  
Db  
121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140  
620 TGCACCTACATTAATGGAATTCGACATCATCTCGAGGACAATATTTTAAAGCTGGAGAACTCA 679  
Db  
141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
680 CATTTTGAACCGCGTGGGAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTT 739  
Db  
161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180  
740 TTAATAGATGGAATTAATCTCTGGAAGTCACTGAGTATTTATGGGGGAGACTTTGCT 799  
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181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
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Db  
201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220  
860 CTCAATGATCCAAAGTTCAATAGTGCACCTCATCTCAGAGAGTCACAATCCTGAAGAT 919  
Db  
221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240  
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Db  
241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
980 ACTCAGCTAGAAATAGTTCAGATATGCAAGATGCTTTGGAGGACAGAAAGTCTGGTG 1039  
Db  
261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
1040 AATAAATGGAACAATTCCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAATGGC 1099  
Db  
281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
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Db  
301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320  
1160 AATCCAGTTGTATGAGGTGTTTACGACTTCAGTAAACATTTTCAAGGGATCAGCCGTG 1219  
Db  
321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
1220 TGTATGTATAGCATGATGTGAGAGGGTTCCTTTGGTCCATATCCCAACAGGGAT 1279  
Db  
341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360  
1280 GGACCCCAACTATCAATGGGTGCTTATCAAGGAGAGTCCCTATTCACGGCCAGGAAT 1339  
Db  
361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
1340 TGTCCAGCAAAACATTTGCTGGTTTGTACTCTACAAAGGACCTTCCTCATGATGTATA 1399  
Db  
381 CysProSerLysThrPheGlyPheAspSerThrLysAspLeuProAspAspValIle 400  
1400 ACCTTTGCAAGAGTATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAATCGCCA 1459

401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
1460 ATAGTGATCAAAACGGATGTAATTTATCAAAATTTGTCTAGACCGAGTGGAT 1519  
Db  
421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValIleValAspArgValAsp 440  
1520 GCAGAGATGACAGTATGATGTTATCGGAACAGATGTTGGGACCGTCTTTAAA 1579  
Db  
441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
1580 GTAGTTTCAATTCCTAAGGAGACTTGTATGATTTAGAGAGGTCTCTCTGGAAGAAATG 1639  
Db  
461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480  
1640 ACAGTTTTCGGGAACCGACTGCTATTTTCCAGCAATGGAGCTTTCACATAAGCAGCAACA 1699  
Db  
481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
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501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
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Db  
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Db  
561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580  
1940 GAAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACATTTTTCGAATGCGTCCGAAG 1999  
Db  
581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
2000 TCGCAGAGCGCTGCTTATTGGCAATTCAGAGCGCAATTAAGAGCGAAAGAGAG 2059  
Db  
601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluArgLysGluGlu 620  
2060 ATCAGATGGATGATCATATCATCAGGACAGATCAAGCCCTTCTCTAGTAGTCTACAA 2119  
Db  
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661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680  
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681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
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701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
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741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgAsp 760  
2480 ACCCAAGAAATTTGAGAGGCGACCCAGGAGTGTCT 2512

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Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
RESULT 2
semaphorin D - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48747
R:Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates
A:Reference number: I48744; MUID:95267431; PMID:7748561
A:Accession: I48747
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-772 <RES>
A:Cross-references: UNIPROT:O08665; EMBL:X85993; NID:g854329; PIDN:CAA59985.1; PID:g8543
C:Genetics:
C:Superfamily: semaphorin
Alignment Scores:
Pred. No.: 1,38e-293 Length: 772
Score: 3989.50 Matches: 730
Percent Similarity: 97.28% Conservative: 21
Best Local Similarity: 94.56% Mismatches: 20
Query Match: 81.48% Indels: 1
DB: 2 Gaps: 1
US-09-774-490-1 (1-2709) x I48747 (1-772)
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QY 260 AACTATCAAGTGGAGAACATGTGCCAAGCTGAATTTATCTTACAAAGAAATGTTG 319
Db 21 AsnTyrAlaAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCATCTTC 379
Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAACCGAGTAGGTGTATGTGGAGCAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTAATATCAAGATTTTCAAAGATTGTGTGCCAGTATCTTACACCAAGA 499
Db 81 AsnLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGGCTCGAAAGACATCCTGAAGAGATGTCTAATTTTCATCAAGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCATCAAT 619
Db 121 LeuGluAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGAATTTGGACATCATCTCGAGCAATATTTTAAAGTGGAGAACTCA 679
Db 141 CysThrTyrIleGluValGlyHisProGluAspAsnIlePheLysLeuGlnAspSer 160
QY 680 CATTTTGAACGGCGCTGGAGAGTCCATATGACCTTAAGCTGTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGATTATCTCTGAACTGCGAGCTGATTTTATGGGGGAGACTTTGCT 799
Db 181 LeuIleAspGlyCysLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTCCGAACTCTTGGGCACCAACCAATCAGGACAGAGCAGCATGATTTCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyAspHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCAATGATCCAAAGTTTCATTTAGTCCCACTCATCTCAGAGAGTGACAAATCCTGAAGAT 919
Db 221 LeuAsnAspProArgPheIleSerAlaHisLeuIleProGluSerAspAsnProGluAsp 240
QY 920 GACAAGATATCTTTTCTTCGTCGAAATGCAATAGATGGAGAACACTCTCGAAAGACT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleGlyGlyHisSerGlyLysAla 260
QY 980 ACTCAGCTAGTAATAGTTCAGATATGCAAGATGACTTTGGAGGGCACAAGAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATCTCTCAAGCTCGTCTGATTTGTCTAGTGCACAGTCAAAATGCC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGCACTCATTTTGTGAACTGCGAGGATGATTTCTTAATCAACTTTTAAGATCCATAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnSerLysAspProLys 320
QY 1160 AATCCAGTTGTATATGGAGTGTTCAGACTTCAGTAACTTTCAAGGATCAGCCGCTG 1219
Db 321 AsnProIleValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGATGAGAAGGTGTTCTTCTTGGTCCATATCCACACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCACTATCAATGGGTGCTTATCAAGAGAGTCCCTATCCAGGCGCAGGAAT 1339
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QY 1400 ACCTTTGCAAGAGTCAATCCAGCCATGATCAATCCAGTGTTCCTATGAACATCCGCCA 1459
Db 401 ThrPheGlyArgSerHisProAlaMetTyrAsnProValPheProIleAsnAsnArgPro 420
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Db 421 IleMetIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 CGAGAGATGGACATGATGATGTTTATCGGAACAGATGTTGGGACCGTCTCTTAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTCTCTGCGAAGAAATG 1639
Db 461 ValValSerValProLysGluThrTrpHisAspLeuGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTTCGGAACCGACTCTATTTCAGCAATGGAGCTTTCACATAAGCAGCAACAA 1699
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QY 1700 CTATATATTTGTTCAACGGCTGGGTTCGCCAGCTCCCTTTACACCGGTGTATATTTAC 1759
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QY 1760 GGAAGAGCTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTGTCTGGGATGTTCT 1819
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QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGCACAAGACGACCAAGATATAAGAAAT 1879
Db 541 SerCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTGATCTGTTTACAGCTTACAC---CATGATAATCACCATGCCACAGC 1936
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QY 1118 GAATGTCAGGATGTTTCTTAATGAACCTTAAAGATCTTAAATCCAGTTGTATATGGA 1177  
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 Db 221 ValPheThrThrSerSerAsnIlePheLysGlySerAlaValCysMetTyrSerMetSer 240  
 QY 1238 GATGTGAGAGGTTGTTCTTGGTCCATATGCGGATGCGGATGCGGATGCGGATGCGGAT 1297  
 Db 241 AspValArgValLeuLeuGlyProTyrAlaHisArgAspGlyProAsnTyrGlnTrp 260  
 QY 1298 GTGCTTATCAAGGAAGTCCCTTATCCAGGCGCAGGAACCTTGTCCAGCAAAACATTT 1357  
 Db 261 ValProTyrGlnGlyArgValProTyrProArgProGlyThrCysProSerLysThrPhe 280  
 QY 1358 GGTGTTTGTACTCTACAAAGGACCTTCTGTATGATGTTTATTAACCTTTGCAAGAGTCA 1417  
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 QY 1418 CCAGCATGTACAATCCAGTGTCTTCTATGAACATCGCCCAATAGTATGATCAAAACGAT 1477  
 Db 301 ProAlaMetTyrAsnProValPheProIleAsnAsnArgProIleMetIleLysThrAsp 320  
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 Db 321 ValAsnTyrGlnPheThrGlnIleValValAspArgValAspAlaGluAspGlyGlnTyr 340  
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 QY 1598 GAGACTGTGTATGTTTGAAGAGTTCGCTGGAGAAATACAGAGTTTTCGGGAACCG 1657  
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 QY 1658 ACTGCTATTTACGAATGAGCTTCCACTAAGCAGCAACTATATATGTTGGTCAACG 1717  
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 QY 1718 GCTGGGTTGCCAGTCCCTTTACACCGGTGTGTATTTACGGGAAGCGTGTCTGAG 1777  
 Db 401 AlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyrGlyLysAlaCysAlaGlu 420  
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 Db 421 CysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySerSerCysSerArgTyrPhe 440  
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 QY 1955 TATGTTGTAGAGATAGTAGCACTTTTGGATTCAGTCCGAGTCCGAGTCCGAGAGCGGTG 2014  
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 Db 541 AsnTyrLeuCysHisAlaValGluHisGlyPheMetGlnThrLeuLeuLysValThrLeu 560

QY 2195 GAATCATTTGACACAGAGCATTTTGAAGAACTTTCTTCATTAAGATGATGATGGAGATGCG 2254  
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 QY 2255 TCTAAGACCAAGAAATGTCTCAATAGCATGACACCTAGCAGAGAGGTCTGTACAGAC 2314  
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 QY 2315 TTTCATGAGCTCATCAACACCCCAATCTCAACAGCATGATGATGATCTTGTGAACAAGTT 2374  
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 QY 2375 TCGAAAAGGACCGCAAAACAACTGCGCAAGCCAGGACATACCCAGGGAACAGTAAAC 2434  
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 G01856  
 semaphorin V - human  
 C:Species: Homo sapiens (man)  
 C>Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
 C:Accession: G01856  
 R:Sekido, Y.  
 submitted to the EMBL Data Library, June 1995  
 A:Reference number: G08634  
 A:Accession: G01856  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-749 <SEK>  
 A:Cross-references: UNIPROT:Q13214; EMBL:U28369; NID:g974283; PIDN:AAD09138.1; PID:g9742  
 C:Superfamily: semaphorin  
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 Pred. No.: 4,95e-152 Length: 749  
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 QY 281 AATGTGCCAAGGCTGAAATTTATCTTACAAAGAAATGTTGGAAATCCAAATGTGTACT 340  
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 QY 341 TTCAATGCTGCGCAACAGCTCCAGTTATCATCTCTTCTTTCGATGAGGAGCGAGT 400  
 Db 47 PheSer---LeuGluArgThrCysCysTyrGlnAlaLeuLeuValAspGluGluArgGly 65  
 QY 401 AGGCTGTATGTTGGAGCAAGATCATATTTTTCATTCGACCTCGTTTAATATC---AAG 457  
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 QY 458 GATTTTCAAAAGATTGTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAGTGGGT 517  
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 QY 518 GGAAGAAGATCTCTGAAAGATGTGCTAATTTTCATCAAGGTACTTAAGCATATATCAG 577  
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Qy	578	ACTCACTGTGACGCTGTGGAAACGGGGCTTTTTCATCCAAATTTGCACCTACATTTGAAAT	637
Db	126	ThrHisLeuLeuAlaCysGlyThrGlyAlaPheHisProThrCysAlaPheValGluVal	145
Qy	638	GGACATCATCTCAGGACAATAATTTTAAAGCTCGGAGAACTCACATTTGTTAAAAACGGCGT	697
Db	146	GlyHisArgAlaGluGluProValLeuArgLeuAspProGlyArgIleGluAspGlyLeu	165
Qy	698	GGGAAGAGTCCATATGACCCCTAAAGCTCTGACAGCATCCCTTTTAAATAGATGAGAAATTA	757
Db	166	GlyIysSerProTyrAspProArgHisArgAlaSerValLeuValGlyGluGluLeu	185
Qy	758	TACTCTGGAACCTGAGCTGATTTTATGGGGCGGAGACTTTCTCTATCTTCCGAACCTCTTGGG	817
Db	186	TyrSerGlyValAlaAlaAspLeuMetGlyArgAspPheThrIlePheArgSerLeuGly	205
Qy	818	CACCACCACCAATCAGCAGACGACATGATTTCAGGTGGCTCAATGATCCAAAGTTTC	877
Db	206	GlnArgProSerLeuArgThrGluProHisAspSerArgTrpLeuAsnGluProLysPhe	225
Qy	878	ATTAGTGCCCACTCATCTCAGAGAGTGACAATCTCGAAGATGACAAAGTATACTTTTTC	937
Db	226	ValIysValPheTrpIleProGluSerGluAsnProAspAspIysIleTyrPhePhe	245
Qy	938	TTCCGTGAAAATGCAATAGATGGAGACACTCT---GGAAAAGCTACTCAGCTAGATA	994
Db	246	PheArgGluThrAlaValGluAlaAlaProAlaLeuGlyArgLeuSerValSerArgVal	265
Qy	995	GGTCAGATATGCAAGATGACTTTGGAGGCGCACAGAGTCTGCTGTAATAAATCGACAACA	1054
Db	266	GlyGlnIleCysArgAsnAspValGlyGlyIleArgSerLeuValIleTyrThrThr	285
Qy	1055	TTCTCTAAAGCTCGTCTGATTTGCTCAGTCGCCAGGTCCAAATGGCATGTGACATCATTTT	1114
Db	286	PheLeuIysAlaArgLeuValCysSerValProGlyValGluGly---AspThrHisPhe	304
Qy	1115	GATCAACTGCGAGGTATTTCTTAATCAACTTTAAGATCCTTAAATCCAGTTGTATAT	1174
Db	305	AspGlnLeuGlnAspValPheLeuLeuSerSerArgAspHisArgThrProLeuLeuTyr	324
Qy	1175	GGAGTGTTTACGACTTCACGTAACATTTTCAAGGGATCAGCCGTGTGTATGTATAGCATG	1234
Db	325	AlaValPheSerThrSerSerSerIlePheGlnGlySerAlaValCysValTyrSerMet	344
Qy	1235	AGTGATGTGAGAGGGTTCCTTTGGTCCATATGCCACAGGGATGAGCCCACTATCAA	1294
Db	345	AsnAspValArgArgAlaPheLeuGlyProPheAlaHisIysGlyGlyProMetHisGln	364
Qy	1295	TGGGTGCCTTTCAAGGAAGAGTCCCTATCCAGGCCAGGAACCTGTCGCCACCAAAACA	1354
Db	365	TrpValSerTyrGlnGlyArgValProTyrProArgProGlyMetCysProSerLysThr	384
Qy	1355	TTTGGTGGTTTTGACTCTACAAAGGACCTTCCTGATGATGTATTAACTTTGCAAGAAGT	1414
Db	385	PheGlyThrPheSerSerThrLysAspPheProAspAspValIleGlnPheAlaArgAsn	404
Qy	1415	CATCCAGCCATGATCAATCCAGTGTTCCTATGACAATCCGCCAATAGTGATGCAAAACG	1474
Db	405	HisProLeuMetTyrAsnSerValLeuProThrGlyGlyArgProPheLeuGlnVal	424
Qy	1475	GATCTAAATTTATCAATTTACAAAATTTGCTAGACCGAGTGGATGAGAAAGATGGACAG	1534
Db	425	GlyAlaAsnTyrThrPheThrGlnIleAlaAlaAspArgValAlaAlaAspGlyHis	444
Qy	1535	TATGATGTTATGTTATCGGAACAGATGTTGGGACCGTCTTTAAAGTAGTTCCTTCAATTCCT	1594
Db	445	TyrAspValLeuPheIleGlyThrAspValGlyThrValLeuIysValIleSerValPro	464
Qy	1595	AAGAGACTTGGTATGATTTAGACAGGTCTCTGCTGGAAGAAATGACAGTTTTTTCGGAA	1654
Db	465	LysGlySerArgProSerAlaGluGlyLeuLeuLeuGluGluLeuHisValPheGluAsp	484

## RESULT 6

RESOUR  
I48744

148/44  
semaphorin A - mouse

C:Species: Mus musculus (house mouse)

C;species: Mus musculus (mouse mouse)  
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004

C;Date: 02-JUL-1996  
C;Accession: T48744

C;Accession: 148/44  
P: Busch, A W : Adams P W : Betz H

R;Puschel, A.W.; Adams, R.  
November 14 041-048 1995

Neuron 14, 941-948, 1995

A:Reference number: I48744; MUID:95267431; PMID:7748561  
 A:Accession: I48744  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-748 <RES>  
 A:Cross-References: UNIPROT:Q62177; EMBL:X85990; NID:g854323; PIDN:CAAS9982.1; PID:g8543  
 C:Genetics:  
 A:Gene: sema  
 C:Superfamily: semaphorin

Alignment Scores:  
 Pred. No.: 1,32e-147 Length: 748  
 Score: 2059.50 Matches: 400  
 Percent Similarity: 66.93% Conservative: 112  
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 DB: 2 Gaps: 15

US-09-774-490-1 (1-2709) x I48744 (1-748)

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DB	27	AsnLeuProArgLeuArgLeuSerPheGlnGluLeuGlnAlaArgHisGlyValArgThr	46
QY	341	TTCAATGGCTTGGCCCAACAGCTCCAGTTATCATACCTCTTTCGATGAGGAAACGGAGT	400
DB	47	PheArg---LeuGluArgThrCysCysTyrGluAlaLeuLeuValAspGluArgGly	65
QY	401	AGCGTGTATGTGGAGAAAGATCACATATTTTCATTCGACCTGGTAAATATC---	457
DB	66	ArgLeuPheValGlyAlaGluAsnHisValAlaSerLeuSerLeuAspAsnIleSerLys	85
QY	458	GATTTTCAAAAGATTGTGGCGAGTACTTACACAGAGAGATGAATGCAAGTGGCT	517
DB	86	ArgAlaLysLysLeuAlaTrpProAlaProValGluTrpArgGluGluCysAsnTrpAla	105
QY	518	GGAAAGACATCCTGAAAGAAATGCTAATTTTCATCAAGGTACTTAAGGCATATATCAG	577
DB	106	GlyLysAspIleGlyThrGluCysMetAsnPheValArgLeuLeuHisAlaLysAsnHis	125
QY	578	ACTCACTGTACGCTGTGGACGGGGCTTTTCATCCAAATTTGC-----	622
DB	126	ThrHisLeuLeuAlaCysArgThrGlyAlaPheHisProThrCysAlaLeuTrpArgTrp	145
QY	623	-----ACCTACATTGAAATTGGACATCATCCTCGAGGACAAATTTTAAG	667
DB	146	AlaThrAlaGlyGlyThrHisAlaSerThrGly-----ProGlu-----	158
QY	668	CTGGAGAACTCACATTTTGAACCGCGCTGGGAAGAGTCCATATGACCCCTAAGCTGCTG	727
DB	159	-----LysLeuGluAspGlyLysGlyLysThrProTyrAspProArgHisArg	174
QY	728	ACAGCATCCCTTTTAATAGATGGAATATATCTGGAACCTGCAAGCTGATTTTATGGG	787
DB	175	ProProSerValLeuValGlyGluGluLeuTyrSerGlyValThrAlaAspLeuMetGly	194
QY	788	CGAGACTTGTCTCTCGAACTCTGGCCACCACCCCAATCAGGACGACGAGCAT	847
DB	195	ArgAspPheThrIlePheArgSerLeuGlyGlnAsnProSerLeuArgThrGluProHis	214
QY	848	GATTCAGGTGGCTCAATGATCCAAAGTTTCATTAGTGGCCACCTCATCTCAGAGAGTGC	907
DB	215	AspSerArgTrpLeuAsnGluProLysPheValLysValPheTrpIleProGluSerGlu	234
QY	908	AATCTGAAGATGACAAAGTATATCTTTTCTTCCTGAAATGCAATAGATGGAGAACAC	967
DB	235	AsnProAspAspLysIleTyrPhePheArgGluSerAlaValGluAlaAlaPro	254
QY	968	TCT---GGAAAGCTACACCTAGATAGATGATGCAAGATGCTTTTGAGGG	1024
DB	255	AlaMetGlyArgMetSerValSerArgValGlyGlnIleCysArgAsnAspLeuGlyGly	274
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DB	275	GlnArgSerLeuValAsnLysTrpThrPheLeuLysAlaArgLeuValCysSerVal	294
QY	1085	CCAGTCCAAATGGCATTCAGACTCATTTTATGAGTGCAGGATGATTTCTTATGAAAC	1144
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QY	1145	TTTAAAGATCCTAAAAATCCAGTTGTATATGGAGTGTTCAGACTTCAGTAAACATTTTC	1204
DB	314	SerArgAspArgGlnThrProLeuLeuTyrAlaValPheSerThrSerSerGlyValPhe	333
QY	1205	AAGGATCAGCCGCTGTGTATGTATAGCATGTGTGTGAGAGGGTGTTCCTTGGTCCA	1264
DB	334	GlnGlySerAlaValCysValTyrSerMetAsnAspValArgArgAlaPheLeuGlyPro	353
QY	1265	TATGCCCAACAGGATGGACCCCACTCATCAATGGGGTCCCTTATCAAGGAGAGTCCCTAT	1324
DB	354	LeuProHisLysGluGlyProThrHisGlnTrpValSerTyrGlnGlyArgValProTyr	373
QY	1325	CCAGGCCAGAACTTGTCCAGCAAAACATTTTGGTGGTGTTCAGTCTACAAAGACCTT	1384
DB	374	ProArgProGlyMetCysProSerLysThrPheGlyThrPheSerSerThrLysAspPhe	393
QY	1385	CCTGATGATGTTAAACCTTTTCAAGAAAGTCCATCCAGCCATGTACAATCCAGTGTTCCT	1444
DB	394	ProAspAspValIleGlnPheGlyArgAsnHisProLeuMetTyrAsnProValLeuPro	413
QY	1445	ATGAACAATCCCCCAATAGTATGATCAAAACGAGTGAATATTATCAATTTTACACAAATGTC	1504
DB	414	MetGlyGlyArgProLeuPheLeuGlnValGlyAlaGlyTyrThrPheThrGlnIleAla	433
QY	1505	GTAGACCCAGTGGATGTCAGAAAGATGCAGATGATGATGTTTATCGGAACAGATGT	1564
DB	434	AlaAspArgValAlaAlaAspGlyHisTyrAspValLeuPheIleGlyThrAspVal	453
QY	1565	GGGACCGTCTTAAAGTAGTTTCAATTCCTAAGGAGACTGTGTATGATTATGAAGAGGT	1624
DB	454	GlyThrValLeuLysValIleSerValProLysGlyArgArgProAsnSerGluGlyLeu	473
QY	1625	CTGTGGAAAGATGACAGTGTTCGGGAACCGAGTCTATTTTACGCAATGAGGCTTCC	1684
DB	474	LeuLeuGluGluLeuGlnValPheGluAspSerAlaAlaIleThrSerMetGlnIleSer	493
QY	1685	ACTAAGCAGCAACACTATATATTGTTCAACCGTGGGTTGCCAGTCCCTCTTACAC	1744
DB	494	SerLysArgGlnGlnLeuTyrValAlaSerArgAlaAlaValAlaGlnIleAlaLeuHis	513
QY	1745	CGTGTGATATTTACGGGAAACGCTGCTGAGTGTTCCTCGCTCGCCGAGACCTTACTGT	1804
DB	514	ArgCysThrAlaLeuGlyArgAlaCysAlaGluCysCysLeuAlaArgAspProTyrCys	533
QY	1805	GCTTGGGATGTTCTGCATGTTCTCGCTATTTTCCACTGCAAGAGACGACACAGAGA	1864
DB	534	AlaTrpAspGlySerAlaCysThrArgPheGlnProThrAlaLysArgArgPheArg	553
QY	1865	CAAGATATAAGAAATGGAGACCACTGACTCACTGTTTCAGACTTACACCATGATATAC	1924
DB	554	GlnAspIleArgAsnGlyAspProSerThrLeuCysSerGly-----AspSerSer	570
QY	1925	CATGCCACACCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACTTTTG	1984
DB	571	HisSerValLeuLeuGluLysValLeu---GlyValGluSerGlySerAlaPheLeu	589
QY	1985	GAATGCACTCGAAGTCCAGAGAGCGCTGCTTATTCGCAATTCAGGCGGGAATGAA	2044
DB	590	GluCysGluProArgSerLeuGlnAlaHisValGlnTrpThrPheGlnGlyAlaGlyGlu	609
QY	2045	GAGCGAAAGAGAGATCAGAGTGCATCATATCATCATCAGACAGATCAAGGCTTCTG	2104
DB	610	AlaAlaHisThrGlnValLeuAlaGluGluArgValGluArgThrAlaArgGlyLeuLeu	629
QY	2105	CTACGTAGTCTACACAGAGAGATTTCAGCAATTTACCTCTGCGCATCGCGTGAACATGGG	2164





Db 445 ArgTyrGluValLeuPheLeuGlyThrAspArgGlyThrValGlnLysValleValLeu 464  
 QY 1592 CTAAGGAGACTTGGTATGATTAGAGAGGTTCTGCTGGAAGAATAACAGACTTTTTCGG 1651  
 Db 465 ProLysAspAsp---GlnGluMetGluGluLeuMetLeuGluGluValGluValPheLys 483  
 QY 1652 GAACCGACTGCTATTCAGCAATGGAGCTTCCATTAAGCAGCAACAATATATATATGTT 1711  
 Db 484 AspProAlaProValLysThrMetThrLysSerLysArgGlnGlnLeuTyrValAla 503  
 QY 1712 TCACCGCTGGGTGCCAGCTCCCTTTACACCGGTGTGATATTCGGGAACGGTGT 1771  
 Db 504 SerAlaValGlyValThrHisLeuSerLeuHisArgCysGlnAlaTyrGlyAlaAlaCys 523  
 QY 1772 GCTGAGTGTGCTCGCCGACACCTTACTGCTGCTGGATGCTTCTGATGCTGCTGCG 1831  
 Db 524 AlaAspCysCysLeuAlaArgAspProTyrCysAlaTyrPaspGlyGlnAlaCysSerArg 543  
 QY 1832 TATTTTCCACTGCCAAGAGACGCAAGACGACAGATATTAAGAAATGGAGACCCACTG 1891  
 Db 544 TyrThrAlaSerSerLysArgArgSerArgGlnAspValArgHisGlyAsnProIle 563  
 QY 1892 ACTCACTGTTACAGCTTACACCATGATATACCATGCGCCAGCCCTGACAGAGATC 1951  
 Db 564 ArgGlnCysArgGlyPhe-----AsnSerAsnAlaAsnLysAsnAlaValGluSerVal 581  
 QY 1952 ATCTATGTTAGAGAAATAGTAGACATTTTGGAAATGAGTCCGAAAGTCGACAGAGCG 2011  
 Db 582 GlnTyrGlyValAlaGlySerAlaAlaPheLeuGluCysGlnProArgSerProGlnAla 601  
 QY 2012 CTGGTCTATTGGCAATTCAGAGGCGAAATGAAGAGCGAAAGAGAGATGAGTGGAT 2071  
 Db 602 ThrValLysTrpLeuPheGlnArgAspProGlyAspArgArgGluLeuAlaGlu 621  
 QY 2072 GATCATATCATCAGACAGATCAAGCCCTTCTGCTAGCTAGTCTACACAGAGATTC 2131  
 Db 622 AspArgPheLeuArgThrGluGlnGlyLeuLeuLeuArgAlaLeuGlnLeuSerAspArg 641  
 QY 2132 GCCAATTACTCTGCCATCGCGTGAACATGGGTTTCATACAACTCTTCTTAAGGTAA 2191  
 Db 642 GlyLeuTyrSerCysThrAlaThrGluAsnAsnPheLysHisValValThrArgValGln 661  
 QY 2192 CTGGAAGTCATTCACACAGAGATTTGGAAGAACTTCTTCAAAAGATGATGATGAGAT 2251  
 Db 662 LeuHisValLeuGlyArgAspAlaValHisAlaAlaLeuPhe----- 675  
 QY 2252 GCTCTAAGACCAAGAAATGCTCAATAGCATGACACCTAGCCAGAGAGTCTGG----- 2305  
 Db 676 -----ProProLeuSerMetSerAlaProProProProGlyAlaGlyProPro 691  
 QY 2306 -----TACAGAGCTTCATGAGCTCATCAACCCCACTCAACACGATGGAT 2356  
 Db 692 ThrProProTyrGlnGluLeuAlaGlnLeuLeuAlaGlnProGluValGlyLeuLeuHis 711  
 QY 2357 GAGTTCCTGTGAACAATTGGAAGAGGACCGAAACAAACAGCTCGGAAAGCCAGACAT 2416  
 Db 712 GlnTyrCysGlnGlyTyrTrpArgHisValProProSerProArgGluAlaProGly--- 730  
 QY 2417 ACCCAGGGAACAGTAACTAAGAGAGCTTACAGAAATAAGAAAGGTAGAACAGG 2476  
 Db 731 -----AlaProArgSerProGluProGlnAspGlnLysLysProArgAsnArg 746  
 QY 2477 AGGACCCAC 2485  
 Db 747 ArgHisHis 749

RESULT 8  
 I48748  
 semaphorin E - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I48748  
 R:Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995  
 A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates  
 A:Reference number: I48744; MUID:95267431; PMID:7748561  
 A:Accession: I48748  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-751 <RES>  
 A:Cross-references: UNIPROT:Q62181; EMBL:X85994; NID:g854331; PIDN:CAAS9986.1; PID:g85433  
 C:Genetics:  
 A:Gene: semE  
 C:Superfamily: semaphorin  
 Alignment Scores:  
 Pred. No.: 8,47e-132 Length: 751  
 Score: 1850.50 Matches: 343  
 Percent Similarity: 65.54% Conservative: 161  
 Best Local Similarity: 44.60% Mismatches: 224  
 Query Match: 37.80% Indels: 41  
 DB: 2 Gaps: 10  
 US-09-774-490-1 (1-2709) x I48748 (1-751)  
 QY 215 AGGATTGCTGCTCTTTCTGGGAGTATTACTTACAGCAAGAGCAAACTATCAGATGGG 274  
 Db 4 ArgAlaIleCysValLeuValGlyValPheIleCysSerIleCys---ValArgGlySer 22  
 QY 275 AAGAACTATGTCGCAAGGCTGAAATATCTCTACAAAGAAATGTTGGAATCCAACTATGTG 334  
 Db 23 SerGlnProGlnAlaArgValTyrLeuThrPheAspGluLeuArgGluThrLysThrSer 42  
 QY 335 ATCATCTTCAATGGCTTGGCCAAAGCTCCAGTTATCATACCTTCTCTTTGGATGAGAA 394  
 Db 43 GluTyrPheSerLeuSerHisGlnGlnLeuAspTyrArgIleLeuLeuMetAspGluAsp 62  
 QY 395 CGGAGTAGCTGTATGTTGGACCAAGCATCACATATTTTCTTCTGCTGCTGCTGCTGCTGCT 454  
 Db 63 GlnAspArgIleTyrValGlySerLysAspHisIleLeuSerLeuAsnIleAsnIle 82  
 QY 455 ---AAGGATTTTCAAAAGATTTGTCGCGCAGTATCTTACACCAAGAGAGATGAATGCAAG 511  
 Db 83 SerGlnGluProLeuSerValPheTrpProAlaSerThrIleLysValGluGluCysLys 102  
 QY 512 TGGGCTGGAAGAAGACATCCTGAAAGATGTGCTAATTTTCACTCAAGGTACTTAAAGCATAT 571  
 Db 103 MetAlaGlyLysAspProThrHisGlyCysGlyAsnPheValArgValIleGlnThrPhe 122  
 QY 572 AATCAGACTCCTGTTAGCCCTGTGGACGGGGCTTTTCTCCTCAATTTGACCTACATTT 631  
 Db 123 AsnArgThrHisLeuTyrValCysGlySerGlyAlaPheSerProValCysThrTyrLeu 142  
 QY 632 GAAATTTGGACATCATCTGAGGACAAATATTTTAAAGCTGGAGAACTCACATTTTGAAC 691  
 Db 143 AsnArgGlyArgArgSerGluAspGlnValPheMetIleAsp---SerLysCysGluSer 161  
 QY 692 GGCCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTTTTAAATAGATGA 751  
 Db 162 GlyLysGlyArgCysSerPheAsnProAsnValAsnThrValSerValMetIleAsnGlu 181  
 QY 752 GAATTTACTCTGGAACTGCGACCTGATTTTATGGCGGAGCTTTGCTGCTATCTTCCGAACT 811  
 Db 182 GluLeuSerSerGlyMetTyrIleAspPheMetGlyThrAspAlaAlaIlePheArgSer 201  
 QY 812 CTTGGGCAACCAACCCCAATCAGGACAGCAGCATGATTTCCAGGTGGCTCAATGATCCA 871  
 Db 202 LeuThrLysArgMetGlnLeuArgThrAspGlnHisAsnSerLysTrpLeuSerGluPro 221  
 QY 872 AAGTTTATTAGTCCACCTCATCTCAGAGAGTGAATCTCTGAAGATGACAAAGATATAC 931  
 Db 222 MetPheValAspAlaHisValIleProAspGlyThrAspProAsnAspAlaLysValTyr 241  
 QY 932 TTTTCTTCTCCGTGAAATGCAATAGATGAGAACACTCTGGAAAGAGCTACTCAGCTACA 991  
 Db 242 PhePhePheLysGluArgLeuThrAspAsnAsnArgSerThrLysGlnIleHisSerMet 261



QY 992 ATAGGTGACATATGCAAGAAATGACTTTGAGGCGCAGACAGTCTGGTGAATAAATGGACA 1051  
DB : : : : :  
DB 262 IleAlaArgIleCysProAsnAspThrGlyGlnArgSerLeuValAsnIleYsrPrThr 281  
QY 1052 ACATTCTCAAGCTCGTCTGATTGCTCAGTGCCAGGTCCTCAAAATGGCAATTCACACTCAT 1111  
DB : : : : :  
DB 282 ThrPheLeuLeuYalaArgLeuValCysSerValThrAspGluAspGlyProGluThrHis 301  
QY 1112 TTGTGATGAATCAGAGATATTTCTTAATGAATCTTAAAGATCTTAAATAATCCAGTTGTA 1171  
DB : : : : :  
DB 302 PheAspGluLeuGluAspValPheLeuLeuGluThrAspAsnProArgThrThrLeuVal 321  
QY 1172 TATGGAGTTTACGATCTCCAGTAACATTTTCAAGGATCAGCGTGTGTATGTATAGC 1231  
DB : : : : :  
DB 322 TyrGlyIlePheThrThrSerSerValPheLeuGlySerAlaValCysValThrHis 341  
QY 1232 ATGAGTGATGTGAGAGGTTGTTCTTGTGTCATATGCCACAGGATGGACCAACTAT 1291  
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DB 342 LeuSerAspIleGlnThrValPheAsnGlyProPheAlaHisGlySerGluGlyProAsnHis 361  
QY 1292 CAATGGTGCTTATCAAGAAAGAGTCCCTATCCACGGCCAGGAACCTTGTCCCGACAA 1351  
DB : : : : :  
DB 362 GlnLeuIleSerTyrGlnGlyArgIleProTyrProArgProGlyThrCysProGlyGly 381  
QY 1352 ACATTT---GGTGGTTTGACTCTACAAAGAGCTTCTGTATGATGTATTAACCTTTGCA 1408  
DB : : : : :  
DB 382 AlaPheThrProAsnMetArgThrThrLysAspPheProAspValValThrPheIle 401  
QY 1409 AGAAGTCATCCAGCCATGACATCCAGTGTTCCTATGAACAAATCCGCAATAGTGATC 1468  
DB : : : : :  
DB 402 ArgAsnHisProLeuMetTyrAsnSerIleSerProIleHisArgArgProLeuIleVal 421  
QY 1469 AAAACGGATGTAATATCAATTTACACAAATTTGCTAGACCGAGTGGATGACAGAGAT 1528  
DB : : : : :  
DB 422 ArgIleGlyThrAspTyrLysThrLysIleAlaValAspArgValAsnAlaAlaAsp 441  
QY 1529 GGACAGTATGATGTATGTTATCGGAACAGATGTGGACCGTCTTTAAAGTAGTTTCA 1588  
DB : : : : :  
DB 442 GlyArgTyrHisValLeuPheLeuGlyThrAspArgGlyThrValGlnLysValValVal 461  
QY 1589 ATTCCTAAGGACACTGGTATGATTTAGAAAGGTTCTCTCGAAGAATGACAGTTT 1648  
DB : : : : :  
DB 462 LeuProThrAsnSerSerAlaSer---GlyGluLeuLeuLeuGluLeuGluValPhe 480  
QY 1649 CCGGAACCGACTGCTATTTTCAGCAATGGAGCTTCCACTAAGCAGCAACACTATATTT 1708  
DB : : : : :  
DB 481 LysAsnHisValProIleThrThrMetGluIleSerSerLysLysGlnGlnLeuTyrVal 500  
QY 1709 GGTTCACCGCTGGGTGCCAGCTCCCTTTACACCGGTGTGATATTTACGGGAAGCG 1768  
DB : : : : :  
DB 501 SerSerAsnGluGlyValSerGlnValSerLeuHisArgCysHisIleTyrGlyThrAla 520  
QY 1769 TGTGCTGAGTGTGCTCCCGCAGACCCCTTACTGTGCTGGAGTGTCTCATGTTCT 1828  
DB : : : : :  
DB 521 CysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyHisSerCysSer 540  
QY 1829 CGCTATTTCCCAAGAGAGCGCACAGACAGACAGATATAAGAAATCGAGACCCA 1888  
DB : : : : :  
DB 541 ArgPheTyrProThrGlyLysArgSerArgGlnAspValArgHisGlyAsnPro 560  
QY 1889 CTGACTCACTGTTACAGCTTACACCATGATATACCATGGCCACCGCTCGAAGAGAGA 1948  
DB : : : : :  
DB 561 LeuThrGlnCysArgGlyPheAsnLeuLysAlaTyr-----ArgAsnAlaAlaGluIle 578  
QY 1949 ATCATCTATGTTGATAGAAATAGTAGCACATTTTGGAAATGAGTCCGGAAGTCGAGAGA 2008  
DB : : : : :  
DB 579 ValGlnTyrGlyValArgAsnAsnSerThrPheLeuGluCysAlaProLysSerProGln 598  
QY 2009 GCGCTGCTATTTGCAATTCAGAGCGCAATTAAGAGCGGAAAGAGAGATCAGAGTG 2068  
DB : : : : :  
DB 599 AlaSerIleLysTrpLeuLeuGln---LysAspLysAspArgLysGluGlyLysLeu 617

QY 2069 GATGATCATATCATCAGGACAGATCAAGGCCCTTCTGTAGTCTTACACAGAGGAT 2128  
DB : : : : :  
DB 618 AsnGluArgIleAlaThrSerGlnGlyLeuLeuIleArgSerValGlnAspSerAsp 637  
QY 2129 TCAGGCAATTTACTCTCGCATCGGTGGAACATGGGTTTCATACAAACTCTTCTTAAGTGA 2188  
DB : : : : :  
DB 638 GlnGlyLeuTyrHisCysIleAlaThrGluAsnSerPheLysGlnThrIleAlaLysIle 657  
QY 2189 ACCCTGGAAAGTCATTGACACAGAGCATTTGGGAAGAACTTCTTCATAAAGATGATGGA 2248  
DB : : : : :  
DB 658 AsnPheLysValLeuAspSer----- 664  
QY 2249 GATGCTCTAAGACCAAGAAATGCTCAATAGCATGACACCTAGCCAGAGGCTCTGGTAC 2308  
DB : : : : :  
DB 665 -----GluMetValAlaValThrAspLysTrpSerProTrpThr 678  
QY 2309 -----AGAGACTTCATGCGCTCATCAAC 2332  
DB : : : : :  
DB 679 TrpAlaGlySerValArgAlaLeuProPheHisProLysAspIleLeuGlyAlaPheSer 698  
QY 2333 CACCCCAATCTCAACACGATGATGTTCTGTGAACAAAGTTTGGAAAAGGACCGCAAAA 2392  
DB : : : : :  
DB 699 HisSerGluMetGlnLeuIleAsnGlnTyrCysLysAspThr-----ArgGlnGlnGln 716  
QY 2393 CACCTCGCAAGAGCCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACAA 2452  
DB : : : : :  
DB 717 GlnLeuGlyGluGluProGlnLysMetArgGlyAspTyrGlyLysLeuLysAlaLeuIle 736  
QY 2453 GAAATAAGAAAGGTAGAAACAGGAGG 2479  
DB : : : : :  
DB 737 AsnSerArgLysSerArgAsnArgArg 745

RESULT 9  
S66498  
M-sema F protein precursor - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C.Accession: S66498  
R.Inagaki, S.; Furuyama, T.; Iwahashi, Y.  
FEBS Lett. 370, 269-272, 1995  
A.Title: Identification of a member of mouse semaphorin family.  
A.Reference number: S66498; MUID:95385809; PMID:7656991  
A.Accession: S66498  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-834 <INA>  
A.Cross-references: UNIPROT:Q64151; EMBL:S79463; NID:gl110598; PIDN:AAB35184.1; PID:gl110598  
C.Superfamily: semaphorin  
F1-21/Domain: signal sequence #status predicted <SIG>  
F1-22-834/Product: M-sema F protein #status predicted <MAT>

Alignment Scores:  
Pred. No.: 6, 88e-65 Length: 834  
Score: 966.00 Matches: 236  
Percent Similarity: 51.3% Conservative: 107  
Best Local Similarity: 35.33% Mismatches: 269  
Query Match: 19.73% Indels: 56  
DB: 2 Gaps: 21

US-09-774-490-1 (1-2709) x S66498 (1-834)

QY 206 TGGTTAACTAGGATGTCTGCTTTTCTGGGGAGTATTACTTACAGCAAGACAAACTAT 265  
DB : : : : :  
DB 8 TrpLeu-----LeuAlaAlaGlyLeuTrpGlyLeuGlyIleGlyAlaGluMetTrpTrp 25  
QY 266 CAGAATGGGAAGAACAAATGTGCCAAGGCTGAAATTTATCTCAACAAAGAAATGTTGGAAATCC 325  
DB : : : : :  
DB 26 -----AsnLeuValProArgLysThrValSerSerGlyGluLeuValThrVal 41  
QY 326 RACATGTGATCATCTTCAATGGCTTGGCCACACAGCTCCAGTTATCATCATCTCTTTT 385  
DB : : : : :  
DB 42 ValArgArgPheSerGlnThrGlyIle-----GlnAspPheLeuThrLeuThrLeu 58





C:Species: Mus musculus (house mouse)  
 C>Date: 09-May-2004 #sequence\_revision 09-May-2004 #text\_change 09-May-2004  
 C:Accession: Jc8059  
 R:Taniguchi, M., and Shimizu, T.  
 Biochem. Biophys. Res. Commun. 314, 242-248, 2004  
 A:Title: Characterization of a novel member of murine semaphorin family.  
 A:Reference number: Jc8059; PMID: 14715272  
 A:Accession: Jc8059  
 A:Molecule type: mRNA  
 A:Residues: 1-1011 <TAN>  
 A:Cross-references: DDBJ:AB091532  
 C:Comment: This protein is a secreted and transmembrane semaphorin protein belonging to elopment and neuronal plasticity in brain, neurogenesis and morphogenesis, and vasculog  
 C:Genetics:  
 A:Gene: Sema6D-1  
 A:Map position: 2  
 C:Keywords: axon guidance; brain; semaphorin; transmembrane protein

Alignment Scores:		Pred. No.:	Length:	1011
Score:	828.00	Matches:	253	
Percent Similarity:	42.89%	Conservative:	133	
Best Local Similarity:	28.11%	Mismatches:	236	
Query Match:	16.91%	Indels:	218	
DB:	2	Gaps:	40	

US-09-774-490-1 (1-2709) x Jc8059 (1-1011)

QY	200	ATGGGCTGTTAACTAGGATTGCTGCTTTCTGGGAGTATTACTTACACAGAGCA	259
DB	1	MetGlyPheLeuLeuLeuTrpPheCysValLeuPheLeuValSerArgLeuArgAla	20
QY	260	AACTATCAGAAATGGGAGAACATGTCGCAAGCTGAAATATCTACAAAGAAATGTTG	319
DB	21	ValSerPheProGluAspAsp	27
QY	320	GAATCCAAACATGTGATC-----ACTTTCAATGGCTTG	352
DB	28	GluProLeuAsnThrValAspTyrHisTyrSerArgGlnTyrProValPheArgGlyArg	47
QY	353	-----GCCAACGTCCTCATACCTTC-----CTTTGGATGAGGAGCGAGT	400
DB	48	ProSerGlyAsnGluSerGlnHisArgLeuAspPheGlnLeuMetLeuLysIleArgAsp	67
QY	401	AGCGTGTATGTCGCAAGATCACATATTTTCATTCGACTGCTTAATCAAGAT	460
DB	68	ThrLeuTyrIleAlaGlyArgAspGlnValTyrThrValAsnLeuAsnGluIleProGln	87
QY	461	TTTCAA-----AAGATTGTGTGGCCAGTATCTTACACCAAGAGATGAA	505
DB	88	ThrGluValIleProSerLysLysLeuThrTyrArgSerArgGlnGlnAspArgGluAsn	107
QY	506	TGCAAGTGGCTGGAAAAGACATCTGGAAGAATGTGCTTAATTCATCAAGTACTTAAG	565
DB	108	CysAlaMetLysGlyLysHis-----LysAspGluCysHisAsnPheIleLysValPheVal	126
QY	566	GCATATAATCAGACTCATTGTACGCTGTGGAAGGGGCTTTTCATCAATTTGTCACC	625
DB	127	ProArgAsnAspGluMetValPheValCysGlyThrAsnAlaPheAsnPrometCysArg	146
QY	626	TACATTGAAATTGGACATCATCTCGAGCAATATTTTAAAGCTGGAGAACTCACATTTT	685
DB	147	Tyr-----TyrArgLeuArgThrLeuGluTyr	155
QY	686	GAA-----AACGGCGTGGGAAGATGCCATATGACCTTAAGCTGTGACAGCA	733
DB	156	AspGlyGluGluIleSerGlyLeuAlaArgCysProPheAspAlaArgGlnThrAsnVal	175
QY	734	TCCCTTTTATAGATGGAGATATATCTCGGAACGTCAGCTCATTTTATGGGGCAGAC	793
DB	176	AlaLeuPheAlaAspGlyLysLeuTyrSerAlaThrValAlaAspPheLeuAlaSerAsp	195
QY	794	TTTGCTATCTTCGAACTCTTGGGCACCACCACTTACAGGACAGCAGCATGATTC	853

DB	136	AlaValIleTyrArgSerMetGlyAspGlySerAlaLeuArgThrIleLysTyrAspSer	215
QY	854	AGGTGGCTCAATGATCCAAAGTTCAATTAGTCCCACTCATCTCAGAGAGTCAACATCT	913
DB	216	LysTrpIleLysGluProHisPheLeu-----HisAlaIleGluTyrGly	230
QY	914	GAAGATGACAAAGATATATCTTTCTTCGTTGAAATGCAATAGATGGAGAACACTCTGA	973
DB	231	-----AsnTyrValTyrPhePhePheArgGluIleAlaValGluHisAsnLeuGly	248
QY	974	AAAGCTACTACGCTAGAAATAGTCATATGCAAGATGACTTTGGAGGGCAGACAGAT	1033
DB	249	LysAlaValTyrSerArgValAlaArgIleCysLysAsnAspMetGlySerGlnArg	268
QY	1034	CTGGTGAATAAA---TGGACAACATCTCTCAAGCTCTCTGATTGCTCAGTGCCAGGT	1090
DB	269	ValLeuGluLysHisIleTrpThrSerPheLeuLysAlaArgLeuAsnCysSerValProGly	288
QY	1091	CCAAATGGCATTCACACTCATTTTGATGAACTGCAG-----GATGTATTCCTAATG	1141
DB	289	AspSerPhePhe-----TyrPheAspValLeuGlnSerIleThrAspIleIleGlnIle	306
QY	1142	AACTTTAAAGATCTTAAATCCAGTTGTATATGAGGTGTTTACGATTCAGATTAACAT	1201
DB	307	Asn-----GlyIleProThrValValGlyValPheThrThrGlnLeuAsnSer	322
QY	1202	TTCAGGATCAGCGCTGTGTATGATAGCATGATGTGAGAGGGTGTCTCTGCT	1261
DB	323	IleProGlySerAlaValCysAlaPheSerMetAspAspIleGluLysValPheLysGly	342
QY	1262	CCATATGCCACAGGATGGACCAACTATCAATGG-----GTCCCTTATCAAGAGAA	1315
DB	343	ArgPheLysGluGlnLysThrProAspSerValTyrThrAlaValPro-----GluAspLys	361
QY	1316	GTCCCTATCCACGGCCAGGAACCTTGTCCCGAGCAAAACATTTGGT---GGTTTCACTCT	1372
DB	362	ValProLysProArgProGlyCysCysAlaLysHisGlyLeuAlaGluAlaTyrLysThr	381
QY	1373	ACAAAGGACCTTCTCTGATGATCTTAACTTTGCAAGAAGTCATCCAGCCCATGACAT	1432
DB	382	SerIleAspPheProAspAspThrLeuAlaPheIleLysSerHisProLeuMetAspSer	401
QY	1433	CCAGTGTCTTCTATCAACAATCGCCCAATAGTATCAAAACGATGTAAATATCAATTT	1492
DB	402	AlaValProProIleAlaAspGluProThrPheThrLysThrArgValArgTyrArgLeu	421
QY	1493	ACACAAATTCGTAGACCGAGTGGATGCAGAGAATGGACATGATGATGTTATGTTATC	1552
DB	422	ThrAlaIleGluValAspArgSerAlaGlyProTyrGlnAsnTyrThrValIlePheVal	441
QY	1553	GGAAACAGATGTGGACCGCTTCTTAAAGTATTTCAATTCCTAAGAGACTTGGTATGAT	1612
DB	442	GlySerGluAlaGlyValValLeuLysValLeuAla-----LysThrSerProPheSer	459
QY	1613	TTA---GAAGAGTCTCTGCTGGAAGAAATGACAGTTTTT-----	1648
DB	460	LeuAsnAspSerValLeuLeuGluGluIleGluAlaTyrAsnProAlaLysCysSerAla	479
QY	1649	-----CGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTTCCACTAAGCAGCAACTA	1702
DB	480	GluSerGluGluAspArgLysValValSerLeuGlnLeuAspLysAspHisAlaLeu	499
QY	1703	TATATTGTTTCAACCGCTGGGTGCCAGCTCCCTTTACACGGGTGTGATTTACGGG	1762
DB	500	TyrValAlaPheSerCysValValArgIleProLeuSerArgCysGluArgTyrGly	519
QY	1763	AAAGCGTGTGCTGAGTGTGCTCCCGCAGACCCCTTACTGTGCTTG---GATGTTCT	1819
DB	520	SerCysLysLysSerCysAlaIleAlaSerArgAspProTyrCysGlyTyrLeuSerGlnGly	539
QY	1820	GCATGTTCTCGTATTTTCCCACTCGAAAGAGACGACCAAGACGACAGATTAAGAAAT	1879

Db 540 ValCysGluArgVal-----ThrLeuGlyMetLeuLeuLeuThrGluAspPhe----- 555  
 QY 1880 GGAGAGCCCACTGACTCACTGTTTCAGAGCTTACACCATGATGATAATCACCATCGCCACAGCCCT 1939  
 Db 556 -----PheAlaPheHisAsnHisSerPro 563  
 QY 1940 -----GAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACATTTTGGAAATGC 1990  
 Db 564 GlyGlyTyrGluGlnAspThrGluTyrGly-----AsnThrAlaHisLeuGlyAspCys 581  
 QY 1991 AGTCGCAAGTCGCAGAGAGCGCTGCTTATGTCATTCGCAATTCAGAGCGGGAATAGAGAGCA 2050  
 Db 582 HisGly-----ValArgTrpGluValGlnSerGlyGluSerAsnGln 595  
 QY 2051 AAAGAGAGATCAGAGCTG-----ValArgTrpGluValGlnSerGlyGluSerAsnGln 2068  
 Db 596 MetValHisMetAsnValLeuLeuThrCysValPheAlaPheValLeuGlyAlaPhe 615  
 QY 2069 -----GATGATCATATCATCAGGACAGATCAAGCCCTT 2101  
 Db 616 IleAlaGlyValAlaValTyrCysTyrArgAspMetPheValArgLysAsnArgLysIle 635  
 QY 2102 CTGCTAGCTAGCTACACAGAGGAT-----TCA 2131  
 Db 636 -----HisLysAspAlaGluSerAlaGlnSerCysThrAspSerSer 649  
 QY 2132 GGCATATTACTCTGCTCATCGGTGGAAACATGGGTTTCATCAAACTCTTCTTAAAGGTAACC 2191  
 Db 650 GlySerPhe-----AlaLysLeuAsnGlyLeuPheAspSerProValLysGluTyr 666  
 QY 2192 CTGGAAGTCATTGACACAGAGCATTTG---GAAGAACTTCTTCATAAAGATCATGATGA 2248  
 Db 667 GlnGlnAsnIleAspSerProLysLeuTyrSerAsnLeu----- 680  
 QY 2249 GATGGCTCTAAGACCAAGAAATG---TCAATAGCATGACACCTAGCCAGAGGTCTGG 2305  
 Db 681 -----ThrSerArgLysGluLeuProProAsnThrAspThrLysSerMetAlaValAsp 698  
 QY 2306 TACAGA-----GACTTCATGCGAGCTCAGC 2329  
 Db 699 HisArgGlyGlnProGluLeuAlaLeuProThrProGluSerThrProValLeu 718  
 QY 2330 AACCAACCCCAATCTCAACAGCATGATGATGTTCTGTGAACAAGATTTGGAAAGG----- 2383  
 Db 719 HisGlnLysThrLeuGlnAlaMetLysSerHisSerGluLysAlaHisSerHisGlyAla 738  
 QY 2384 GACCGAAACACAGCTCGGCAA-----AGCCAGGACATACCCCA----- 2422  
 Db 739 SerArgLysGluHisProGlnPhePheProSerSerProProHisSerProLeuSer 758  
 QY 2422 ----- 2422  
 Db 759 HisGlyHisIleProSerAlaIleValLeuProAsnAlaThrHisAspTyrAsnThrSer 778  
 QY 2423 ---GGGAACAGTAACAAATGGAAGCATTACAGAAATAAG----- 2461  
 Db 779 PheSerAsnSerAsn-----AlaHisLysAlaGluLysLysLeuGlnSerMetAspHis 796  
 QY 2462 -----AAGGTAGAACAGGAGGACCCAGAAATTTGAGAGGCGACCCAGGAGTGTTC 2512  
 Db 797 ProLeuThrLysSerSerLysArgGluHisArg-----ArgSerVal 811  
 RESULT 12  
 148745  
 semaphorin B - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: 148745  
 R:Puschel, A.W.; Adams, R.H.; Betz, H.  
 Neuron 14, 941-948, 1995  
 A>Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates  
 A:Reference number: 148744; MUID:95267431; PMID:7748561  
 A:Accession: 148745

A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-760 <RES>  
 A:Cross-references: UNIPROT:Q62178; EMBL:X85991; NID:g854325; PIDN:CAA59983.1; PID:g854  
 C:Genetics:  
 A:Gene: semB  
 C:Superfamily: semaphorin  
 Alignment Scores:  
 Pred. No.: 1-72e-52 Length: 760  
 Score: 802.00 Matches: 204  
 Percent Similarity: 49.32% Conservatives: 122  
 Best Local Similarity: 30.88% Mismatches: 251  
 Query Match: 16.38% Indels: 84  
 DB: 2 Gaps: 23  
 US-09-774-490-1 (1-2709) x 148745 (1-760)  
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 Db 30 AlaSerGlyThrGlyGlyGlnGlyProMetProArgValLysTyr-----HisAla 46  
 QY 317 TTGGAATCCAAACAATGTGATCACTTCAATGCTTGGCCCAACAGCTCCAGTTATCATACC 376  
 Db 47 GlyAspGlyHisArgAlaLeuSerPhePheGlnGlnLysGlyLeuArgAspPheAspThr 66  
 QY 377 TTCTTTTGGATGAGAACGGAGTAGGTGTATGTTGGAGCAAGAGATCACATATTTTCA 436  
 Db 67 LeuLeuLeuSerAspAspGlyAsnThrLeuTyrValGlyAlaArgGluThrValLeuAla 86  
 QY 437 TTCGACCTGGTGTAAAT-----ATCAAGGATTTTCAAAAGATTTGTGTGCCCA 481  
 Db 87 LeuAsnIleGlnAsnProGlyIleProArgLeuLysAsnMet-----IleProTrpPro 104  
 QY 482 GTATCTTACACAGAGAGATCAATGCAAGTGGGTGGAAAGACATCTCTGAAGAAATGT 541  
 Db 105 AlaSerGluArgLysLysThrGluCysAlaPheLysLysLysSerAsnGluThrGlnCys 124  
 QY 542 GCTAATTTTCATCAAGTACTTAAGGCATATATACAGATCACTTGTACCGCTGTGGAACG 601  
 Db 125 PheAsnPheIleArgValLeuValSerTyrAsnAlaThrHisLeuTyrAlaCysGlyThr 144  
 QY 602 GGGGCTTTTCATCCAAATTTGCACCTACATTTGAAATTTGGACATCATCTCTGAGCAATAT 661  
 Db 145 PheAlaPheSerProAlaCysThrPheIleGluLeu-----GlnAspSerLeuLeu 161  
 QY 662 TTTAAGCTGGAGAACTCATTTTGAAGCGCCGTGGGAAGAGTCCATATACCCCTAAG 721  
 Db 162 LeuProIleLeuIleAspLysValMetAspGlyLysGlyGlnSerProLeuThrLeuPhe 181  
 QY 722 CTGCTGACAGCATCCCTTTAATAGATGGAATATATCTCTGGAACCTGACGTGATTT 781  
 Db 182 ThrSerThrGlnAlaValLeuValAspGlyMetLeuTyrSerGlyThrMetAsnAsnPhe 201  
 QY 782 ATGGGCGGAGACTTTTCTATCTTCGCACTCTTGGGCACCCACCACCCCAATAGGACAGAG 841  
 Db 202 LeuGlySerGluProIleLeuMetArgThrLeuGlySerHisProValLeuLysThrAsp 221  
 QY 842 CAGCATGATTCAGGTGGCTCAAT---GATCCAAAGTTCAATAGTGGCCCACTCATCTCA 898  
 Db 222 IlePhe---LeuArgTrpLeuHisAlaAspAlaSerPheValAlaAla----- 236  
 QY 899 GAGAGTGACATCTCTGAAGATGACAAAGTATATCTTTCTCCGTGAAATCAATAGAT 958  
 Db 237 -----IleProSerThrGlnValValTyrPhePheGluGluThrAlaSerGlu 253  
 QY 959 GGAGAACACTCTGGAAAGAGCTACTCACGCTAGATAGTGCAGATATGCAAGAACTGACTTT 1018  
 Db 254 PheAspPhePheGluGluLeuTyrIleSerArgValAlaGlnValCysLysAsnAspVal 273  
 QY 1019 GGAGGGCACAGAGTCTGTGTAATTAATGACAACTCTCTCAAGCTCGTCTGATTTGC 1078  
 Db 274 GlyGlyGluLysLeuLeuGlnLysLysTrpThrThrPheLeuLysAlaGlnLeuLeuCys 293





QY 656 -----AATATTTTAAAGCTGGAGAACTCACATTTTGAATAACGCGCTGG----- 700  
 Db 161 TyrAlaAsnLeuThrHisLeuProArgSerGluTyrValIleGlyValGlyLeuGlyIle 180  
 QY 701 ---AAGAGTCCATACACCTTAAGCTGCTGACAGCATCCCTTTTAAATAGATGA----- 751  
 Db 181 AlaLysCysProIlyrAspProLeuAspAsnSerThrAlaIleTyrValGluAsnGlyAsn 200  
 QY 752 -----GAATATATCTCTGGAAGCTGACAGCTGATTTTATGGGCGAGACTTT 796  
 Db 201 ProGlyGlyLeuProGlyLeuTyrSerGlyThrAsnAlaGluPheThrLysAlaAspThr 220  
 QY 797 GCTATCTTCGAACCTCTGGGACACACCCCAATC----- 832  
 Db 221 ValIlePheArgThrAspLeuTyrAsnThrSerAlaLysArgLeuGluTyrLysPheLys 240  
 QY 833 AGGACAGAGCAGCATATCCAGTGCCTCAATGATCCAAAGTTCATTAGTCCACCTC 892  
 Db 241 ArgThrLeuLysTyrAspSerLysTrpLeuAspLysProAsnPheValGlySerPheAsp 260  
 QY 893 ATCTCAGAGAGTACCAATCTGAAGATGACAAAGTATATCTTTTCTCCGTCGAAATGCA 952  
 Db 261 IleGlyGlu-----TyrValTyrPhePheArgGluThrAla 273  
 QY 953 ATAGATGGAGAACACTCTGTGAAGCTACTCAGCTAGATAGGTGAGATATCAAGAT 1012  
 Db 274 ValGluTyrIleAsnCysGlyLysAlaValTyrSerArgIleAlaArgValCysLysLys 293  
 QY 1013 GACTTTGGGGGACAGAGTCTGGTGAATAATGACACATCTCTCAAGCTCTCTG 1072  
 Db 294 AspValGlyGlyLysAsnLeuAlaHisAsnTrpAlaThrTyrLeuLysAlaArgLeu 313  
 QY 1073 ATTGTGTCAGTCCAGTCCAAATGCGATTCACACTCATTTTGCATCACTGACAGGATGA 1132  
 Db 314 AsnCysSerIleSerGlyGlu-----PheProPheTyrPheAsnGluIleGlnSerVal 331  
 QY 1133 TTCCTAAGAACCTTTAAAGATCCTAAAGATCCAGTTGTATATGGAGTGTTCAGACTCC 1192  
 Db 332 TyrGlnLeuProSerAspLysSerArg-----PhePheAlaThrPheThrThrSer 348  
 QY 1193 AGTAACATTTTCAAGGATCAGCGGTGTATGTATATGATGATGATGATGATGAGAGGGTG 1252  
 Db 349 ThrAsnGlyLeuIleGlySerAlaValCysSerPheHisIleAsnGluIleGlnAlaLa 368  
 QY 1253 TTCCTTGGTCCATATGCCACAGGATGGACCAACTATCAATGGGTGCT---TATCAA 1309  
 Db 369 PheAsnGlyLysPheLysGluGlnSerSerSerAsnSerAlaTrpLeuProValLeuAsn 388  
 QY 1310 GGAAGAGTCCCTTATCCAGCGGAGGAACCTGTCAGCAAAACATTTGGTGTGTTTGAC 1369  
 Db 389 SerArgValProGluProArgProGlyThrCys-----ValAsn 401  
 QY 1370 TCTAAGAGACCTCTCTGATGATGTATTAACCTTGCAGAGATGATCATCAGCCATGTAC 1429  
 Db 402 AspThrSerAsnLeuProAspThrValLeuAsnPheIleArgSerHisProLeuMetAsp 421  
 QY 1430 AATCCAGTGTTCCTATGAACATCCGCCAATAGTATCAAAACGAGTGTAAATTATCAA 1489  
 Db 422 LysAlaValAsnHisGluHisAsnProValTyrTyrLysArgAspLeu-----Val 439  
 QY 1490 TTTTACAAATTTCTGTAGAC-----CGAGTGGATGCGAAGATGCGACATGATGATTT 1543  
 Db 440 PheThrLysLeuValValAspLysIleArgIleAspIleLeuAsnGlnGluTyrIleVal 459  
 QY 1544 ATGTTTATCGAAGACAGATGTGGGCGGTCTTTAAAGTAGTTTCAATCTCTAAGAGACT 1603  
 Db 460 TyrTyrValGlyThrAsnLeuGlyArgIleTyrLysIleValGln----- 474  
 QY 1604 TGTATGATTTAAGAGGTTCTGCTGGAAGAATACAGTCTTTTCGG-----GAACCG 1657  
 Db 475 TyrTyrArgAsnGlyGluSerLeuSerLysLeuLeuAspIlePheGluValAlaProAsn 494

QY 1658 ACTGCTATTTTCCAGCAATGAGCTTCCACTAAGCAGCAACAACATATATATGTTTCAACG 1717  
 Db 495 GluAlaIleGlnValMetGluIleSerGlnThrArgLysSerLeuTyrIleGlyThrAsp 514  
 QY 1718 GCTGGGGTTCGCCAGCTCCCTTTTACACCGGTGTATATTTACGGGAAGCGTGTCTGAG 1777  
 Db 515 HisArgIleGlyGlnIleAspLeuAlaMetCysAsnArgTyrAspAsnCysPheArg 534  
 QY 1778 TTTTGCTCGCCGAGACCTTACTGTGTCTGGATGGTGTCTGCA-----TGTTCCTCGC 1831  
 Db 535 Cys-----ValArgAspProTyrCysGlyTyrAspLysGluAlaAsnThrCysArgPro 552  
 QY 1832 TATTTTCCCACTGCAAGAGAGCGACAGACGACAGATATAGAATGAGACCCCACTG 1891  
 Db 553 Tyr-----GluLeuAspLeuLeuGlnAspValAlaAsn----- 563  
 QY 1892 ACTCACTGTTTACAGCTTACACCATGATATACCATGGCCACAGCCCTGAAGAGAGAATC 1951  
 Db 564 ---GluThrSerAspIleCysAspSerSer-----ValLeuLysLysLysIle 578  
 QY 1952 ATC-----TATGGTGTAGAGAAATAGTACACATTTTTCGAATGCGAGTCCGAGTCCGAG 2005  
 Db 579 ValValThrTyrGly-----GlnSerValHisLeuGlyCysPheValLysIlePro 595  
 QY 2006 AGAGCGCTG-----GTCTATTGCGCAATTCAGAGGCGGAATGAAGAGCGAATA 2053  
 Db 596 GluValLeuLysAsnGluGlnValThrTrp---TyrHisHisSerLysAspLysGlyArg 614  
 QY 2054 GAAGAGATCAGAGTGGAT-----GATCATATCATCAGACACAGATCAAGGCTTCGTGCTA 2107  
 Db 615 TyrGluIleArgTyrSerProThrLysTyrIleGluThrGluArgGlyLeuValVal 634  
 QY 2108 COTAGTCTACAACAGAGGATTCAGGCAATTCCTCTGCCAT 2149  
 Db 635 ValSerValAsnGluAlaAspGlyGlyArgTyrAspCysHis 648

RESULT 14  
 JH0798  
 fasciclin IV precursor - American bird grasshopper  
 C:Species: Schistocerca americana (American bird grasshopper)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C:Accession: JH0798  
 R:Kolodkin, A.; Mathes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Goo  
 A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance i  
 A:Reference number: JH0798; PMID:93040225; PMID:1418998  
 A:Accession: JH0798  
 A:Molecule type: mRNA  
 A:Residues: 1-730 <KOL>  
 A:Cross-references: UNIPROT:Q26473; GB:I00709; NID:g160844; PID:g160845  
 A:Experimental source: embryo  
 C:Comment: This protein plays a role in growth cone guidance in the developing central  
 C:Keywords: glycoprotein; transmembrane protein  
 F;1-2/Domain: signal sequence #status predicted <SIG>  
 F;23-730/Product: fasciclin IV #status predicted <MAT>  
 F;23-627/Domain: extracellular #status predicted <EXT>  
 F;628-652/Domain: transmembrane #status predicted <TM>  
 F;653-730/Domain: intracellular #status predicted <INT>  
 F;44,71,63,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
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 Best Local Similarity: 31.05% Mismatches: 225  
 Query Match: 15.66% Indels: 127  
 DB: 2 Gaps: 29

US-09-774-490-1 (1-2709) x JH0798 (1-730)

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 Db 5 LeuValAlaValAlaAlaLeuLeuTrp---ValAlaLeuHisAlaAla----- 20





A:Residues: 1-656 <KOL>  
A:Cross-references: GB:I26082  
C:Genetics:  
A:Gene: sema1  
A:Cross-references: FlyBase:FBgn0011259

Alignment Scores:  
Pred. No.: 3,61e-47 Length: 656  
Score: 731.50 Matches: 199  
Percent Similarity: 46.92% Conservative: 129  
Best Local Similarity: 28.47% Mismatches: 248  
Query Match: 14.94% Indels: 123  
DB: 2 Gaps: 24

US-09-774-490-1 (1-2709) x B49423 (1-656)

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DB 3 AspCysGlnAsnTyrIleArgIleMetValProSerProGlyArgLeuPheValCys 22  
QY 596 GGAACGGGGCTTTTCATCAATTTGC---ACCTCAATTGAAATTGGACATCATCCTGAG 652  
DB 23 GlyThrAsnSerPheArgProMetCysAsnThrTyrIle-----IleSer 37  
QY 653 GACAATATTTTAAGCTGAGACTCACATTTTGAACGGCGCTGGAGAGTCCATAT 712  
DB 38 AspSerAsnTyrThrLeuGluAlaThr-----LysAsnGlyGlnAlaValCysProTyr 55  
QY 713 GACCTTAAGCTGACAGCATCCCTTTTAATAGATGGAGAAATATATCTCTGGAACCTGCA 772  
DB 56 AppProArgHisAsnSerThrSerValLeuAlaAspAsnGluLeuTyrSerGlyThrVal 75  
QY 773 GCTGATTTTATGGGGGAGACTTGTCTATCTTCGGAACCTCTTGGGCACCAACCACCAATC 832  
DB 76 AlaAspPheSerGlySerAspProIleIleTyrArg-----GluProLeu 90  
QY 833 AGGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAGTTCATTAGTGGCCACCTC 892  
DB 91 GlnThrGluGlnTyrAspSerLeuSerLeuAsnAlaProAsnPheValSerPhe--- 109  
QY 893 ATCTCAGAGTGCACAACTCTGAAGATGACAAAGTATATCTTTTCTCGTGAATGCA 952  
DB 110 -----ThrGlnGlyAspPheValTyrPhePheArgGluThrAla 123  
QY 953 ATAGATGGAGAACACTCTGGAAGAGTACTACGCTAGAAATAGGTGAGATATGCAAGAT 1012  
DB 124 ValGluPheIleAsnCysGlyLysAlaIleTyrSerArgValAlaArgValCysLysTyr 143  
QY 1013 GACTTTGGAGGACAGAGTCTGGTGAATAATGACAAACATTCCTCAAGCTCTCTG 1072  
DB 144 AspLysGlyGlyProHisArgPheArgAsnArgTyrThrSerPheLeuLysSerArgLeu 163  
QY 1073 ATTTGCTCAGTGCAGGTCCAAATGCGATGACATTCATTTGATCAACTGAGGATGTA 1132  
DB 164 AsnCysSerIleProGly-----AspTyrProPheTyrPheAsnGluIleGlnSerAla 181  
QY 1133 TTCCTTAATG-----AACTTTAAAGATCTCTAAATAATCCAGTTCTATATGAGTGT 1183  
DB 182 SerAsnLeuValGluGlyGlnTyrGlySerMetSerSerLysLeuIleTyrGlyValPhe 201  
QY 1184 AGCACTTCAGTAAACATTTTCAAGGATCAGCGCTGTGTATGTATGATGATGATGATG 1243  
DB 202 AsnThrProSerAsnSerIleProGlySerAlaValCysAlaPheAlaLeuGlnAspIle 221  
QY 1244 AGNAGGGTTCCTTGGTCCATATGCCAGGGATGGACCCCACTATCAATGGGTGCT 1303  
DB 222 AlaAspThrPheGluGlyGlnPheLysGluGlnThrGlyIleAsnSerAsnTrpLeuPro 241  
QY 1304 TAT---CAAGGAGAGTCCCTTATCCAGCGCCAGGAACTTGTCCACGAAAAACATTGGT 1360  
DB 242 ValAsnAsnAlaLysValProAspProArgProGlySerCys----- 255  
QY 1361 GGTTCCTACTACAAAGGACCTTCTCTGATGATGTTTATAACCTTTTGAAGAGTCAATCCA 1420

DB 256 ---HisAsnAspSerArgAlaLeuProAspProThrLeuAsnPheIleLysThrHisSer 274  
QY 1421 GCCATGTACAATCCAGTGTTCCTATGAAATCCCAATAGTATGATCAAAACGAGTGA 1480  
DB 275 LeuMetAspGluAsnValProAlaPhePheSerGlnProIleLeuValArgThrSerThr 294  
QY 1481 AATTATCAATTTTACACAAATTCCTGATAGC---CGAGTGGATGCAGAAATGCAGAC--- 1534  
DB 295 IleTyrArgPheThrGlnIleAlaValAspAlaGlnIleLysThrProGlyGlyLysThr 314  
QY 1535 TATGATGTATGTTATCGGAACAGATGTGGACCGTCTTAAAGTAGTCTTCAATTCCT 1594  
DB 315 TyrAspValIlePheValGlyThrAspHisGlyLysIleLysSerValAsnAlaGlu 334  
QY 1595 AAGGAGACTGTTGATGAT---TTAGAAGAGTCTCTGCTGGAAGAATAGACAGTTCGG 1651  
DB 335 SerAlaAspSerAlaAspLysValThrSerValIleGluGluIleAspValLeuThr 354  
QY 1652 GAACCGACTGCTATTTTCACATGAGCTTTCACCTAAGCAGCA----- 1696  
DB 355 LysSerGluProIleArgAsnLeuGluIleValArgThrMetGlnTyrAspGlnProLys 374  
QY 1697 -----CAACTATATATTGTTCAACGCTGGGGTTCGCCAGCTC 1735  
DB 375 AspGlySerTyrAspAspGlyLysIleIleValThrAspSerGlnValAlaIle 394  
QY 1736 CTTTACACCGGTGT---GATATTACGGGAAACGCTGCTGAGTGTTCCTCGCCCGA 1792  
DB 395 GlnLeuHisArgCysHisAsnAspLysIleThrSerCysSerGluCysValAlaLeuGln 414  
QY 1793 GACCTTACTGCTGCTGGATGCTGTGCA-----TGT----- 1825  
DB 415 AspProTyrCysAlaTrpAspLysIleAlaGlyLysCysArgSerHisGlyAlaProArg 434  
QY 1826 -----TCTCGCTATTTT-----CCC 1840  
DB 435 TrpLeuGluAsnTyrPheTyrGlnAsnValAlaThrGlyGlnHisAlaLysPro 454  
QY 1841 ACTGCAAGAGAGACGACAGACGACCAAGATATAAGAAATGGAGACCCACTGACTCTGT 1900  
DB 455 SerGlyLysIleAsnSerLys-----AspAlaAsnAlaGlyGluGlyLysGlyPheArg 472  
QY 1901 TCAGCTTACACCATGATTAATCAGCATGGCCACAGCCCTGAGAGAGATCATCTATGT 1960  
DB 473 AsnAspMetAspLeuAspSerArgGlnSerLysAspGlnGluIleIleAspAsn 492  
QY 1961 GTAGAGATAGTACACATTTTGGATGCTGAGTCCGAACTCCGAGAGCGCTGCTAT 2020  
DB 493 IleAspLysAsnPheGlu-----GlyProGlnThrSerAlaAspIleIleAsn 508  
QY 2021 TGGCAATTCAGAGCGCAAAATGAAGCGCAAAAGAGATCAGATGATGATCATATATC 2080  
DB 509 AlaGlnTyr-----ThrValGluThrLeuVal 517  
QY 2081 ATCAGACAGATCAAGGCCTTCTGTACGTAGTCTTCAACAGAGAGATTCAGGCAATTC 2140  
DB 518 MetAlaValLeuAlaGlySerIlePheSerLeuLeuValGlyPhePheThrGlyTyrPhe 537  
QY 2141 CTC-----TGCATCGGTGGACATGGGTTTCATACAACTCTTCTTAAGGTAACC 2191  
DB 538 CysGlyArgArgCysHisLysAspGluAspAsp-----Asn 549  
QY 2192 CTGGAAGTCAATTCACACA-----GAGCATTTGGAAGAACTTCTTCATAAAGATGATGAT 2245  
DB 550 LeuProTyrProAspThrGluTyrGluTyrPheGluGlnArgGlnAsnValAsnSerPhe 569  
QY 2246 GGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAGGCTCTG 2305  
DB 570 ProSerSerCysArgIleGlnGlnProLysLeuLeuProGlnValGluGluValThr 589  
QY 2306 TACAGAGCTTCTATGAGCTCATCAACCCCACTCTCAACAGATGATGATGATGATGAT 2365

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Db      590 TyrAlaGluProValLeuLeuProGlnProProProProAsnLysMet----- 605
QY      2366 GAACAAGTTTGGAAAAAGGGACCGAAACAACGTCGGCAAGGCCACATACCCAGGG 2425
Db      606 -----HisSerProLys 609
QY      2426 AACAGTAAACAATGGAAGCACTTACAAGAAAAATAAGAAAGGTAGAAACAGGAGGACC 2482
Db      610 AsnThrLeuArgLysProProMetHisGlnMetHisGlnGlyProAsnSerGluThr 628

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Search completed: March 8, 2005, 21:13:45  
 Job time : 169.5 secs

GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 8, 2005, 20:54:21 ; Search time 452.5 Seconds  
(without alignments)  
6131.370 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 4896  
Sequence: 1 aatctttttttatcatgatg.....aggcttttttttcttaataacc 2709

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cn2\_1/USPTO spoal\_p/US09774490/runat 08032005 140757 14842/app query.fasta\_1.2887  
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4201	85.8	771	1 SM3A_HUMAN	Q14563 homo sapien
2	4057.5	82.9	772	1 SM3A_RAT	Q63548 rattus norv
3	4035.5	82.4	772	1 SM3A_MOUSE	Q08665 mus musculu
4	3784.5	77.3	772	1 SM3A_CHICK	Q90607 gallus gall
5	3609.5	73.7	774	2 Q8JW9	Q8jiw9 xenopus lae
6	3207.5	65.5	778	1 S3AB_BRARE	Q9w686 brachydanio
7	3075.5	62.8	860	1 S3AA_BRARE	Q9w7j1 brachydanio
8	2258	46.1	777	2 Q8BH34	Q8bh34 m mus muscu
9	2252	46.0	777	2 Q8BMF6	Q8bm6 mus musculu
10	2247.5	45.9	777	1 SM3D_HUMAN	Q95025 homo sapien
11	2245.5	45.9	777	2 Q6UW77	Q6uw77 homo sapien
12	2245	45.9	761	1 SM3D_CHICK	Q90663 gallus gall
13	2125	43.4	764	1 SM3D_BRARE	Q9w696 brachydanio
14	2118	43.3	749	1 SM3B_HUMAN	Q13214 homo sapien
15	2059.5	42.1	748	1 SM3B_MOUSE	Q62177 mus musculu
16	2044	41.7	775	1 SM3E_HUMAN	Q15041 homo sapien

17	2030	41.5	775	2 Q9QX23	Q9qx23 mus musculu
18	2020	41.3	775	1 SM3E_MOUSE	P70275 mus musculu
19	2008.5	41.0	685	2 Q66KH4	Q66kh4 xenopus lae
20	2005.5	41.0	756	2 Q8QGU9	Q8qgu9 gallus gall
21	1993	40.7	785	1 SM3E_CHICK	Q42337 gallus gall
22	1940	39.6	785	1 SM3F_HUMAN	Q13275 homo sapien
23	1928	39.4	785	1 SM3F_MOUSE	Q88632 mus musculu
24	1894	38.7	751	1 SM3C_CHICK	Q42336 gallus gall
25	1862.5	38.0	751	2 Q6NXW7	Q6nxw7 mus musculu
26	1850.5	37.8	751	1 SM3C_MOUSE	Q62181 mus musculu
27	1849.5	37.8	751	1 SM3C_HUMAN	Q99585 homo sapien
28	1830	37.4	782	2 Q9NS98	Q9ns98 homo sapien
29	1765.5	36.1	725	2 Q7L9D9	Q7l9d9 homo sapien
30	1668	34.1	695	2 Q6DFQ0	Q6dfq0 xenopus tro
31	1662	33.9	591	2 Q7SM97	Q7sm97 homo sapien
32	1653	33.8	695	2 Q6PF60	Q6pf60 xenopus lae
33	1639	33.5	301	2 Q8GJ2	Q8gj2 homo sapien
34	1606	32.8	574	2 Q6ZQD8	Q6zqd8 mus musculu
35	1570	32.1	287	2 Q7SMQ2	Q7smq2 homo sapien
36	1516.5	31.0	573	2 Q6PI51	Q6pi51 homo sapien
37	1271.5	26.0	268	2 Q75PK9	Q75pk9 oryzias lat
38	1176.5	24.0	457	2 Q9HBR1	Q9hbr1 homo sapien
39	1139.5	23.3	403	2 Q8BKQ6	Q8bkq6 mus musculu
40	1080	22.1	296	2 Q9J129	Q9j129 rattus norv
41	1048.5	21.4	830	2 Q6NRA4	Q6nra4 xenopus lae
42	1010	20.6	861	2 Q6GTM9	Q6gtm9 mus musculu
43	1003	20.5	861	1 SM4D_MOUSE	Q09126 mus musculu
44	981.5	20.0	862	1 SM4D_HUMAN	Q92854 homo sapien
45	976.5	19.9	799	2 Q8BJC1	Q8bjc1 mus musculu

## ALIGNMENTS

RESULT 1  
SM3A\_HUMAN  
ID SM3A\_HUMAN STANDARD; PRT; 771 AA.  
AC Q14563;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Semaphorin 3A precursor (Semaphorin III) (Sema III).  
GN Name=SEMA3A;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=94094332; PubMed=8269517;  
RA Kolodkin A.L., Matthes D.J., Goodman C.S.;  
RT "The semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules..";  
RL Cell 75:1389-1399(1993).  
RN [2]  
RP SEQUENCE OF 1-37 FROM N.A.  
RA Woessner J., Minx P., Hinds K., Stromatt C.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBSJ databases.  
RN [3]  
RP SEQUENCE OF 39-182 FROM N.A.  
RA Rohlfing T., Tin-Wollam A.M., Duckels G.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBSJ databases.  
CC -!- FUNCTION: Induces the collapse and paralysis of neuronal growth cones. Could serve as a ligand that guides specific growth cones by a motility-inhibiting mechanism. Binds to the complex neuropilin-1/plexin-1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy third of the protein.  
CC -!- SIMILARITY: Belongs to the semaphorin family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 Sema domain.



QY 1640 ACAGTTTTCGGGAACCGCTGCTATTTCAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699  
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATTGGTTCAACGGCTGGGTTGCCAGCTCCCTTACACGGGTGCTATTTAC 1759  
 Db 501 LeuTyrlleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
 QY 1760 GGGAAACGCTGCTGAGTGTTCCTCGCCCGCAGACCTTACTGTCTTGGATGCTTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaIleArgGln 540  
 QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGAGCAGCAGCAAGATATAAGAAAT 1879  
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCCACTGACTGCTTACAGCTTACAGCTTACAGCTTACAGCTTACAGCTTAC 1939  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580  
 QY 1940 GAAGAGAGATCATCTATGCTGTAGAGATAGTAGCACATTTTGAATGCCAGTCCGAG 1999  
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
 QY 2000 TCGCAGAGAGCGCTGCTTATTTGGCAATTCAGAGCGCAATTCAGAGCGCAATTCAG 2059  
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGlu 620  
 QY 2060 ATCAGAGTGCATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTACAA 2119  
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeu 640  
 QY 2120 CAGAAGGATTACAGCAATTTACCTTCCCATGGTGGTGAACATGGTTCATACAACTCT 2179  
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThr 660  
 QY 2180 CTTAAGGTAAACCTGGAAGTCTTATTCAGCAGAGCAATTTGGAAGAACTTCTTCA 2239  
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680  
 QY 2240 GATGATGGAGATGGCTTAAAGCAACCAAGAAATGTCCATAGCATGACCTAGCAGAG 2299  
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGln 700  
 QY 2300 GTCGTGTACAGAGCTTCATGCTGAGCTCATCAACCCCACTCAACACGATGATGAG 2359  
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAsp 720  
 QY 2360 TTCTGTGAACAAGTTTGGAAAGGGACCGCAACCAACGTCGCAAGGCCAGGACATACC 2419  
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
 QY 2420 CAGGGAAACAGTAACAATGGAAGCCTTACAGAAATAAGAAAGGTGAACAGGAGG 2479  
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArg 760  
 QY 2480 ACCCAGGAATTCAGAGGCGCCCGAGGAGTCTC 2512  
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2

SM3A\_RAT  
 ID SM3A\_RAT STANDARD; PRT; 772 AA.  
 AC Q63548;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Semaphorin 3A precursor (Semaphorin III) (Sema III).  
 GN Name:Sema3a;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;

[1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Wistar; TISSUE=Brain;  
 RX MEDLINE=97073089; PubMed=8915837;  
 RX DOI=10.1002/(SICI)1096-9861(199611)375:3<378::AID-CNE33>3.0.CO;2-#;  
 RA Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaagen J.;  
 RT "Anatomy of rat semaphorin III/collapsin-1 mRNA expression and  
 relationship to developing nerve tracts during neuroembryogenesis.";  
 RL J. Comp. Neurol. 375:378-392(1996).  
 CC -!- FUNCTION: May be involved in guiding growing axons towards their  
 targets by forming a molecular boundary that instructs axons to  
 engage in the formation of specific nerve tracts. Binds to  
 neuropilin.  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- DEVELOPMENTAL STAGE: At E11, expression was restricted to the  
 olfactory pit, the basal and rostral surface of the telencephalic  
 vesicle, the eye anlage, the epithelium of rathe's pouch, and  
 somites. At later developmental stages, it was widely distributed  
 in neuronal as well as in mesenchymal and epithelial structures  
 outside the nervous system. After birth, mesenchymal levels  
 decreased rapidly and expression became restricted to specific  
 sets of neurons in the CNS. In the mature CNS, it is detectable in  
 mitral cells, neurons of the accessory bulb and cerebral cortex,  
 cerebellar purkinje cells, as well as a subset of cranial and  
 spinal motoneurons.  
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy  
 third of the protein.  
 CC -!- SIMILARITY: Belongs to the semaphorin family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 1 Sema domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 modified and this statement is not removed. Usage by for commercial  
 entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL, X95286; CAA64607.1; -;  
 DR RGD; 3657; Sema3a.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003659; Plexin-like.  
 DR InterPro; IPR002165; Plexin\_repeat.  
 DR InterPro; IPR001627; Sema.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF01403; Sema; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00423; PSI; 1.  
 DR SMART; SM00630; Sema; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 DR PROSITE; PSS1004; SEMA; 1.  
 KW Developmental protein; Glycoprotein; Immunoglobulin domain;  
 KW Multigene family; Neurogenesis; Signal.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 21 772 Semaphorin 3A.  
 FT DOMAIN 31 514 Sema.  
 FT DOMAIN 577 665 Ig-like C2-type.  
 FT DOMAIN 728 770 Arg/Lys-rich (basic).  
 FT DISULFID 650 723 By similarity.  
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 125 125 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 772 AA; 8808 MW; 240907812FF9F2D2 CRC64;

Alignment Scores:

Pred. No.:	0	Length:	772
Score:	4057.50	Matches:	740
Percent Similarity:	98.58%	Conservative:	21
Best Local Similarity:	95.85%	Mismatches:	10
Query Match:	82.87%	Indels:	1
DB:	1	Gaps:	1

US-09-774-490-1 (1-2709) x SM3A_RAT (1-772)	Db	341	CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp	360
200 ATGGCGTGTAACTAGGATGTCTGCTTTCTGGGAGTATTACTTACACGAAGCA	QY	1280	GGACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCACGGCAGAACT	1339
1 MetGlyTrpPheThrGlyIleAlaCysLeuPheTrpGlyIleLeuLeuThrAlaArgAla	Db	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGCTGAAATATCTCCACAAAGAAATGTTG	QY	1340	TGTCACGACAAAACAAATTTGGTGGTTTGTCTCTACAAAGGACCTTCTCGATGATGTTATA	1399
21 AsnTyrAlaAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	Db	381	CysProSerLysThrPheGlyPheAspSerThrLysAspLeuProAspAspValIle	400
320 GAATCCAAAGTGTATCTCTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATCCTTC	QY	1400	ACCTTTGCAAGAGTCATCCAGCCATGACCAATCCAGTGTTCCTTATGAACAATCGCCCA	1459
41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	Db	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProIleAsnAsnArgPro	420
380 CTTTGGATGAGGAACGGAGTAGGTGTATGTTGGAGCAAGAAAGATCATATTTTCATTC	QY	1460	ATAGTGATCAAAACCGGATGTAATATCAATTTTACAAATTTGTCTGAGACCGAGTGGAT	1519
61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	Db	421	IleMetIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
440 GACCTGTTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGCA	QY	1520	GCAGAAGATGACAGTATGATGTTTATGTTATTCGGAACAGATGTTGGGACCGTCTTTAAA	1579
81 AsnLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	Db	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
500 GATGAATGCAAGTGGCTCGAAAGACATCTCTGAAAGAAATGTCTTAATTTTCATCAAGGTA	QY	1580	CTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGAAGAAATG	1639
101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	Db	461	ValValSerValProLysGluThrTrpHisAspLeuGluGluValLeuLeuGluMet	480
560 CTTAAGGCATATAATCAGACTCACCTGTAGCGCTGTGGAAACGGGGCTTTTTCATCAATT	QY	1640	ACAGTTTTTTCGGAAACCGACTGCTATTTTTCAGCAATGGAGCTTTCACATAAGCAGCAACA	1699
121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	Db	481	ThrValPheArgGluProThrThrIleSerAlaMetGluLeuSerThrLysGlnGln	500
620 TGCACTACATTAATGCAATCTCTGAGGCAATATTTTAAAGCTGGAGAACTCA	QY	1700	CTATATATTTGTTCAACGGCTGGGTGCTCCAGGCTCCCTTTACACGGTGTGATTTTAC	1759
141 CysThrTyrIleGluValGlyHisProGluAspAsnIlePheLysLeuGlnAspSer	Db	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr	520
680 CATTGTAAGAACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGATCCCTT	QY	1760	GGAAAGCGTGTCTGAGTGTGCTCCGCGAGACCTTACTGCTGCTGGATGGTCT	1819
161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	Db	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer	540
740 TTAATAGATGGAATTAATCTCTGAACTGGAGCTGATTTTATGGGGAGACTTGTCT	QY	1820	GCATCTTCTCGCTATTTTCCCACTGCAAGAGACGACACAAGACGACAAGATAAAGAAAT	1879
181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	Db	541	SerCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn	560
800 ATCTTCGCAACTCTTGGGCACCAACCAATCAGACAGACAGCATGATTTCCAGGTGG	QY	1880	GGAGACCACTGACACTGTTTCAGACTTA --- CACCATGATAATCAACATGCCACACAGC	1936
201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp	Db	561	GlyAspProLeuThrHisCysSerAspLeuGlnHisHisAspAsnHisGlyHisSer	580
860 CTCATGATCCAAAGTTTATAGTGCCTCATCTCTCAGAGAGTGACAATCTCGAGAT	QY	1937	CCTGAAGAGAGAAATCATCTATGCTGAGAGATACTAGCACATTTTTCGAATGCAGTCCG	1996
221 LeuAsnAspProArgPheIleSerAlaHisLeuIleProGluSerAspAsnProGluAsp	Db	581	LeuGluGluLysGlyIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerPro	600
920 GACAAAGTATCTTTTCTTCCTGGAATGCAATAGATGGAGAACACTCTGGAAGCT	QY	1997	AACTCGCAGAGACCGCTGCTCTATTGGCAATTTCCAGAGCGCAAAATGAAAGCGAAAGAA	2056
241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGlyHisSerGlyLysAla	Db	601	LysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluAspArgLysGlu	620
980 ACTCAGCTAGATAGTCTAGATATCAAGAAATGACTTTGGAGGGCAGCAAGTCTGGTG	QY	2057	GAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTCTA	2116
261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal	Db	621	GlulIleArgValGlyAspHisIleIleArgThrGluGlnGlyLeuLeuLeuArgSerLeu	640
1040 AATAAGTGAACAACATCTCTCAAGCTCGTCTGATTTGTCAGTGCAGGTCAAATGGC	QY	2117	CAACAGAGGATTCAGGCAATTTACCTCTGCATCGGTGGACATGGGTTCATACAAACT	2176
281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	Db	641	GlnLysLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheMetGlnThr	660
1100 ATTGACACTCATTTCATGAGTGTAGTGTATTCCTAATGAACCTTAAAGATCTCTAAA	QY	2177	CTTCTTAAGGTAAACCTCGAAGTCAATGACACAGAGCAATTTTGGAAAGAACTTCTTCAAAA	2236
301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnSerLysAspProLys	Db	661	LeuLeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLys	680
1160 AATCAAGTTGTATTCGAGTGTTTTACGATCTTCAGTAAACATTTTCAAGGGATCAGCCGTG	QY	2237	GATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCATAGATGACCTAGTCCAG	2296
321 AsnProIleValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	Db	681	AspAspAspGlyAspGlySerLysThrLysGluMetSerSerSerMetThrProSerGln	700
1220 TGTATGTATAGCATGATGTGAGAGGGTGTCTTCTGGTCCATATGCCACACGGAT	QY	2297	AGGCTCTGGTACAGAGCTTCATGCTCAGCTCATCAACCCCACTCAACAGCATGGAT	2356
	Db	701	LysValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAsp	720



QY 2357 GAGTTCGTGAACAAGTTTGGAAAAGGACCGGAAACAAACGTCGCGAAAGGCCAGGACAT 2416  
 |||||  
 Db 721 GiuPheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHis 740  
 |||||  
 QY 2417 ACCCCAGGACAGTAAACAAATGGAAGCAGCTTACAGAAATAAGAAAGTAAACAGG 2476  
 |||||  
 Db 741 SerGlnGlySerSerAsnLysTrpLysHisMetGlnGluSerLysLysGlyArgAsnArg 760  
 |||||  
 QY 2477 AGGACCACAGCAATTTGAGAGGCGCCAGGAGTGTC 2512  
 |||||  
 Db 761 ArgThrHisGluPheGluArgAlaProArgSerVal 772  
 |||||  
 RESULT 3  
 SM3A\_MOUSE  
 ID SM3A\_MOUSE STANDARD; PRT; 772 AA.  
 AC 008665; Q622180; Q62215;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Semaphorin 3A precursor (Semaphorin III) (Sema III) (Semaphorin D) (Sema D).  
 GN Name=Sema3a; Synonyms=SEMA3, SemD;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NR1; TISSUE=Embryo;  
 RX MEDLINE=95267431; PubMed=7748561; DOI=10.1016/0896-6273(95)90332-1;  
 RA Puschel A.W., Adams R.H., Betz H.;  
 RT "Murine semaphorin D/collapsin is a member of a diverse gene family  
 and creates domains inhibitory for axonal extension.";  
 RL Neuron 14:941-948(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97470885; PubMed=9331345; DOI=10.1016/S0896-6273(00)80368-2;  
 RA Taniguchi M., Yuasa S., Fujisawa H., Naruse I., Saga S., Mishina M.,  
 RA Yagi T.;  
 RT "Disruption of semaphorin III/D gene causes severe abnormality in  
 peripheral nerve projection.";  
 RL Neuron 19:519-530(1997).  
 RN [3]  
 RP SEQUENCE FROM M.A.  
 RA Kimura T., Fishman M.C.;  
 RT "cDNA sequence of mouse collapsin/semaphorin III.";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ Databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McQuinn P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez J.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]

RP SEQUENCE OF 107-772 FROM N.A.  
 RX TISSUE=Fetal brain;  
 RC MEDLINE=95267432; PubMed=7748562; DOI=10.1016/0896-6273(95)90333-X;  
 RA Messersmith E.K., Leonardo E.D., Shatz C.J., Tessier-Lavigne M.,  
 RA Goodman C.S., Kolodkin A.L.;  
 RT "Semaphorin III can function as a selective chemorepellent to pattern  
 sensory projections in the spinal cord.";  
 RL Neuron 14:949-959(1995).  
 CC -!- FUNCTION: Plays a role in growth cones guidance. May function to  
 pattern sensory projections by selectively repelling axons that  
 normally terminate dorsally.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DEVELOPMENTAL STAGE: Expressed early in embryonic development  
 (E11) in distinct regions of the neuroectoderm and mesoderm.  
 CC Expression became more extensive at later stages.  
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy  
 third of the protein.  
 CC -!- SIMILARITY: Belongs to the semaphorin family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 1 Sema domain.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X85993; CAA59985.1; -;  
 DR EMBL; D85028; BAAL19773.1; -;  
 DR EMBL; L41541; AAL7761.1; -;  
 DR EMBL; BC057588; AAH57588.1; -;  
 DR EMBL; L40484; AAA73934.1; -;  
 DR PIR; I48747; I48747.  
 DR PIR; I58169; I58169.  
 DR MGD; MGI:107558; Sema3a.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR002165; Plexin\_repeat.  
 DR InterPro; IPR001627; Sema.  
 DR Pfam; PF00047; igf\_1.  
 DR Pfam; PF01403; Sema; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS51004; SEMA; 1.  
 KW Developmental protein; Glycoprotein; Immunoglobulin domain;  
 KW Multigene family; Neurogenesis; Signal.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 21 772 Semaphorin 3A.  
 FT DOMAIN 31 514 Sema.  
 FT DOMAIN 579 665 Ig-like C2-type.  
 FT DOMAIN 728 770 Arg/Lys-rich (basic).  
 FT DISULFID 650 723 By similarity.  
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 125 125 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 193 193 D -> N (in Ref. 5).  
 FT CONFLICT 207 207 H -> D (in Ref. 1).  
 FT CONFLICT 253 253 D -> G (in Ref. 1).  
 FT CONFLICT 352 352 F -> L (in Ref. 5).  
 FT CONFLICT 403 403 A -> G (in Ref. 1).  
 FT CONFLICT 571 572 QH -> ED (in Ref. 1).  
 FT CONFLICT 616 620 EDRKE -> RRSKR (in Ref. 1).  
 FT CONFLICT 623 623 R -> K (in Ref. 5).  
 SQ SEQUENCE 772 AA; 88799 MW; E89A0852B10AEC3 CRC64;  
 Alignment Scores:  
 Pred. No.: 0 Length: 772  
 Score: 4035.50 Matches: 737  
 Percent Similarity: 98.32% Conservative: 22  
 Best Local Similarity: 95.47% Mismatches: 12  
 Query Match: 82.42% Indels: 1  
 DB: 1 Gaps: 1

US-09-774-490-1 (1-2709) x SM3A\_MOUSE (1-7772)

QY 200 ATGGGCTGTTAACTAGGATGCTGCTCTTTCTGGGAGTATTACTTACAGCAAGACA 259  
 Db 1 MetGlyTrpPheThrGlyIleAlaCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20  
 QY 260 AACTATCAGAATGGGAAGAACCAATGTGCCAAGGCTGAAATTTATCCTACAAAGAAATGTTG 319  
 Db 21 AsnTyrAlaAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40  
 QY 320 GAATCCACAATGTGATCACTTTCAATGCTTGGCCACACAGCTCCAGTTATCATCACTTC 379  
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
 QY 380 CTTTGGATGAGAAAGGAGTGGTGTATGTTGGAGCAAGATCACATATTTTCATTC 439  
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80  
 QY 440 GACCTGGTTTAATCAAGGATTTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGAAGA 499  
 Db 81 AsnLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100  
 QY 500 GATGAATGCAATGGGCTGGAAAAGACATCCTGAAAGATGTGCTAAATTTCAATCAAGTGA 559  
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120  
 QY 560 CTTAAGGCATATAATCAGACTCACCTGTAGCTGTGGAAAGGGGCTTTTCATCCAATT 619  
 Db 121 LeuGluAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140  
 QY 620 TGCACCTCATATTGAAATGGACATCATCTCTGAGCAATATTTTAAAGTGGAGAACTCA 679  
 Db 141 CysThrTyrIleGluValGlyHisProGluAspAsnIlePheLysLeuGlnAspSer 160  
 QY 680 CATTTGAAAAGCGCGTGGAGAGTCCATATGACCTTAAGCTGCTGACAGATCCCTT 739  
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180  
 QY 740 TTAATAGATGGAGATTACTCTGGAAGTGGAGTGGATTTTATGGGGAGACTTTGCT 799  
 Db 181 LeuIleAspGlyLeuLeuTyrSerGlyThrAlaAlaAspPheMetCylArgAspPheAla 200  
 QY 800 ATCTTCCGAACCTCTGGGCACCACCAATCAGGACAGACAGCATGATTCAGAGTGG 859  
 Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220  
 QY 860 CTCATATGATCCAAAGTTCATATGATGCTCCCATCTCATCTCAGAGATGACATCTGAAGAT 919  
 Db 221 LeuAsnAspProArgPheIleSerAlaHisLeuIleProGluSerAspAsnProGluAsp 240  
 QY 920 GACAAAGTATCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGAAAGCT 979  
 Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
 QY 980 ACTCAGCTAGATAGCTCAGATATGCAAGAATGACTTTGGAGGGCAGCAAGTCTGGTG 1039  
 Db 261 ThrHisAlaArgIleGlyGlnCysLysAsnAspPheGlyHisArgSerLeuVal 280  
 QY 1040 AATAATGACAAATCTCCTCAAGCTCGTCTGATTTGCTCAGTGCAGGCTCAAAATGGC 1099  
 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
 QY 1100 ATTGACACATTTTCATGACTGCAAGGATGATTTCTTAATGAATTTAAAGATCCTAAA 1159  
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnSerLysAspProLys 320  
 QY 1160 AATCCAGTTGATATGAGTGTTCAGCTTCCAGTAAACATTTTCAAGGGATCAGCCGTG 1219  
 Db 321 AsnProIleValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
 QY 1220 TGATGCTATAGCATGATGAGAGAGGCTGCTTCTGGTCCATATGCTCCACAGGAT 1279  
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360

QY 1280 GGACCCAACTATCAATGGTGCCTTTATCAAGGAAGAGTCCCTATCCACGGCCAGAACT 1339  
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
 QY 1340 TGTCCACACAAAACATTTGGTGGTTTCACTCTACAAAGGACCTTCTCTGATGATGTTATA 1399  
 Db 381 CysProSerLysThrPheGlyPheAspSerThrLysAspLeuProAspAspValIle 400  
 QY 1400 ACCTTTGCAAGAAGTCATCCAGGCATGACCAATCCAGTGTTCCTATCAACAATCGCCCA 1459  
 Db 401 ThrPheAlaArgSerHisProAlaMetLysAsnProValPheProIleAsnAsnArgPro 420  
 QY 1460 ATAGTGATCAAAACCGGATGTAATTTATCAAAATTTTACAAAATTTGCTGAGACCGAGTGGAT 1519  
 Db 421 IleMetIleLysThrAspValAsnTyrGlnPheThrGlnIleValIleAspArgValAsp 440  
 QY 1520 GCAGAAGATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579  
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
 QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATGATGATGATGATGATGATGATGATGATGAT 1639  
 Db 461 ValValSerValProLysGluThrHisAspLeuGluValLeuLeuGluGluMet 480  
 QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTTACCAATGGAGCTTTCACATTAAGCAGCAACAA 1699  
 Db 481 ThrValPheArgGluProThrThrIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATGTTTCAACGGCTGGGTGCGCAGCTCCCTTTACACCGGTGATATTTAC 1759  
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
 QY 1760 GGGAAAGCGTGTGAGTGTGCTGCGCGAGACCTTACTGCTGCTGGATGCTTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
 QY 1820 GCATCTTCTCGCTATTTTCCCACTCAAGAGACGACACAGCAAGCAAGATATAAGAAAT 1879  
 Db 541 SerCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCACTGACTGACTGTTTACACTTA---CACCATGATTAATCACCATGCCACAGC 1936  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuGlnHisHisAspAsnHisHisGlyProSer 580  
 QY 1937 CCTGAAGAGAGAAATCATCTATGCTGTAGAGATAGTAGCACATTTTGGAAATGCACTCG 1996  
 Db 581 LeuGluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerPro 600  
 QY 1997 AAGTCGACAGAGCGCTGCTTATTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAAGAA 2056  
 Db 601 LysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluAspArgLysGlu 620  
 QY 2057 GAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTCTA 2116  
 Db 621 GluIleArgMetGlyAspHisIleIleArgThrGluGlnGlyLeuLeuLeuArgSerLeu 640  
 QY 2117 CAACAGAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAATGGAATGGGTTCATACAACT 2176  
 Db 641 GlnLysLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheMetGlnThr 660  
 QY 2177 CTTCTTAAGGTTAACCTCGGAGTCAATTCACACAGAGCATTTTGGAAAGAACTTCTTCAATAA 2236  
 Db 661 LeuLeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLys 680  
 QY 2237 GATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAG 2296  
 Db 681 AspAspAspGlyAspGlySerLysIleLysGluMetSerSerSerMetThrProSerGln 700  
 QY 2297 AAGTCTGTGTACAGAGACTTCATGAGCTCATCAACCCCACTCATCAACAGATGGAT 2356  
 Db 701 LysValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAsp 720

QY 2357 GAGTCTGTGCAACAGTTTGGAAAGGCGGAAACACAGCTCGGCAAGGCCAGGACAT 2416  
 DB 721 GluPheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHis 740  
 QY 2417 ACCCCAGGAGCAAGTAAACAAATGGAACACTTACAAGAAATTAAGAAAGTACAAACAGG 2476  
 DB 741 SerGlnGlySerSerAsnLysTrpLysHisMetGlnGluSerLysLysGlyArgAsnArg 760  
 QY 2477 AGGACCCAGCAATTTGAGAGGCGCACCCAGGAGTGT 2512  
 DB 761 ArgThrHisGluPheGluArgAlaProArgSerVal 772

RESULT 4  
 SM3A\_CHICK  
 ID SM3A\_CHICK STANDARD; PRT; 772 AA.  
 AC Q90607;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Semaphorin 3A precursor (Collapsin-1) (COLL-1).  
 GN Name=SEMA3A; Synonyms=COLL1;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 322-329; 362-372; 395-403 AND 666-680.  
 RX TISSUE=Brain;  
 RA MEDLINE=94006554; PubMed=8402908;  
 RA Luo Y., Rable D., Raper J.A.;  
 RT "Collapsin: a protein in brain that induces the collapse and paralysis of neuronal growth cones.";  
 RL Cell 75:217-227(1993).  
 CC -!- FUNCTION: Induces the collapse and paralysis of neuronal growth cones. Could serve as a ligand that guides specific growth cones by a motility-inhibiting mechanism. Binds to neuropilin.  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- TISSUE SPECIFICITY: Expressed at relatively high levels in brain and muscle, moderate levels in lung, bursa, and heart and virtually absent in liver. Collapsin-1, -2, -3, and -5 bind to overlapping but distinct axon tracts.  
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy third of the protein.  
 CC -!- SIMILARITY: Belongs to the semaphorin family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 1 Sema domain.

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 CC EMBL; U02528; AAC59638.1; --  
 DR PIR; A49069; A49069.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003659; plexin-like.  
 DR InterPro; IPR002165; plexin\_repeat.  
 DR InterPro; IPR001627; Sema.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00403; Sema; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00423; PSI; 1.  
 DR SMART; SM00630; Sema; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS51004; SEMA; 1.  
 DR Developmental protein; Direct protein sequencing; Glycoprotein;  
 KW Immunoglobulin domain; Multigene family; Neurogenesis; Signal.

FT SIGNAL 1 22 Potential.  
 FT CHAIN 23 772 Semaphorin 3A.  
 FT DOMAIN 31 514 Sema.  
 FT DOMAIN 576 665 IG-like C2-type.  
 FT DOMAIN 728 770 Arg/Lys-rich (basic).  
 FT DISULFID 650 723 By similarity.  
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 125 125 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 772 AA; 88867 MW; E91E09DE0CC940AC CRC64;

Alignment Scores:  
 Pred. No.: 8,74e-297 Length: 772  
 Score: 3784.50 Matches: 683  
 Percent Similarity: 95.34% Conservative: 53  
 Best Local Similarity: 88.47% Mismatches: 35  
 Query Match: 77.30% Indels: 1  
 DB: 1 Gaps: 1

US-09-774-490-1 (1-2709) x SM3A\_CHICK (1-772)

QY 200 ATGGGCTGTTAACTAGGATTCTGTCTTTCTGGGAGTATTACTTACAGCAAGCA 259  
 DB 1 MetGlyTrpLeuArgGlyIleAlaLeuSerLeuGlyValLeuLeuAlaGlyArgVal 20  
 QY 260 AACTATCAGAATGGGAAGAACAAATGTCCAAGCTGAAATTTATCTTACAAAGAAATGTTG 319  
 DB 21 AsnCysGlnHisValLysAsnValProArgLeuLysLeuSerTyrlsGluMetLeu 40  
 QY 320 GAATCCACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATCTTC 379  
 DB 41 GluSerAsnAsnIleValAsnPheAsnGlyLeuAlaAsnSerSerSerTyrlsHisThrPhe 60  
 QY 380 CTTTGGATGACGACGAGTAGGTGTATGTTGGAGCAAGAGTACACATATTTTCATTC 439  
 DB 61 LeuLeuAspGluGluArgSerArgLeuTyrlsValGlyAlaLysAspHisIlePheSerPhe 80  
 QY 440 GACCTGGTTTAAATCAAGGATTTTCAAAAGATTTGTGTGCCAGTATCTTACACCAAGA 499  
 DB 81 AsnLeuValAsnIleLysGluTyrlsGlnLysIleValTrpValSerHisSerArgArg 100  
 QY 500 GATGAATGAATGGGCTGGAAAGACATCTCTGAAGAAATGCTGAATTTTCATCAAGTTA 559  
 DB 101 AspGluCysLysTrpAlaGlyLysAspIleLeuArgGluCysAlaAsnPheIleLysVal 120  
 QY 560 CTTAAGGCATATAATCAGACTCCTGTACGCTGTGGAACGGGGCTTTTCATCAAT 619  
 DB 121 LeuLysThrTyrlsAsnGlnThrHisLeuTyrlsAlaCysGlyThrGlyAlaPheHisProMet 140  
 QY 620 TGCACCTACATTAATGAATTCATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 679  
 DB 141 CysThrTyrlsGluValGlySerHisProGluAspAsnIlePheArgMetGluAspSer 160  
 QY 680 CATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTGTGTGACAGCATCCCTT 739  
 DB 161 HisPheGluAsnGlyArgGlyLysSerProTyrlsAspProLysLeuLeuThrAlaSerLeu 180  
 QY 740 TTAATAGATGGAGAAATTATCTCTGAACTGAGCTGATTTTATGGGGAGACTTTGCT 799  
 DB 181 LeuValAspGlyGluLeuTyrlsSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
 QY 800 ATCTTCCGAACCTCTTGGGACCAACCAATCAGGACAGAGCATGATTTCCAGGTGG 859  
 DB 201 IlePheArgThrLeuGlyHisHisIlePheProLysIleArgThrGluGlnHisAspSerArgTrp 220  
 QY 860 CTCATATGATCCAAAGTTCAATTAGTGTCCACCTCATCTCTCAGAGAGTGACAAATCCTGAAGAT 919  
 DB 221 LeuAsnAspProArgPheIleSerAlaHisLeuIleProGluSerAspAsnProGluAsp 240  
 QY 920 GACAAAGTATATCTTTTCTTCGTTGAAATGAAATAGATGGAGAACACTCTCGAAGACT 979  
 DB 241 AspLysIleTyrlsPhePheArgGluAsnAlaIleAspGlyGluHisThrGlyLysAla 260

QY 980 ACTCAGCTAGATAGGTGAGATATGCAAGAAATGACTTTGGAGGCGCACAGAGTCTGGTG 1039  
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
 QY 1040 AATAAATGACAAATCTCTAAAGCTGCTGATTTGCTAGTCCAGGTCAAATGGC 1099  
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
 QY 1100 ATTGACACTCATTTGATGAACCTGAGGATGATTCCTAATCAATTTAAAGATCCTAAA 1159  
 Db 301 IleAspThrHisPheAspGlnLeuGlnAspValPheLeuMetCasnSerLysAspProLys 320  
 QY 1160 AATCAGATTGTATATGAGTGTATACGACTTCAGATAACATTTCAAGGGATCAGCCGTG 1219  
 Db 321 AsnProIleValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
 QY 1220 TGTATGTATAGATGATGTGAGAGGGTGTCTTGGTGTCCATATGCCACAGGGAT 1279  
 Db 341 CysMetTyrSerMetThrAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360  
 QY 1280 GGACCCAACTATCAATGGTGCCTTATCAAGGAGTCCCTATCCAGTCCAGGCGGCAACT 1339  
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
 QY 1340 TGTCCAGCAAAACATTTTGGTGGTGTGACTCTCAAAAGGAGCTTCTGATGATGTATA 1399  
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspGluValIle 400  
 QY 1400 ACTTTGCAAGAGTATCCAGCCATGTACATCCAGTGTTCCTATGAAATCAATCCGCA 1459  
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProIleAsnSerArgPro 420  
 QY 1460 ATATGATCAAAACCGATTAATATCAATTTACAAATTTGCTGAGACCGAGTGGAT 1519  
 Db 421 IleMetIleLysThrAspValAspTyrGlnPheThrGlnIleValValAspArgValAsp 440  
 QY 1520 CGAAGAGTGGACAGTATGATGTATGTTTATCGGAACAGATGTGGGACCGTCTTAAA 1579  
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspIleGlyThrValLeuLys 460  
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAAAGAGTTCCTGCGAAGAAATG 1639  
 Db 461 ValValSerIleProLysGluThrTrpHisGluLeuGluValLeuLeuGluMet 480  
 QY 1640 ACAGTTTTTCGGGACCGACTGCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699  
 Db 481 ThrValPheArgGlnProThrValIleSerAlaMetLysIleSerThrLysGlnGln 500  
 QY 1700 CTATATATTGGTTCAACGGCTGGGTGGCCAGCTCCCTTTACACGGGTGATATTAC 1759  
 Db 501 LeuTyrIleGlySerAlaThrGlyValSerGlnLeuProLeuHisArgCysAspValTyr 520  
 QY 1760 GGGAAAGCTGTGCTGAGTGTGCTGCTGCGCCAGACCTTACTGTGCTGGATGTTCT 1819  
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540  
 QY 1820 GCATGTTCTCGTATTTTCCCTGCAAGAGCGCACAGCGCAAGATATAGAAAT 1879  
 Db 541 SerCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560  
 QY 1880 GGAGACCCACTGACTCACTGTTCCAGACTTAA--CACCATGATAATCACCATGCCACAGC 1936  
 Db 561 GlyAspProLeuThrHisCysSerAspLeuGlnHisHisAspAsnProSerGlyGlnThr 580  
 QY 1937 CCTGAAGAGAGAAATCATCTGCTGTAGAGATATAGTACACATTTTGGAAATGCGTCCG 1996  
 Db 581 LeuGluGluLysIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerPro 600  
 QY 1997 AGTCCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAAATCAAGAGCGCAAGAA 2056  
 Db 601 LysSerGlnArgAlaIleValTyrTrpGlnPheGlnLysGlnAsnAspHisLysVal 620  
 QY 2057 GAGATCAGAGTGGATCATATCATCAGGACAGATCAAGGCGCTTCTGCTAGCTAGTCTA 2116

Db 621 GluIleLysValAspArgMetIleArgThrGluGlnGlyLeuLeuLeuArgSerLeu 640  
 QY 2117 CAACAGAGGATTCAGGCAATTTACCTCTGCTCCTGCGGTGGAACTGGGTTCATACAACT 2176  
 Db 641 GlnArgArgSerGlyIleTyrPheCysHisAlaValGluHisGlyPheIleGlnThr 660  
 QY 2177 CTTCTTAAGGTAAACCTCGAAAGTTCATTCACAGACAGACATTTTGGAAAGAACTTCTTCAAAA 2236  
 Db 661 LeuLeuLysValThrLeuGluValIleAspThrAspHisLeuGluGluLeuHisLys 680  
 QY 2237 GATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCATAGCATGACACCTAGCCAG 2296  
 Db 681 GluGluAspAlaAspAlaSerLysThrLysAspAlaThrAsnSerMetThrProSerGln 700  
 QY 2297 AAGTCTCTGTCACAGAGCTTCATGACGCTCATCAACACCCCACTCTCAACACGATGGAT 2356  
 Db 701 LysIleTyrTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAsp 720  
 QY 2357 GAGTCTCTGTCGAACAGTTTGGAAAGGACCGCAAAACAACTCGGCAAGGCCAGACAT 2416  
 Db 721 GluPheCysGluGlnValTyrLysArgAspArgLysGlnArgGlnArgProAlaAsn 740  
 QY 2417 ACCCCAGGGAACAGTAACAAATGGAGCATTACAGAAATATAGAAAGGTAGAAACAGG 2476  
 Db 741 AlaGlnValAsnThrAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArg 760  
 QY 2477 AGGACCCAGCAATTTGAGAGGCGCACCCAGGAGTGTCT 2512  
 Db 761 ArgThrHisGluPheGluArgAlaProArgSerVal 772  
 RESULT 5  
 OBJINS  
 ID Q8JTW9 PRELIMINARY; PRT; 774 AA.  
 AC Q8JTW9;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Semaphorin 3A.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Head;  
 RA Tannahill D., Nielsen J., Regan A.G.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY030051; AAK38166.1; -.  
 DR HSSP; Q92854; 1OLZ.  
 DR GO; GO:0016020; C.membrane; IEA.  
 DR GO; GO:0004872; F.receptor activity; IEA.  
 DR GO; GO:0007275; P.development; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR001005; Myb DNA binding.  
 DR InterPro; IPR003659; Plexin-like.  
 DR InterPro; IPR002165; Plexin\_repeat.  
 DR InterPro; IPR001627; Sema.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF01437; PSI; 1.  
 DR Pfam; PF01403; Sema; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00423; PSI; 1.  
 DR SMART; SM00630; Sema; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00037; MYB 1; UNKNOWN 1.  
 SQ SEQUENCE 774 AA; 89319 MW; 3127FD2E0CCD5FA4 CRC64;  
 Alignment Scores:  
 Pred. No.: 1.228-282 Length: 774  
 Score: 3609.50 Matches: 654

Percent Similarity:	93.67%	Conservative:	71
Best Local Similarity:	84.50%	Mismatches:	46
Query Match:	73.72%	Indels:	3
DB:	2	Gaps:	3
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QY	260	AACTATCAGAATGGGAAGAACATGTGCCAAGSCTGAAATATCTACAAAGAAATGTTG	319
DB	21	AsnCysGlnAsnValLysAsnAsnValProArgLeuArgLeuSerTyrLysGluMetVal	40
QY	320	GAATCCAAACATGTGATCTTCAATGGCTTGGCCCAACAGCTCCAGTATTATCATCTTC	379
DB	41	GluSerAsnAsnLeuIleThrPheAsnGlyTrpProAsnSerSerSerTyrAsnThrPhe	60
QY	380	CTTTGGATGAGAACGGAGTAGGCTGTATGTTGGAGCAAGATCACATATTTTCATTC	439
DB	61	ValLeuAspGluGluArgGlyArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGTTAAATATCAAGATTTTCAAAAGATGTGTGCCAGTATCTTACACCAGACA	499
DB	81	AsnLeuAlaAsnValLysGluPheGlnLysIleLeuTrpProValThrAsnIleArgArg	100
QY	500	GATGAATGCAAGTGGCTCGAAAAGACATCTCTGAAAGATGTGCTAAATTTCAAGGTA	559
DB	101	AspGluCysLeuTrpAlaGlyLysAspIleValLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATAATCAGACTCACTGTACGCTGTGGAACGGGGCTTTTCATCCAAT	619
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QY	620	TGCACCTACATTAATGGACATCATCTCTGAG---GACAAATTTTAAAGCTGAGAAC	676
DB	141	CysThrTyrIleAspValGlyHisTyrProGluGlnAspAsnValPheLysLeuGluAsp	160
QY	677	TCACATTTTGAACCGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGCATCC	736
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DB	201	AlaIlePheArgThrLeuGlyAsnHisHisProIleArgThrGluGlnHisAspSerArg	220
QY	857	TGGCTCAATGATCCAAAGTTTATTAGTGCACCTCATCTCAGAGAGTGACAAATCCTGAA	916
DB	221	TrpLeuAsnAspProArgPheIleGlyAlaTyrLeuValProGluSerAspAsnProGlu	240
QY	917	GATGACAAAGTACTTTTCTTCGCTGAAAATGCAATAGATGGAGAACACTCTCGAAA	976
DB	241	AspAspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisThrLysLys	260
QY	977	GCTACTCAGCTAGATAGGTGAGATATGCAAGAATGATTTTGGAGGGGACAGAGTCTG	1036
DB	261	AlaThrHisAlaArgIleGlyGlnLeuCysLysAsnAspPheGlyGlyHisArgSerLeu	280
QY	1037	GTGAATTAATGACACATCTCTCAAGCTCTCTGATTTGCTAGTCCAGGTCCTCAAT	1096
DB	281	ValAsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsn	300
QY	1097	GGCATTGACACTCATTTTTCATCAACTGCAAGGATGTATTCTCAATCAACTTTAAAGATCT	1156
DB	301	GlyIleAspThrHisPheAspGluLeuGlnAspValValLeuMetAsnSerLysAspPro	320
QY	1157	AAAAATCCAGTTGTATGGAGTGTATACGATTCAGCTTCCAGTAACTTTTCAAGGGATCAGCC	1216

DB	321	LysAsnProValValTyrAlaValPheThrThrSerSerAsnIlePheLysGlySerAla	340
QY	1217	GTGTGTATGTATAGCATGATGATGAGAGGGTGTCTCTTTGGTCCATATATCCACAGG	1276
DB	341	ValCysMetTyrSerLeuThrAspIleArgValPheLeuGlyProTyrAlaHisArg	360
QY	1277	GATGACCAACTATCAATGGTGCTTATTCAGGAAGAGTCCCTTATCCAGGCGCAGA	1336
DB	361	AspGlyProAsnTyrGlnTrpValProPheGlnGlyArgValProTyrProArgProGly	380
QY	1337	ACTTCTCCAGCAAAACATTTTGGTGGTGTGATCTACAAAGAGCTTCTCTGATGATGT	1396
DB	381	ThrCysProArgGlnThrPheGlyGlyPheAspSerThrLysAspLeuProAspGluVal	400
QY	1397	ATAACCTTTGCAAGAAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACATCGC	1456
DB	401	IleMetPheAlaArgSerHisProAlaMetTyrAsnProValPheProIleAsnAsnArg	420
QY	1457	CAATAGTGTATCAAAACCGATGTAATATCAATTTTACAAATTTGCTAGACCGAGTG	1516
DB	421	ProIleIleIleLysThrGluValAspTyrGlnPheThrGlnIleValValAspArgVal	440
QY	1517	GATGCAGAGATGGACAGTATGATGTATTCGGAACAGATGTGGGACCGTCTT	1576
DB	441	GluAlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspMetGlyThrIleLeu	460
QY	1577	AAAGTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGAAGAA	1636
DB	461	LysValValSerValProLysGluThrTrpThrAspLeuGluGluValLeuLeuGluGlu	480
QY	1637	ATGACAGTTTTCGGAAACCGACTGCTATTTACAGCAATGGAGCTTTCCTAAGCAGCAA	1696
DB	481	MetThrValPheArgGluProThrAlaIleSerAlaMetGluIleSerThrLysGlnGln	500
QY	1697	CAACTATATATGTTTCAACGGCTGGGCTGCCAGCTCCCTTTACACGGGTGTATATT	1756
DB	501	GlnLeuTyrIleGlySerSerValGlyValSerGlnLeuProLeuHisArgCysAspVal	520
QY	1757	TACGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGAGCCCTTACTGTGTTGGATGCT	1816
DB	521	TyrGlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGly	540
QY	1817	TCTGCATGTTCTCGCTATTTTCCCACCTCAAGAGACGCCAAGACGACAGATATAAGA	1876
DB	541	SerSerCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArg	560
QY	1877	AATGAGACCCACTGACTGACTGTTTCAGACTTA---CACCATGATAATCACCATGCCAC	1933
DB	561	AsnGlyAspProLeuThrHisCysSerAspLeuGlnHisGlnAspAspProHisArgGln	580
QY	1934	AGCCCTGAAGAGAGAAATCATCTATGCTAGAGAATAGTACACATTTTGGAAATGCAGT	1993
DB	581	SerLeuGluGluLysIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSer	600
QY	1994	CCGAAGTCGACAGAGCGCTGCTCTATTGGCAATTTCCAGAGCGCAAAATGAAGAGCAAAA	2053
DB	601	ProLysSerGlnArgAlaLeuValPheTrpGlnPheGlnLysGlnAsnGluGluLysLys	620
QY	2054	GAAGAGATCAGATGGATGATCATATCATCAGGACAGATCAAGCGCTCTCTGCTAGTGT	2113
DB	621	AspGluIleLysValAspGluArgLysIleLysThrGluHisGlyLeuLeuArgThr	640
QY	2114	CTACAACAGAGGATTCAGGCAATTTACCTCTGCCATCGGTGGACATGGGTTCATACAA	2173
DB	641	LeuLysLysArgAspSerGlyIleTyrTyrCysAsnAlaValGluHisGlyPheMetGln	660
QY	2174	ACTCTTCTTAAGGTAACCTCGAAATCATTCACACAGAGCATTTTGGAAAGAACTTCTCAT	2233
DB	661	ThrLeuLeuLysValThrLeuGluIleIleAspThrGluHisLeuAspGluLeuHis	680
QY	2234	AAAGATGATGAT---GGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACCT	2290
DB	681	LysGluAspGluGlyGlyAspSerHisLysHisLysGluProSerAsnSerMetSerPro	700





QY 974 AAAGCTACTCAGCTAGATAGTCTAGATATGCAAGAAATGACTTTGGAGGCGACAGAT 1033  
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QY 1034 CTGGTGAATAAATGGACAACATTCCTCAAGCTCGCTGATTTGCTCAGTGCAGGTCCA 1093  
Db 280 LeuValAsnLysTrpThrPheLeuLysAlaArgLeuValCysSerValProGlyLeu 299  
QY 1094 AATGGCAATGACACTCATTTTGTATGAACAGTGCAGATGTATTCTTAATGAACTTTAAAGAT 1153  
Db 300 AsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeuMetSerLysAsp 319  
QY 1154 CCTAAAATCCAGTGTATATGAGTGTTCAGACTTCCAGTCCAGTAACTTTCAAGGATCA 1213  
Db 320 ProLysAsnProIleIleTyAlaValPheThrThrSerSerAsnIlePheLysGlySer 339  
QY 1214 GCCGTGTATGATAGCATGAGTGTGAGAGGGTGTCTTCGTCCATATGCCAC 1273  
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QY 1274 AGGATGGACCCCAACTATCAATGGTGCCTTATCAAGGAGAGTCCCTTATCCAGGCCA 1333  
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QY 1334 GGAACCTGTCCAGCAAAACATTTGGTGTGTTTGTACTCTCAAGAGACCTTCTGTATGAT 1393  
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QY 1394 GTTATACCTTTGCAAGAGTCAATCCAGCATGATCAATCCAGTGTTCCTATGACAAAT 1453  
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Db 420 HisProIleIleIleLysThrAspValAspTyGlnPheThrGlnIleValValAspArg 439  
QY 1514 GTGGATGCAAGATGCAAGATGATGATGTTATGTTATCGGAACAGATGTGGACCGTT 1573  
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QY 1574 CTTAAAGTAGTTTCAATTCCTAAGGAGACTGTTGATGATTAGAACAGTTCCTCGTGA 1633  
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QY 1754 ATTTACGGAAACGCTGCTGAGTGTTCCTCGCCGAGACCTTACTGCTGCTGGAT 1813  
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QY 1814 GGTTCCTGCACTGTTCTCGCTATTTCCTGCAAGAGACGCAAGACAGCAAGATATA 1873  
Db 540 GlySerGlnCysSerArgTyrlPheProThrAlaLysArgArgThrArgGlnAspIle 559  
QY 1874 AGAAATGGAGACCCACTGACTCTCTCTCAGACTTA---CACCATGATAATCACCATGCC 1930  
Db 560 ArgAsnGlyAspProLeuThrGlnCysSerAspLeuGlnHisAspGluAlaAspGly 579  
QY 1931 CACAGCCCT---GAAAGAGATCATCTATGTTGTAGAGATAGTACCATTTTGGAA 1987  
Db 580 GluAlaGlyLeuLeuAspLysThrValTyrlGlyValGluAsnSerSerPheLeuGlu 599  
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QY 2048 CGAAAAAGAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTA 2107

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QY 2108 CTTAGTCTACAAACAGAGGATTTCAGCAATTAATCTCTGCTCGCTGGAACATGGTTC 2167  
Db 640 ArgSerLeuHisGlnLysAspSerGlyValTyrlTyrlCysHisAlaValGluHisGlyPhe 659  
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QY 2228 CTTTCAAGATGATCATGAGATGCTCTTAAGACCAAGAAATGTCCTAATAGCATGACA 2287  
Db 680 LeuHisArgAspPro-----ProAspThrAsnAspProAlaAsnGly----- 693  
QY 2288 CTTAGCCAGAGCTGTTACAGACACTTCATCGACTCATCAACACCCCAATCTCAAC 2347  
Db 694 -----LysMetTrpTyrlArgAspPheLeuSerLeuLeuAsnProProSerProAsn 710  
QY 2348 AGATGATGATGTTCTGTAACAAGTTTGGAAAGGACCGAAACAAACAGCTCGGAAAGG 2407  
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QY 2408 CCAGCA-----CATACCCCGAGGAAC 2428  
Db 731 AlaAsnLeuLeuHisAlaSerGlnSerHisThrSerGlnIleLeuHisSerGlnSer 750  
QY 2429 AGTAACTAATGAAGCAGCTTACAGAAATAAGAAAGGTAGAAACAGGAGGAGCCACGAA 2488  
Db 751 HisAlaLysTrpLysLeuLeuGlnGluAsnLysLysGlyArgAsnArgArgThrHisGlu 770  
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Db 771 MetGlnArgAlaProArgSerVal 778  
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ID S3AA BRARE AC Q9W7J1;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Semaphorin 3aa precursor (Semaphorin 1A) (Semaphorin 21A) (Sema-21A).  
GN Name=sema3aa; Synonyms=sema21a;  
OC Brachydanio rerio (Zebrafish)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=99313409; PubMed=10386838; DOI=10.1016/S0361-9230(99)00038-6;  
RA Yee C.S., Chandrasekhar A., Halloran M.C., Shoji W., Warren J.T.,  
RA Kuwada J.Y.;  
RT "Molecular cloning, expression, and activity of zebrafish semaphorin 21a."  
RL Brain Res. Bull. 48:581-593(1999).  
CC -!- FUNCTION: May influence outgrowth by a variety of growth cones including those of the posterior lateral line ganglion.  
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -!- DEVELOPMENTAL STAGE: Expressed in highly specific patterns within the developing embryo.  
CC -!- SIMILARITY: Belongs to the semaphorin family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 Sema domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)



or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

[illegible]

Alignment Scores:

Alignment Scores:		
Pred. No.:	1.85e-239	Length: 860
Score:	3075.50	Matches: 561
Percent Similarity:	76.73%	Conservative: 105
Best Local Similarity:	64.63%	Mismatches: 97
Query Match:	62.82%	Indels: 105
DB:	1	Gaps: 6

US-09-774-490-1 (1-2709) X S3AA BRARE (1-860)

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Qy		260	AACATCAGAATGGGAAGAACAACTGTGCCAAGGCTGAAATATCTCACAAAATAATGTG	319
Db		21	AlaProGlnHisThrLysGluAsnValProArgLeuLysLeuSerTyrAsnGluMetLeu	40
Qy		320	GAAATCCAACAATGTGCATCACTTTCAATGGCTTGGCCAACAGCTCCAGTTTTCATACCTTC	379
Db		41	GluSerSerAsnLeuValThrPheThrGlyLeuAlaAsnSerSerGlyTyrAspThrPhe	60
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Qy		440	GACCTGGTTAATATC---AAGATTTCAAAGATTGTGGCCAGTACTTTACACCAGA	496
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Qy		497	AGAGATGAATGCAAGTGGCTGGAAAGACATCTCGAAGAAATGTGCTTAATTTTCATCAAG	556
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Qy		557	GTACTTAAGGCATATAATCAGACTCACTTGTAAGCTGTGGAAACGGGGCTTTTCATCCA	616
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Qy		617	ATTTCACCTACATGAAATTCGACATCATCTCTGAGGACAAATATTTTTAAAGCTGGAGAAC	676
Db		141	IleCysSerPheLeuGluMetGlyLysArgAlaGluaspAsnIlePheArgLeuaspAla	160
Qy		677	TCACATTTTGAACCGCGCTGGGAAGAGTCCATATGACCCCTAAGCTGTGCAGCATCC	736

161	AsnTyrPheGluAsnGlyArgGlyLysSerProTyrAspProLysMetGlnSerSerSer	180
737	CTTTTAATAGATGGAGAATTATACTCTGGAACTGCAGCTGATTTTATGGGGCAGACTTTT	796
181	LeuLeuLeuAspGlyGluLeuTyrSerGlyThrSerAlaAspPheMetGlyArgAspPhe	200
797	GCTATCTTCGAACTCTTGGGCACACACCACCAATCAGGACAGACGACGATGATTCAGG	856
201	AlaIlePheArgThrLeuGlySerHisHisProIleArgThrGluGlnHisAspSerArg	220
857	TGGCTCAATGATCCAAAGTTTCATTAGTGGCCACTCATCTCAGAGAGTACAATCTCTGAA	916
221	TrpLeuAsnGluProArgPheLeuGlyIleHisLeuIleProGluSerAspAsnProGlu	240
917	GATGACAAAGTATATCTTTTCTTCGCTGAAAATGCAATAGATGAGAGAACTCTGGAAAA	976
241	AspAspLysIlePheLeuPhePheLysGluAsnAlaMetAspGlyGluHisThrGlyLys	260
977	GCTACTCACGCTAGAAATAGTCTAGATGACGAAGATGACTTTTGGAGGGCACAAGA	1036
261	AlaThrIleSerArgIleGlyGlnLeuCysLysAsnAspMetGlyGlyHisArgSerLeu	280
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1277	GATGCACCCAACTATCAATGGTGCTTATCAAGAAAGAGTCCCTATCCACGGCCAGGA	1336
361	AspGlyProAsnTyrGlnTrpValProPheGlnGlyArgValProTyrProArgProGly	380
1337	ACTTGTCCCGACAAAACATTTGGTGGTTTTGACTCTACAAAGGACCTTCTGTATGATGTT	1396
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1397	ATAACCTTTGCAAGAAGTCATCCAGCAGCATGTACAAATCCAGTGTTCCTATGACAAATCGC	1456
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1457	CCAATAGTGATCAAAACGGAGTAAATATCAATTTACAAAATGTGCTAGACCGAGTG	1516
421	ProIleValValArgThrAsnValGluTyrGlnPheThrGlnLeuValValAspArgVal	440
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441	GluAlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspLeuGlyThrValLeu	460
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461	LysValValThrIleProArgGluSerTrpHisAspLeuGluGluValValLeuGluGlu	480
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1697	CAACTATATATGTGTTCAACGGCTGGGGTGTGCCAGCTCCCTTTACACCGGTGTGATAT	1756
501	GlnLeuTyrLeuGlySerAspLeuGlyLysSerGlnMetProLeuHisArgCysGluVal	520
1757	TACGGGAAAGCGTGTGTGAGTGTGTGCTCGCCCGAGACCTTACTGTGCTTGGGATGCT	1816
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Db      574 pValyTyrGlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis-- 593
QY      1930 CCACAGCCCTTGAAGAGAGATCATCTATGTTGTAGAGAATAGTAGCACATTTTGTGAATG 1989
Db      594 -GluThrAlaAspGluValIlePheGlyIleGluPheAsnSerThrPheLeuGluCy 613
QY      1990 CAGTCCGAGTGCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAATGAAGAGCG 2049
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QY      2050 AAAAGAAGAGATCAGAGTGCATCATCATCAGCAGCAGATCAAGCGCTCTGCTAG 2109
Db      633 sArgGluGluLeuLysProAspGluArgIleIleLysThrAspTyrGlyLeuLeuIleAr 653
QY      2110 TAGTCTACACAGAGATTACGGCAATTACCTCTGCCATGCGTGGTGAACATGGGTTCAT 2169
Db      653 gSerLeuGlnLysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIle 673
QY      2170 ACAAACTCTTCTTAAGGTAACTTGAAGTCAATGACAGAGCATTTGGAAGAACTTCT 2229
Db      673 eHisThrIleValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsn---Th 692
QY      2230 TCATAAGATGATGATGAGATGGCTCTAAGACCAAGAAATGTCATAGCATGACACC 2289
Db      692 rGlnArgAlaGluTyrGlnGluGluGlnValLysAspLeuLeuAlaGluSer----- 709
QY      2290 TAGCCAGAAAGTCTGTGACAGAGACTTCATGAGCTCATCAACCAACCCCAATCTCAAC 2349
Db      710 -----ArgLeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---Se 726
QY      2350 GATGATGATGCTGTGTGAACAAGTTTGGAAAGGGACCGAAGACGTCGCAAGGCC 2409
Db      726 rLeuAspGlnTyrCysGluGlnMetTrpTyrLysGluLysArgGlnArgAsnLys-- 745
QY      2410 AGGACATACCCAGGAGAACTAACAATGAGAGCACTTACAGAAATTAAGAAAGTTAG 2469
Db      746 -----GlySerProLysTrpLysHisMetGlnGluMetLysLysLysAr 760
QY      2470 AAACAGGAGGACCCAC---GAATTGAGAGGGACCCAGGAGGTGTC 2512
Db      760 gAsnArgArgHisArgAspLeuAspGluLeuGlnArgSerVal 775

RESULT 9
Q8BMF6 PRELIMINARY; PRT; 777 AA.
AC Q8BMF6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE enriched library, clone:6030494C20 product:SEMAPHORIN 3D homolog.
DE Name=Sema3d;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]_
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]_
RN [3]_
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]_
RN [4]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]_
RN [5]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwa K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]_
RN [6]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK031704; BAC27522.1; -
DR HSP; Q92854; 10LZ.
DR MGD; MGI:1860118; Sema3d.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 777 AA; 89562 MW; B7204D82288B89CE CRC64;
Alignment Scores:
Pred. No.: 6,62e-173 Length: 777
Score: 2252.00 Matches: 427
Percent Similarity: 72.11% Conservative: 147
Best Local Similarity: 53.64% Mismatches: 191
Query Match: 46.00% Indels: 31
DB: 2 Gaps: 13
US-09-774-490-1 (1-2709) x Q8BMF6 (1-777)

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Db 710 -----ArgLeuArgTyrIleGlnIleLeuSerSerProAsnPhe---Se 726

QY 2350 GATGGATGATCTCTGGAACAAGTTTGGAAAGGCGACGAAACAACAGTCGGCAAGGCC 2409

Db 726 rLeuAspGlnTyrCysGluGlnMetTrpTyrIleGluArgGlnArgAsnLys-- 745

QY 2410 AGGACATACCCAGGAAACAGTACAAATGGAAGGACCTTACAGAAATAAGAAAGGTAG 2469

Db 746 -----GlySerProLysTrpLysHisMetGlnGluMetLysLysLysAr 760

QY 2470 AAAACAGGAGGACCCAC---GAATTTTCAGAGGGCACCCAGGAGTGTC 2512

Db 760 gAsnArgArgHisLeuAspLeuAspGluLeuGlnArgSerVal 775

RESULT 10

SM3D HUMAN STANDARD; PRT; 777 AA.

AC 095025; 08NC01.

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE 25-OCT-2004 (Rel. 45, Last annotation update)

DE Semaphorin 3D precursor.

GN Name=SEMA3D;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Mead K., Graves T., Wilson C.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE OF 327-777 FROM N.A.

RC TISSUE=Testis;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.L., Feigold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Induces the collapse and paralysis of neuronal growth

CC cones. Could potentially act as repulsive cues toward specific

CC neuronal populations. Binds to neuropilin (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy

CC third of the protein.

CC -!- SIMILARITY: Belongs to the semaphorin family.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: Contains 1 Sema domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; AC004957; -; NOT ANNOTATED CDS.

DR EMBL; BC029590; AAH29590.1; ALT\_INIT.

DR Genew; HGNC:10726; SEMA3D.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003659; Plexin-like.

DR InterPro; IPR002165; Plexin\_repeat.

DR InterPro; IPR001627; Sema.

DR Pfam; PF01403; Sema; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00423; PSI; 1.

DR SMART; SM00630; Sema; 1.

DR PROSITE; PS00835; IG-LIKE; 1.

DR PROSITE; PS01004; SEMA; 1.

KW Developmental protein; Glycoprotein; Immunoglobulin domain;

KW Multigene family; Neurogenesis; Signal.

FT SIGNAL 1 39 Potential.

FT CHAIN 40 777 Semaphorin 3D.

FT DOMAIN 44 531 Sema.

FT DOMAIN 592 680 IG-like C2-type.

FT DOMAIN 739 773 Arg/Lys-rich (basic).

FT DISULFID 665 731 By similarity.

FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 607 607 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 724 724 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 777 AA; 89651 MW; 3F7B0D7AF50F53BD CRC64;

Alignment Scores:

Pred. No.: 1.53e-172 Length: 777

Score: 2247.50 Matches: 414

Percent Similarity: 73.94% Conservative: 142

Best Local Similarity: 55.05% Mismatches: 175

Query Match: 45.90% Indels: 21

DB: 1 Gaps: 10

US-09-774-490-1 (1-2709) x SM3D\_HUMAN (1-777)

QY 275 AAGAACAAATGTCCCAAGCTGAAATATCTCTCAAGAAGAAATGTGTGAATCCCAATGTG 334

Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58

QY 335 ATCACTTCAATGGCTGGCCCAACAGCTCCAGTTATCATCTCTCTTTGGATGAGGAA 394

Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuAspGluGlu 78

QY 395 CGAGTAGGCTGTATGTCGACCAAGGATCATATTTTCATTCGACCTGGTTAATATC 454

Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98

QY 455 ---AAGGATTTTCAAAAGATTGTGGCCAGTATCTTACACAGAGAGAGATGAATCAAG 511

Db 99 AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118

QY 512 TGGGCTGGAAGAGACATCTGAAAGATGTCTAAATTTTCATCAAGTACTTAAAGCATAT 571

Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138

QY 572 ATCAGACTCACTTGTACGCTGTGGACGGGGGCTTTTCATCCAATTTGCACCTACATT 631

Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158

QY 632 GAAATTTGACATCATCTCGAGACAAATATTTTAAAGCTGGAGAACTCACATTTTGAAC 691

Db 159 AspLeuGlyValTyrLysGluAspIlePheLysLeuAspThrHisAsnLeuGluSer 178

QY 692 GCGCTGGGAAGAGTCCATATCACCTACCTAGCTGTCGACAGCATCCCTTTTAATAGTGA 751

Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198

QY 752 GAATTATCTCTGGAACTGCACCTGATTTTATGGGGCGAGACTTGTCTCTTCCGAAT 811

Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218



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 QY 219 LeuGlyProThrHisAspHisHisTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238  
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 QY 863 AATGATCCAAATTCATTAGTCCCACTCTATCTCAGAGAGTGACAACTCTGAAGATGAC 922  
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 QY 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258  
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 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCCTGCTGAAGAAATG 1639  
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 QY 479 ValValSerIleSerLysGluLysTrp---AsnMetGluValValLeuGluLeu 497  
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 QY 498 GlnIlePheLysHisSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517  
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 QY 1700 CTATATATTTGGTTCAACGGCTGGGTTCGCCAGCTCCCTTTTACACGGTGTGATATTAC 1759  
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 QY 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537  
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 QY 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgProTyrCysAlaTrpAspGlyAsn 557  
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 QY 1820 GCATGTTCTCGTATTTTCCACTGCAAGAGACGACAGACGACCAAGATATAGAAAT 1879  
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 QY 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr 577  
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 QY 1880 GGAGACCCCACTGACTCTGTTTACAGACTTACACCATGATAATCACCATGCCACAGCCCT 1939

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 QY 2000 TCGCAGACAGCGTGTCTATTGGCAATTCAGAGCGCAATTCAGAGCAAGAAAGAG 2059  
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 QY 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636  
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 QY 2060 ATCAGATGGATGATCATATCATCAGACAGATCAAGCCTTCTCTCTAGTGTACAA 2119  
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 QY 2300 GTCTGGTACAGACATTCATGCTGATCATCAACACCCCAATCTCAACACGATGATGAG 2359  
 Db |||||  
 QY 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerProAsnPhe---SerLeuAspGln 729  
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 ID Q6UW77 PRELIMINARY; PRT; 777 AA.  
 AC Q6UW77;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Collapsin-2.  
 GN ORFNames=UNQ760;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.H., Yaneura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 effort to identify novel human secreted and transmembrane proteins: a  
 bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; AY358937; AAQ89296.1; -.



Qy	983	CACGCTAGAAATAGGT	CAGATATCAAGAATGACTTTGGAGGGC	CACAGAAGTCTGGTGAAT	1042
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Qy	1103	GACACTCAATTTTCATGAACTCGAGGATGTATTCCTAATGAACCTTTAAAGATCCATAAAAT	1162		
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Qy	1163	CCAGTTGTATATGAGAGTGTTCACGACTCCAGTAAACATTTTCAAGGATCAGCCGCTGTGT	1222		
Db	339	ProValValTyrrGlyValPheThrThrThrSerSerIlePheIysGlySerAlaValCys	358		
Qy	1223	ATGTATAGCATGATGTGACAAGGGTGTCTTGGTCCATATCCACACGGGATGGA	1282		
Db	359	ValTyrrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrrAlaHisIysGlySer	378		
Qy	1283	CCCAACTCATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGGCCAGAACTTGT	1342		
Db	379	AlaAspHisArgTrpValGlnTyrrAspGlyArgIleProTyrrProArgProGlyThrCys	398		
Qy	1343	CCACGACAAACATTTGGTGGT---TTGACTCTCAAAAGGACCTTCTCGATGATGTATA	1399		
Db	399	ProSerLysThrTyrrAspProLeuIleLysSerThrArgAspPheProAspAspValIle	418		
Qy	1400	ACCTTTGCAAGAAGTCATCCAGCCATGTACATCCAGTGTTCCTATGAACAATCGCCCA	1459		
Db	419	SerPheIleIysArgHisSerValMetTyrrLysSerValTyrrProValAlaGlyIlePro	438		
Qy	1460	ATAGTGATCAAAACGGATGTAAATATTCAATTTACACAAATTCGTAGACCCAGATGGAT	1519		
Db	439	ThrPheLysArgIleAsnValAspTyrrArgLeuThrGlnIleValValAspHisValIle	458		
Qy	1520	GCAGAAAGATGGACAGTATGATGTATTGTTTATCGGAACAGAGTGTGGGACCGTCTTTAAA	1579		
Db	459	AlaGluAspGlyGlnTyrrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478		
Qy	1580	GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCCTCGTGGGAAGAAATG	1639		
Db	479	ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluLeuLys	497		
Qy	1640	ACAGTTTTTCGGAAACCGACTGCTATTTCAGCAATCGAGCTTCCACTAAGCAGCAACAA	1699		
Db	498	GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln	517		
Qy	1700	CTATATATTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTATC	1759		
Db	518	LeuTyrrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyrr	537		
Qy	1760	GGGAAACGGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTGGGATGGTTCT	1819		
Db	538	GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrrCysAlaTrpAspGlyIys	557		
Qy	1820	GCATGTTCTCGCTATTTTCCCATCTGCAAGAGACGACAGACAGCAAGATATAAGAAAT	1879		
Db	558	AlaCysSerArgTyrrAlaProThrSerLysArgAlaArgArgGlnAspValLysTyrr	577		
Qy	1880	GGAGACCCACTGACTCACTTTCAGACTTATCACCATGATAATCACCATGCCACAGCCCT	1939		
Db	578	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596		
Qy	1940	GAGAGAGAAATCATATGTTGTGTAGAGATATGATAGACATTTTGGAAATGCAGTCCGAAG	1999		
Db	597	AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616		
Qy	2000	TCCGAGAGCGCTGGTCTATTGGCAATTCACAGCGCGAAATCAAGACGCGAAAGAGAG	2059		
Db	617	SerGlnGlnAlaThrIleLysTrpTyrrIleGlnArgSerGlyAspGluHisArgGluGlu	636		



Db 178 PropheAlaSerValMetAlaAspGluTyrLeuTyrAlaGlyThrAlaSerAspPheLeu 197  
 QY 785 GGGCGAGACTTTGCTATCTCCGAACCTCTGGG-----CACCAACCAACCAATCAGG 835  
 Db 198 GlyLysAspThrAlaLeuThrArgSerLeuGlyProSerHisAspHisTyrIleArg 217  
 QY 836 ACAGAGCAGATGATCCAGGTGGCTCAATGATCCAAAGTTCAATTAGTCCCACTCCTC 895  
 Db 218 ThrAspIleSerGluHisTyrTrpLeuThrGlyAlaLysPheIleAlaThrPheProfile 237  
 QY 896 TCAGAGAGTGCACATCTCGAAGATGACAAAGTATATCTTTCTCCGTGGAATGCAATA 955  
 Db 238 ProAspThrTyrAsnProAspAspLysIleTyrPhePhePheArgGluLeuSerGln 257  
 QY 956 GATGGAGAACACTCTCGAAGAGTACTACGCTAGATAGGTGAGTATGCAAGATGAC 1015  
 Db 258 AspSerSerThrSerAspLysThrIleLeuSerArgValGlyArgValCysLysAsnAsp 277  
 QY 1016 TTTGGAGGCGACAGAAGTCTGGTGAATAATGGAACAATCTCTCAAGCTGCTGATTT 1075  
 Db 278 MetGlyGlyGlnArgSerLeuIleAsnLysTrpThrPheLeuLysAlaArgLeuVal 297  
 QY 1076 TGCTCAGTCCAGGTCCAAATGSCATTGACACTCATTTTGTATGATGAACTGCAGGATGATTC 1135  
 Db 298 CysSerIleProGlyProGluGlyAlaAspThrHisPheAspGluLeuGlnAspIlePhe 317  
 QY 1136 CTAATGAACCTTTAAAGATCCTAAATCCAGTTGTATGAGTGTGTTACGACTTCCAGT 1195  
 Db 318 LeuLeuSerThrArgAspGluArgAsnProLeuValTyrGlyValPheThrThrSer 337  
 QY 1196 AACATTTTCAAGGGATCAGCGTGTGTATGATGATGATGATGATGATGATGATGATGAT 1255  
 Db 338 SerValPheLysGlySerAlaValCysValTyrSerMetAlaAspIleAlaValPhe 357  
 QY 1256 CTTGTGTCATATGCCAGGAGTGCACCAACTATCAATGATGATGATGATGATGATGATGAT 1315  
 Db 358 AsnGlyProTyrAlaHisLysGluSerAlaAspThrHisPheAspGluLeuGlnTyrGlyArg 377  
 QY 1316 GTCCCTATCCAGGCGAGAACTCTGCCAGCAAACTTTGGTGGT---TTTGACTCT 1372  
 Db 378 IleProTyrProArgProGlyThrCysProSerLysThrTyrAspProLeuIleLysSer 397  
 QY 1373 ACAGAGACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1432  
 Db 398 ThrArgAspPheProAspGluValIleSerPheIleLysArgHisProLeuMetTyrLys 417  
 QY 1433 CCAGTGTCTTCTATGAACATCCGCCAATGATGATGATGATGATGATGATGATGATGATGAT 1492  
 Db 418 SerValTyrProLeuThrGlyGlyProValPheThrArgIleAsnValAspTyrArgLeu 437  
 QY 1493 ACACAAATTTGCTAGACGAGTGGATGAGAGATGAGAGATGATGATGATGATGATGATGATGAT 1552  
 Db 438 ThrGlnIleValValAspHisValMetAlaGluAspGlyGlnTyrAspValIlePheLeu 457  
 QY 1553 GGAACAGATGTTGGGACGTTCTTAAAGTAGTTTCAATTCCTAAGAGAGACTGTTGATGAT 1612  
 Db 458 GlyThrAspIleGlyThrValLeuLysAlaValSerIleThrLysGluLysTrp---Thr 476  
 QY 1613 TTAGAGAGTTCGCTGAGAGAAATGACAGTTTTCGGGAACCGACTGCTATTTTCAGCA 1672  
 Db 477 LysGluGluValValLeuGluGluLeuGlnIlePheLysHisProSerPheIleSerThr 496  
 QY 1673 ATGGAGCTTTTCACTAAGCAGCAACAACTATATATGTTTCAACGCTGGGTGGTGGCCAG 1732  
 Db 497 MetGluIleSerGlnLysGlnGlnLeuTyrIleGlySerArgAspGlyLeuValGln 516  
 QY 1733 CTCCTTTTACCGGTGTGATATTTACGGGAAAGCTGTGCTGAGTGTGCTCGCCCGCA 1792  
 Db 517 LeuSerLeuHisArgCysHisThrTyrGlyLysAlaCysAlaAspCysCysLeuAlaArg 536  
 QY 1793 GACCTTACTGCTTGGATGCTTCTGATGTTCTGCTATTTTCCCTGCTCAAGAGA 1852  
 Db 537 AspProTyrCysAlaTrpAspGlyAsnSerCysSerArgTyrAlaProThrSerLysArg 556

QY 1853 CCACAAAGCAGCAGATATAAGAAATGGAGACCCCACTGACTCACTGTTTCAGACTTAC 1912  
 Db 557 ArgAlaArgArgGlnAspValLysTyrGlyAspProValAlaGlnCysTrpAspValGlu 576  
 QY 1913 CATGATATCACCAGTCCAGCCCTGAAGAGAGAAATCATATGCTGTAGAGAAATAGT 1972  
 Db 577 AspSerIleSerHis---GluThrAlaAspGluLysValIlePheGlyIleGluPheAsn 595  
 QY 1973 AGCACAATTTTGGATGCTCCAGTCCGAGAGAGCCCTGCTATTATGGCAATTCAG 2032  
 Db 596 SerThrPheLeuGluCysIleProLysSerGlnGlnAlaSerIleArgTrpTyrIleGln 615  
 QY 2033 AGCGAAATGAAGAGCGAAAGAGATCAGAGTGGATGATCATCATCATCATCATCATCAT 2092  
 Db 616 ArgSerGlyGluGluHisArgGluGluLeuLysAlaAspGluArgIleIleLysThrGlu 635  
 QY 2093 CAAGCCTCTCTGCTAGTGTCTACACAGAGAGGATTCAGGCAATACCTCTGCCATGG 2152  
 Db 636 HisGlyLeuLeuIleArgSerLeuGlnArgAspAlaGlyAlaTyrPheCysLysAla 655  
 QY 2153 GTGGAACTGGTTCATACAAACTCTTTAAAGTAAACCTCGAAGTCAATTCACACAGAG 2212  
 Db 656 GlnGluHisThrPheIleHisThrIleValLysLeuAsnLeuAsnValIleGluAsnGly 675  
 QY 2213 CATTTGGAAGAACTTCTTCATAAAGATGATGATGATGATGATGATGATGATGATGATGAT 2272  
 Db 676 GlnMetGluSer---ThrGlnLysThrGluAspGluGluGly-----ArgVal 690  
 QY 2273 TCCAATAGATCAGACCTAGCCAGAGGTCTCGTACAGAGACTTTCAGCTGATCATCAAC 2332  
 Db 691 ArgAspLeuLeuThrGluSer---ArgLeuArgTyrLysAspTyrIleGlnLeuValSer 709  
 QY 2333 CACCCCAATCTCAACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2392  
 Db 710 SerProSerPhe---SerLeuAspGluTyrCysGluGlnMetTrpHisArgGluLysArg 728  
 QY 2393 CAACCTCGCAAGACCGACATACCCAGGAGACAGTAACAAATGGAAGCACTTACAA 2452  
 Db 729 ArgGlnArgAsnLysGlyGly-----AlaLysTrpLysHisValGln 742  
 QY 2453 GAAATTAAGAAAGTAGAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2503  
 Db 743 GlnMetLysLysLysArgAsnArgHisHisGluProAlaArgProPro 759

RESULT 13  
 SM3D BRARE  
 ID SM3D BRARE STANDARD; PRT; 764 AA.  
 AC Q9W6G6;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Semaphorin 3D precursor (Semaphorin 2) (Semaphorin 22) (Sema-22).  
 GN Name=sema3d; Synonyms=sema2, sema22;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99112778; PubMed=9915572;  
 RX DOI=10.1002/(SICI)1097-0177(199901)214:1<13::AID-DVDY23.0.CO;2-3;  
 RA Halloran M.C., Severance S.M., Yee C.S., Gemza D.L., Raper J.A.,  
 RA Kuwada J.Y.  
 RT "Analysis of a Zebrafish semaphorin reveals potential functions in  
 RT vivo."  
 RL Dev. Dyn. 214:13-25(1999).  
 CC -!- FUNCTION: May play a role in the guidance of several axon  
 CC pathways.  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- DEVELOPMENTAL STAGE: Expressed in a dynamic and restricted pattern  
 CC during the period of axon outgrowth.

CC -!- SIMILARITY: Belongs to the semaphorin family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 1 Sema domain.  
 CC -----  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----

DR EMBL; AF124485; RAD21310.1; -;  
 DR ZFIN; ZDB-GENE-990715-2; sema3d.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003659; Plexin-like.  
 DR InterPro; IPR001627; Sema.  
 DR Pfam; PF01403; Sema; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00423; PSI; 1.  
 DR SMART; SM00630; Sema; 1.  
 DR PROSITE; PS1004; Sema; 1.  
 DR Developmental protein; Glycoprotein; Immunoglobulin domain;  
 KW Multigene family; Neurogenesis; Signal.  
 FT SIGNAL 1 41 Potential.  
 FT CHAIN 42 764 Semaphorin 3D.  
 FT DOMAIN 48 535 Sema  
 FT DOMAIN 61 740 Ig-like C2-type.  
 FT DOMAIN 741 762 Arg/Lys-rich (basic).  
 FT DISULFID 668 733 By similarity.  
 FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 490 490 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 610 610 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 764 AA; 87859 MW; A3ED95C2C479D7AE CRC64;

Alignment Scores:

Pred. No.:	1,21e-162	Length:	764
Score:	2125.00	Matches:	390
Percent Similarity:	71.37%	Conservative:	156
Best Local Similarity:	50.98%	Mismatches:	191
Query Match:	43.40%	Indels:	28
DB:	1	Gaps:	11

US-09-774-490-1 (1-2709) x: SM3D\_BRARE (1-764)

QY	215	AGATTGCTGCTCTTTCTGGGAGTATTACTTACAGCAAGACCAACTATCAGATGGG	274
DB	20	ArgPheSerCysAlaTrpTrpSerThrSerValMetLeuPhePheSerLeuProGluGly	39
QY	275	-----AAGAACAACTGCGAAGCTGAAATTATCTACAGCAAGACCAACTATCAGATGGG	325
DB	40	AsnCysMetLysGluSerLeuProArgValLysLeuGlyTrpLysAspLeuLeuHisSer	59
QY	326	AACAATGTGATCACTTCAATGGCTTGGCCACAGCTCCAGTTATCATCTCTCTTTTG	385
DB	60	ArgSerValProPheThrGlySerSerGluGlyGlnHisPheGlnThrValLeuLeu	79
QY	386	GATGAGAACGAGTAGGCTGTATGTTGGAGCAAGAGTCACATATTTTCATCGACCTG	445
DB	80	AspGluGluArgSerArgLeuLeuGlyAlaLysAspHisValTrpLeuLeuAspPro	99
QY	446	GTTAATATC- --AAGATTTCCTCAAAAGATGTGTGGCCAGTATCTTACACCAAGAGAT	502
DB	100	AspAsnIleAsnLysHisProLysLysLeuSerTrpProAlaSerArgAspArgValGlu	119
QY	503	GAATGCAAGTGGCTGGAAAGACATCTCGAAAGATGTGCTTAATTTTCATCAAGTACT	562
DB	120	MetCysIleLeuAlaGlyLysAsnProLeuThrGluCysAlaAsnPheIleArgValLeu	139
QY	563	AGGCATATAATCAGACTCATTGTACGCTGTGGNACGGGGCTTTTCATCAATTGC	622
DB	140	HisSerTyrAsnArgThrHisValTyrAlaCysGlyThrGlyAlaPheHisProThrCys	159

QY	623	ACCTACATTGAAATTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGAGAACTCACAT	682
DB	160	AlaPheLeuGluIleLysGlyHisLysGluAspArgTrpLeuLeuLeuHisSerAsnThr	179
QY	693	TTTGAACACGGCGTGGGAAGAGTCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTA	742
DB	180	MetGluSerGlyArgMetLysCysProPheAspProAsnGlnProPheAlaSerValLeu	199
QY	743	ATAGATGAGAAATTAATCTCTGGAAGTCTGAGTCTGATTTTATGGGCGGAGACTTCTATC	802
DB	200	ThrAspGlnTyrLeuTyrAlaGlyThrAlaSerAspPheLeuGlyLysAspSerThrPhe	219
QY	803	TTCCCAACTCTTGGG-----CACCAACACCAATCAGACAGACGAGCATGATCC	853
DB	220	ThrArgSerLeuGlyProProHisGlnGlnTyrIleArgThrAspIleSerGluAsp	239
QY	854	AGTGGCTCAATGATCCAAAGTTCATTAGTGCACCTCACTCATCTGACAGAGTGAATCTCT	913
DB	240	TyrTrpIleAsnGluGlyLysPheIleSerAlaHisProIleSerAspThrTyrAsnPro	259
QY	914	GAAGATGACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGGGAGAACACTCTGA	973
DB	260	AspAspAspLysIleTyrPhePheArgGluAlaSerArgAspGlySerThrThrAsp	279
QY	974	AAAGCTACTCAGCTAGATAGTGCATATGCAAGATGACTTTGGAGGGCAGACAGT	1033
DB	280	LysSerValLeuSerArgValAlaArgIleCysArgAsnAspValGlyGlyLeuArgSer	299
QY	1034	CTGGTGAATAATGACAACTCTCTCTAAAGTCTCTGATTTGCTGCTGCTGCTGCTGCTG	1093
DB	300	LeuThrAsnLysTrpThrPheLeuLysAlaArgLeuValCysSerIleProGlyPro	319
QY	1094	ATGCGATTGACACTCATTGATCACTGAGGAGTATCTCTTAATGAACCTTTAAAGAT	1153
DB	320	AspGlyValAspThrHisPheAspGluLeuGlnAspIlePheLeuLeuProSerArgAsp	339
QY	1154	CCTAAAAATCCAGTTGTATATGGAGTGTTCAGACTTCAGTAACTTTTCAAGGATCA	1213
DB	340	GluLysAsnProMetValTyrGlyValPheThrThrThrSerSerIlePheLysGlySer	359
QY	1214	GCCGTGTGTATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1273
DB	360	AlaValCysValTyrThrMetGluAspIleArgAlaAlaPheAsnGlyProTyrAlaHis	379
QY	1274	AGGATGACCACTATCAATGCTGCTTATCAAGGAAGAGTCCCTATCCAGGCCA	1333
DB	380	LysGluGlyProAspHisArgTrpValGluLysGlyArgIleProTyrProArgPro	399
QY	1334	GGAACTTGTCCAGCAAAACATTTGGT---GGTTTGTACTCTCAAAAGGACCTTCTGT	1390
DB	400	GlyThrCysProSerArgThrTyrAspProHisIleLysThrThrLysAspPheProAsp	419
QY	1391	GATGTTATAACCTTTGCAAGAGTATCATCCAGCCATGATCAATCCAGTGTTCCTATGAC	1450
DB	420	GluValIleSerPheIleArgLeuHisProLeuMetTyrGlnSerValHisProMetThr	439
QY	1451	AATCCCAATAGTATCAAAACGATGTAATATCAATTTACACAAATGTCGTAGAC	1510
DB	440	GlyArgProIlePheThrArgIleAsnThrGluTyrArgLeuThrGlnIleValAsp	459
QY	1511	CGAGTGGATGCAAGAGATGGACAGTATGATGTTATGTTTATCGGAACAGATGTTGGACC	1570
DB	460	ArgValAlaAlaGluAspGlyGlnTyrAlaValMetPheLeuGlyThrAspMetGlySer	479
QY	1571	GTTCTTAAGTAGTTCATTCTAAGGAGACTTGGTATGATGATGATGATGATGATGATGATG	1630
DB	480	ValLeuLysValValSerIleThrGlnGlnAsnTrp---SerSerGluGluIleLeu	498
QY	1631	GAAGAAATGACAGTTCCTGGGAAACCGACTGCTATTTCAGCAATGGAGCTTTCCACTAAG	1690
DB	499	GluGluLeuGlnValPheLysAsnProSerProIleLeuAsnMetGluValSerSerLys	518

```
QY 1691 CAGCACAATATATATTGGTTCAACGGCTGGGTTGCCAGCTCCCTTACACCGGTGT 1750
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
519 GlnGlnGlnLeuValGlyGlySerAspGlyLeuValGlnValSerLeuHisArgCys 538
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1751 GATATTACGGGAACGGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTCG 1810
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
539 GlnIleTyGlyGlnGlyCysAlaGluCysCysLeuAlaArgAspProTyCysAlaTrp 558
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1811 GATGTTCTGCTGCTTCTCGCTATTTTCCCACTGCAAGAGCGCAAGACGACGAAT 1870
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
559 AspGlyThrGlnCysSerArgTyIleProAlaSerLysArgAlaArgGlnAsp 578
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1871 ATAAGAAATGAGACCACTGACTCTGCTTACACTTACACCTATTAATCACCATGCG 1930
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
579 IleLysHisGlyAspProSerHisCysTrpAspThr-----GluAspValLeuGly 596
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1931 CACAGCCCTGAAGAGAGATCATCTATGTTGTAGAGAAATAGTAGACATTTTGGAAATCG 1990
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
597 ArgAsnValGluGlnLysValLeuTyGlyValGluSerAsnSerPheLeuGluCys 616
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1991 AGTCCGAAGTTCGAGAGAGCGCTGTCTATTGTCATTTCCAGAGCGCAATGAAGACGA 2050
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
617 ValSerLysSerGlnGlnAlaLeuIleArgTrpPheValLeuLysProGlyValAspHis 636
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2051 AAAGAAGATCAGATGATGATGATCATATCATCAGACAGATCAAGCGCTTCTGTACT 2110
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
637 ArgGlnGluIleLysProAspGluArgValLeuIleThrAspArgGlyLeuLeuIleArg 656
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2111 AGTCTACACAGAGATTCAGCAATTAACCTGCGCTGCGGTGGAACATGGTTCATA 2170
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
657 TrpLeuGlnArgGlyAspAlaGlySerTyPheCysThrSerGlnGluHisArgPheThr 676
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2171 CAAACTCTTCTTAAGTAACCTCGAAGTCATTGACACAGACATTTGGAAGAACTTCT 2230
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
677 ArgThrLeuLeuHisValSerLeuHisIleLeuAspArgGlyGlnIleAsn-----Ala 694
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2231 CATAAAGATGATGATGATGATGCTCTTAAGACCAAGAAATGTCCAAATAGCATGACCT 2290
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
695 HisGlnProAlaIleArgGluSerSerGluAsnProAlaValThrGlu-----Pro 711
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2291 AGCCGAAGTCTGTGTACAGAGATTCATGCGCTCATCAACACCCCAATCTCAACAG 2350
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
712 ArgGlnArg-----TyrLysAspTyLeuArgMetLeuSerGlyPro---AlaArgSer 728
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2351 ATGGATGAGTCTGTGAACAAAGTTTGGAAAAGCGCCGAAACCAAGCTCGCAAGGCCA 2410
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
729 LeuAspGluTyrcysGluThrMetTrpHisArgGluLysGlnLysGlnLys----- 746
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2411 GGACATACCCCGGAACAGTAAACAATGGAAGCACTTACAGAAATAAGAAAGTAGA 2470
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
747 -----GlyLysTrpLysHisValGlnGlnLeuArgLysSerArg 759
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2471 AACAGAGAGACCCAC 2485
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
760 AsnArgArgHis 764

RESULT 14
SM3B HUMAN
ID SM3B HUMAN STANDARD; PRT; 749 AA.
AC Q13214; Q8TB71; Q8TDV7; Q93018; Q96GX0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 3B precursor (Semaphorin V) (Sema V) (Sema A(V)).
GN Name=SEMA3B; Synonyms=SEMA5;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP
RZ
RA
SEQUENCE FROM N.A.
MEDLINE=96210603; PubMed=8633026; DOI=10.1073/pnas.93.9.4120;
Sekido Y., Bader S., Latif F., Chen J.-Y., Duh F.-M., Wei M.-H.,
```

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RA Albanesi J.P., Lee C.-C., Lerman M.I., Minna J.D.;
RT "Human semaphorins A(V) and IV reside in the 3p21.3 small cell lung
RT cancer deletion region and demonstrate distinct expression patterns.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:4120-4125(1996).
[2]
RP SEQUENCE FROM N.A.
RA Dante M., Wamsley P.;
RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Koyama N.;
RT "Semaphorin 3B (SEMA3B) cDNA.";
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushin T.B., Ioshizuka S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN VARIANTS NSCLC CYS-348; HIS-397 AND ILE-415.
RX MEDLINE=20535986; PubMed=11085536;
RA Lerman M.I., Minna J.D.;
RT "The 630-kb lung cancer homozygous deletion region on human chromosome
RT 3p21.3: identification and evaluation of the resident candidate tumor
RT suppressor genes.";
CC Cancer Res. 60:6116-6133(2000).
CC -!- FUNCTION: Inhibits axonal extension by providing local signals to
CC specify territories inaccessible for growing axons (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity). Accumulates in the
CC endoplasmic reticulum.
CC -!- TISSUE SPECIFICITY: Expressed abundantly but differentially in a
CC variety of neural and nonneural tissues.
CC -!- DISEASE: Defects in SEMA3B are found in non-small cell lung cancer
CC (NSCLC) cell lines.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U28369; AAC09138.1; -
CC EMBL; U73167; AAC02731.1; -
CC EMBL; AB083186; BAB88870.1; -
CC EMBL; BC009113; AAH09113.1; -
CC EMBL; BC024220; AAH24220.1; -
CC PIR; G01856; G01856.
CC Genew; HGNC:10724; SEMA3B.
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DR H-InvDB; HIX0003319; --  
 DR MIM; 601281; --  
 DR GO; GO:0005783; C:cytoplasmic reticulum; TAS.  
 DR GO; GO:0007411; Praxon guidance; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003659; plexin-like.  
 DR InterPro; IPR002165; plexin\_repeat.  
 DR InterPro; IPR001627; Sema.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF01403; Sema; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00423; PSI; 1.  
 DR SMART; SM00630; Sema; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS51004; Sema; 1.  
 DR Disease mutation; Glycoprotein; Immunoglobulin domain;  
 KW Multigene family; Signal.  
 FT SIGNAL 1 24 Potential.  
 FT CHAIN 25 749 Semaphorin 3B.  
 FT DOMAIN 30 513 Sema.  
 FT DOMAIN 573 659 IG-like C2-type.  
 FT DOMAIN 699 702 Poly-Gly.  
 FT DOMAIN 724 744 Arg-rich (basic).  
 FT DISULFID 644 710 By similarity.  
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 124 124 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 427 427 R-linked (GlcNAc...) (Potential).  
 FT VARIANT 348 348 R -> C (in NSCLC).  
 FT VARIANT 397 397 FTId=VAR 014221.  
 FT VARIANT 415 415 D -> H (in NSCLC).  
 FT VARIANT 415 415 FTId=VAR 014222.  
 FT VARIANT 415 415 T -> I (in NSCLC).  
 FT CONFLICT 29 36 /FTId=VAR 014223.  
 FT CONFLICT 308 308 PRLRISFQ -> HAFGSPSKV (in Ref. 2).  
 FT CONFLICT 332 332 Q -> RPPPAE (in Ref. 3).  
 FT CONFLICT 332 332 Missing (in Ref. 4).  
 SQ SEQUENCE 749 AA; 83121 MW; 1F3B8F63F59444F3 CRC64;  
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 Score: 2118.00 Length: 749  
 Percent Similarity: 67.22% Matches: 404  
 Best Local Similarity: 51.53% Conservative: 123  
 Query Match: 43.26% Mismatches: 185  
 DB: 1 Gaps: 72  
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 Db 13 LeuAlaLeuLeuTrpAlaValGlyLeuGlySerAlaAla-----Pro 26  
 QY 281 AATGTGCCAAGGCTGAATATCTTCAAAAGAAATGTTGGAATCCAAATGTGATCACT 340  
 Db 27 SerProProArgLeuArgLeuSerPheGlnGluLeuGlnAlaTrpHisGlyLeuGlnThr 46  
 QY 341 TTCAATGGCTTGGCCCAACAGCTCCAGTTATCATACCTCTCTTTGGATGAGGACGAGT 400  
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 QY 401 AGCTGTATGTGGAGCAAGATCATATTTTCATTCGACCTGGTTAATATC---ANG 457  
 Db 66 ArgLeuPheValGlyAlaGluAsnHisValAlaSerLeuAsnLeuAspAsnIleSerLys 85  
 QY 458 GATTTTCAAAGATGTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAGTGGGCT 517  
 Db 86 ArgAlaLysLysLeuAlaTrpProAlaProValGluTrpArgGluGluCysAsnTrpAla 105  
 QY 518 GGAAGACATCTCTGAAGAAATGTGCTAATTTCAATCAAGGTACTTAAGCATATATCAG 577  
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 QY 638 GCACATCATCTGAGGACAATATATTTTAAAGCTGGAGAACTCACATTTTGAACCGCCGT 697  
 Db 146 GlyHisArgAlaGluLupProValLeuLeuAspProGlyArgIleGluAspGlyLys 165  
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 Db 166 GlyLysSerProTyrAspProArgHisArgAlaAlaSerValLeuValGlyGluGluLeu 185  
 QY 758 TACTCTGAACTGCAGCTGATTTTATGGGGGAGACTTTTGTCTATCTTCGAACTCTGGG 817  
 Db 186 TyrSerGlyValAlaAlaAspLeuMetGlyArgAspPheThrIlePheArgSerLeuGly 205  
 QY 818 CACCACCAATCAGACAGAGCAGCATGATTCAGGTGGCTCAATGATCAAAAGTTC 877  
 Db 206 GlnArgProSerLeuArgThrGluProHisAspSerArgTrpLeuAsnGluProLysPhe 225  
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 Db 226 ValLysValPheTrpIleProGluSerGluAsnProAspAspAspLysIleTyrPhePhe 245  
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 QY 1115 GATGAACCTGCAGGATGTATTCCTAATGAATTTAAAGATCTTAAAGATCCAGTCTGTAT 1174  
 Db 305 AspGlnLeuGlnAspValPheLeuLeuSerSerArgAspHisArgThrProLeuLeuTyr 324  
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 QY 1355 TTGTGTGTTTGAATCTACAAAGACCTTCTGTATGATGTTTATTAACCTTTCAGAGAGT 1414  
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 QY 1415 CATCCAGCATGTACAATCCAGTGTTCCTATGAACAATCCGCCAATAGTGATCAAAACG 1474  
 Db 405 HisProLeuMetTyrAsnSerValLeuProThrGlyArgProLeuPheLeuGlnVal 424  
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 QY 1535 TATGATGTATGTTTATCGAACAGATGTGGACCGCTTCTTAAAGTACTTTCAATTCCT 1594  
 Db 445 TyrAspValLeuPheIleGlyThrAspValGlyThrValLeuLysValIleSerValPro 464  
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 Db 465 LysGlySerArgProSerAlaGluGlyLeuLeuGluGluLeuHisValPheGluAsp 484







Db 47 PheArg---LeuGluArgThrCysCysfyrGluAlaLeuValAspGluGluArgGly 65  
 QY 401 AGGCTGTATGTTGGAGCAAGATCACATATTTTCATTCGACCTGGTTAATATC---AAG 457  
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 QY 518 GAAAGACATCCTGAAGAATGTCTAATTTTCATCAAGTACTTAAGCATATAATCAG 577  
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 QY 578 ACTCATGTAGCTGTGGACGGGGCTTTTCATCCAAATTCG----- 622  
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 Db 146 AlaThrAlaGlyGlyThrHisAlaSerThrGly-----ProGlu----- 158  
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 Db 159 -----LysLeuGluAspGlyLysGlyLysThrProTyrAspProArgHisArg 174  
 QY 728 ACAGCATCCCTTTTAATAGATGGAGAAATATATCTCTGGAACCTGACGATTTATGGG 787  
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 Db 195 ArgAspPheThrIlePheArgSerLeuGlyGlnAsnProSerLeuArgThrGluProHis 214  
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 Db 494 SerLysArgGlnGlnLeuTyrValAlaSerArgAlaAlaValAlaGlnIleAlaLeuHis 513  
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 QY 1925 CATGCCACACCCCTGAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTG 1984  
 Db 571 HisSerValLeuLeuGluLysLysValLeu---GlyValGluSerGlySerAlaPheLeu 589  
 QY 1985 GAATCAGCTCGAAGTCCGACAGAGCGTGTGTTTATTCGCAATTCAGAGCGGGAATGAA 2044  
 Db 590 GluCysGluProArgSerLeuGlnAlaHisValGlnTrpThrPheGlnGlyAlaGlyGlu 609  
 QY 2045 GAGCGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2104  
 Db 610 AlaAlaHisThrGlnValLeuAlaGluGluArgValGluArgThrAlaArgGlyLeuLeu 629  
 QY 2105 CTAGTGTCTTCAACAGAGATTCAGCAATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2164  
 Db 630 LeuArgGlyLeuArgArgGlnAspSerGlyValTyrLeuCysValAlaValGluGlnGly 649  
 QY 2165 TTCATACAACTCTTCTTAAGTAACTCCCTGGAAGTCAATTCAGACAGAGCATTTGGAAGAA 2224  
 Db 650 PheSerGlnProLeuArgArgLeuValLeuHisValLeuSerAlaAlaGlnAlaGluArg 669  
 QY 2225 CTTCTTCTATAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2284  
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 Db 701 GlyGlyAlaAsnSerLeu-----ArgMet 708  
 QY 2396 CGTCCGCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGGAAGCAC----- 2446  
 Db 709 CysArgProGlnProGlyHis-----HisSerValAla 719  
 QY 2447 TTACAGAAATATAGAAAGGTAGAACAGGAGGAGCCAC-----GAAATGAG 2494  
 Db 720 AlaAspSerArgArgLysGlyArgAsnArgMetHisValSerGluLeuArgAlaGlu 739

QY 2495 AGGCACCCAGGAGT 2509  
Db ||| |||||  
740 ArgGlyProArgSer 744

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Job time : 552.5 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 01:12:06 ; Search time 11629 Seconds  
(without alignments)  
11287.744 Million cell updates/sec

Title: US-09-774-490-1  
Perfect score: 2709  
Sequence: 1 aatctttatttcatcgatg.....aggcttttttctactataacc 2709

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

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1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2508.4	92.6	2530	6	CQ812254 Sequence
3	2508.4	92.6	2530	6	AX743092 Sequence
4	2508.4	92.6	2530	6	BD084822 Diagnosis
5	2508.4	92.6	2530	9	HUMHSEM
6	2508.4	92.6	2530	11	G31703
7	2508.4	92.6	2601	6	AR040598
8	2508.4	92.6	2601	6	I47054
9	2457	90.7	2509	6	CQ716140 Sequence
10	2050	75.7	4013	10	BC057588
11	2050	75.7	5952	10	MUSC1
12	2027.6	74.8	2913	10	MMRNASEMD
13	1909.4	70.5	2319	10	RNSIITCN1
14	1883.8	69.5	2319	10	MUSC0SE
15	1744	64.4	3263	5	GH02528
16	1612.4	59.5	1998	10	MUSSEMAIII
17	1477	54.5	2325	5	AY030051
18	1415.2	52.2	1481	6	I11900
19	1069.2	39.5	2337	5	AF083382

20	1035.8	38.2	3148	5	AF086761	AF086761 Danio rer
21	718.6	26.5	2331	6	E27342	E27342 Novel polyP
22	718.6	26.5	3871	6	AX376280	AX376280 Sequence
23	718.6	26.5	3871	6	AX697241	AX697241 Sequence
24	718.6	26.5	3871	9	AY358937	AY358937 Homo sapi
25	718.6	26.5	3880	6	E27343	E27343 Novel polyP
26	697.2	25.7	2715	5	GGU28240	U28240 Gallus gall
27	688	25.4	4041	5	BC080392	BC080392 Xenopus l
28	652	24.1	169408	2	AC073110	AC073110 Homo sapi
29	650.4	24.0	179640	9	AC006322	AC006322 Homo sapi
30	647.4	23.9	6474	6	AX743098	AX743098 Sequence
31	647.4	23.9	6474	9	AB002329	AB002329 Homo sapi
32	645.6	23.8	179711	9	AC146275	AC146275 Pan trogl
33	615.6	22.7	2615	5	AF022947	AF022947 Gallus ga
34	599.4	22.1	2337	6	AX155172	AX155172 Sequence
35	596.4	22.0	2898	10	AF034744	AF034744 Mus muscu
36	596.4	22.0	2935	10	BC057956	BC057956 Mus muscu
37	595.8	22.0	2872	10	MMRNASEMA	X85990 M.musculus
38	594.8	22.0	2328	6	CQ768868	CQ768868 Sequence
39	594.8	22.0	2328	10	MMSEMH	Z80941 M.musculus
40	594.8	22.0	3982	6	CQ768869	CQ768869 Sequence
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LOCUS AX207154 2709 bp DNA linear PAT 30-AUG-2001  
DEFINITION Sequence 1 from Patent WO0155455.  
ACCESSION AX207154  
VERSION AX207154.1 GI:15394943  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Jin,S.  
TITLE Resistance sequences and uses thereof  
JOURNAL Patent: WO 0155455-A 1 02-AUG-2001;  
Millennium Pharmaceuticals, Inc. (US) ; Jin, Shengfang (US)  
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DEFINITION Sequence 6 from Patent WO2004038020.
ACCESSION CQ812254
VERSION CQ812254.1 GI:47601874
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Wittig,R., Poustka,A., Mollenhauer,J. and Schendendorf,D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 6 06-MAY-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)
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 ACCESSION AX743092  
 VERSION AX743092.1 GI:305777056  
 KEYWORDS Homo sapiens (human)  
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 ORGANISM Homo sapiens  
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 REFERENCE 1  
 AUTHORS Alltalo, K., Karkkainen, M. and Karila, K.  
 TITLE Neurophilin/vegfr c/vegfr 3 materials and methods  
 JOURNAL Patent: WO 03029814-A 9 10-APR-2003;  
 LUDWIG INSTITUTE FOR CANCER RESEARCH (US); Licentia Ltd. (FI)  
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ORIGIN



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RESULT 5 HUMHSEM HUMHSEM 2530 bp mRNA linear PRI 08-MAY-1995  
LOCUS Homo sapiens semaphorin-III (Hsma-III) mRNA, complete cds.  
DEFINITION L26081  
ACCESSION L26081.1 GI:799328  
VERSION

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE

JOURNAL  
MEDLINE  
PUBMED

COMMENT

FEATURES  
source

gene  
CDS

semaphorin.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1. (bases 1 to 2530)  
Kolodkin, A.L., Matthes, D.J. and Goodman, C.S.  
The semaphorin genes encode a family of transmembrane and secreted  
growth cone guidance molecules  
Cell 75 (7), 1389-1399 (1993)  
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On May 8, 1995 this sequence version replaced gi:436559.  
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ORIGIN

Query Match 92.6%; Score 2508.4; DB 9; Length 2530;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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G31703  
LOCUS  
DEFINITION  
G31703 SW581973 Eric D. Green Homo sapiens STS genomic, sequence tagged site.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
REFERENCE  
AUTHORS  
Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F., Weintraub, L.A., Mohr-Ridwell, R.M., Peluso, D.C., Fulton, R.S., Leckie, M.P. and Green, E.D.  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
JOURNAL  
COMMENT  
Green, E.D.  
Human chromosome 7 STSs (1997)  
Unpublished (1997)  
Synonyms: SEMIII  
GDB\_DSEG: SEMIII  
Contact: Eric D. Green  
Genome Technology Branch  
National Human Genome Research Institute/NIH  
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892  
Tel: 3014020201  
Fax: 3014024735  
Email: egreen@nhgri.nih.gov  
Primer A: CCTGTGAGTCACTTGCACAG  
Primer B: GGTATGCTGCGCTTTGCCG  
STS size: 230  
PCR Profile:  
Presoak: 0 degrees C for 0.00 minute(s)  
Denaturation: 92 degrees C for 0.17 minute(s)  
Annealing: 55 degrees C for 1.00 minute(s)  
Polymerization: 72 degrees C for 1.00 minute(s)  
PCR Cycles: 35  
Thermal Cycler: PerkinElmer 9600  
Protocol:  
Template: 30-100 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/ul  
Total Vol: 10 ul  
Buffer:  
MgCl2: 1.5 mM  
KCl: 100 mM  
Tris-HCl: 10 mM  
NH4Cl: 5 mM  
pH: 8.6  
This STS has been incorporated into the NHGRI chromosome 7 physical map, but was developed by another investigator. See GenBank record: L26081 For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID=92128937].  
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primer\_bind complement (2215. .2235)  
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Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db	1329	AGTGGATGCGAGAAGATGGAACAGTATGATTTATGTTTATCGGAACAGATTTGGGACCGT	1388
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Db	1389	TCCTTAAGTATGTTTCAATTCCTTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGA	1448
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Qy	2653	CCAATTATAAATTAATCCATGAGTAACCTTCCTAATAGGCTTTTTTTTCC	2702
Db	2469	CCAATTATAAATTAATCCATGAGTAACCTTCCTAATAGGCTTTTTTTTCC	2518
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LOCUS	AR040598	Sequence 53 from patent US 5807826.	PAT 29-SEP-1999
DEFINITION	AR040598		
ACCESSION	AR040598		
VERSION	AR040598.1	GI:5959961	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2601)		
AUTHORS	Goodman,C.S., Kolodkin,A.L., Matthes,D., Bentley,D.R. and O'Connor,I.		
TITLE	Semaphorin gene family		
JOURNAL	Patent: US 5807826-A 53 15-SEP-1998;		
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LOCUS I47054 2601 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 53 from patent US 5639856.

ACCESSION I47054

VERSION I47054.1 GI:2471019

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 2601)

Goodman,C.S., Kolodkin,A.L., Matthes,D., Bentley,D.R. and O'Connor,T.

TITLE Semaphorin gene family

JOURNAL Patent: US 5639856-A 53 17-JUN-1997;

FEATURES location/Qualifiers

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/organism="unknown"

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 313 AATGTTGNAATCAAAATGATGATCACTTCAATGGCTTGGCCACAGCTCAGTTATCA 372

Db 129 AATGTTGNAATCAAAATGATGATCACTTCAATGGCTTGGCCACAGCTCAGTTATCA 188

Qy 373 TACCTTCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGAGCAAAAGGATCACATTT 432

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VERSION CQ716140.1 GI:42276997  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof  
JOURNAL Patent: WO 02068579-A 2074 06-SEP-2002; PE Corporation (NY) (US)

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Submitted (03-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 125 Row: 0 Column: 7

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677910.

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ORIGIN

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Best Local Similarity 88.1%; Pred. No. 0;

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## ORIGIN

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VERSION X85993.1 GI:854329
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1
Puschel, A.W., Adams, R.H. and Betz, H.
MURINE SEMAPHORIN D/COLLAGEN IS A MEMBER OF A DIVERSE GENE FAMILY
AND CREATES DOMAINS INHIBITORY FOR AXONAL EXTENSION
Neuron 14 (5), 941-948 (1995)
95267431
PUBMED 7748561
REFERENCE 2 (bases 1 to 2913)
AUTHORS Adams, R.H.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-1995) R.H. Adams, Max-Planck-Institute fuer
Hirnforschung, Deutschordenstr. 46, D- 60528 Frankfurt, FRG
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ORIGIN





ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1  
Giger, R.I.  
AUTHORS Unpublished  
JOURNAL 2 (bases 1 to 2319)  
REFERENCE 2  
Giger, R.I.  
AUTHORS Direct Submission  
JOURNAL Submitted (22-JAN-1996) R.I. Giger, Netherlands Inst. for Brain  
Research, Meibergdreef 33, 1105 AZ, Amsterdam, NETHERLANDS  
Location/Qualifiers

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DEFINITION Mus musculus collapsin/semaphorin III mRNA, complete cds.
ACCESSION L41541
VERSION L41541.1 GI:18654369
KEYWORDS collapsin/semaphorinIII.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2319)
AUTHORS Kimura,T. and Fishman,M.C.
TITLE cDNA sequence of mouse Collapsin/SemaphorinIII
JOURNAL Unpublished
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FEATURES

source

Location/Qualifiers

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VERSION U02528.1 GI:410078  
KEYWORDS  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE  
AUTHORS Luo, Y., Raible, D. and Raper, J. A.  
TITLE Collapsin: a protein in brain that induces the collapse and  
paralysis of neuronal growth cones  
JOURNAL Cell 75 (2), 217-227 (1993)  
MEDLINE 94006554  
PUBMED 8402908  
REFERENCE  
AUTHORS Luo, Y.  
TITLE Direct Submission  
JOURNAL Submitted (13-OCT-1993) Yuling Luo, Department of Neuroscience,  
University of Pennsylvania, School of Medicine, Philadelphia, PA  
19104 USA  
FEATURES  
source  
1..3263  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 01:06:12 ; Search time 1465 Seconds  
(without alignments)  
10946.470 Million cell updates/sec

Title: US-09-774-490-1  
Perfect score: 2709  
Sequence: 1 aatctttatttctgatg.....aggcttttttcttaataacc 2709

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:.\*  
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2: Geneseqn1990s:.\*  
3: Geneseqn2000s:.\*  
4: Geneseqn2001as:.\*  
5: Geneseqn2001bs:.\*  
6: Geneseqn2002as:.\*  
7: Geneseqn2002bs:.\*  
8: Geneseqn2003as:.\*  
9: Geneseqn2003bs:.\*  
10: Geneseqn2003cs:.\*  
11: Geneseqn2003ds:.\*  
12: Geneseqn2004as:.\*  
13: Geneseqn2004bs:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2709	100.0	2709	4	Aah47049 Semaphori
2	2517	92.9	2848	10	Ade25679 Human cdn
3	2508.4	92.6	2530	2	Aax75767 Human sem
4	2508.4	92.6	2530	6	Abs76512 cDNA enco
5	2508.4	92.6	2530	10	Add08933 Human sem
6	2508.4	92.6	2530	11	Adn95334 Human BEC
7	2508.4	92.6	2530	12	Adq19750 Human sof
8	2508.4	92.6	2601	2	Aaq87442 Human sem
9	2508.4	92.6	3023	12	Adq23894 Human sof
10	1415.2	52.2	1481	2	Aaq92331 Human col
11	718.6	26.5	2331	2	Aax89112 Human bra
12	718.6	26.5	3871	3	Aax37109 Human PRO
13	718.6	26.5	3871	4	Aaf54421 DNA enco
14	718.6	26.5	3871	4	Aas46098 Human DNA
15	718.6	26.5	3871	8	ACA89548 Human enco
16	718.6	26.5	3871	8	ACA73558 Human sec
17	718.6	26.5	3871	8	ACA05873 Human sec
18	718.6	26.5	3871	8	ACA66707 cDNA enco
19	718.6	26.5	3871	8	ACF20282 Human sec
20	718.6	26.5	3871	8	ACF19668 Human sec

21	718.6	26.5	3871	8	ACD21956	Acc21956 Human sec
22	718.6	26.5	3871	8	ACF13121	Accf13121 Human sec
23	718.6	26.5	3871	8	ACD25224	Accd25224 Human sec
24	718.6	26.5	3871	8	ACF00273	Accf00273 Human sec
25	718.6	26.5	3871	8	ACA72330	Acca72330 Novel hum
26	718.6	26.5	3871	8	ACD04854	Accd04854 Novel hum
27	718.6	26.5	3871	8	ACD18315	Accd18315 Human sec
28	718.6	26.5	3871	8	ACD08322	Accd08322 Human sec
29	718.6	26.5	3871	8	ACA88756	Acca88756 Novel hum
30	718.6	26.5	3871	8	ACA70198	Acca70198 Human sec
31	718.6	26.5	3871	8	ACD12420	Accd12420 Novel hum
32	718.6	26.5	3871	8	ACC74335	Acc74335 Human sec
33	718.6	26.5	3871	8	ACD15963	Accd15963 Human sec
34	718.6	26.5	3871	8	ACD25331	Accd25331 Novel hum
35	718.6	26.5	3871	8	ACD18008	Accd18008 Human sec
36	718.6	26.5	3871	8	ACC88295	Acc88295 Human sec
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39	718.6	26.5	3871	8	ABX98326	Abx98326 Human CDN
40	718.6	26.5	3871	8	ACD14077	Accd14077 Human PRO
41	718.6	26.5	3871	8	ACD09857	Accd09857 Human sec
42	718.6	26.5	3871	8	ACC88602	Acc88602 Human sec
43	718.6	26.5	3871	8	ACD21342	Accd21342 Human sec
44	718.6	26.5	3871	8	ABX75714	Abx75714 Human CDN
45	718.6	26.5	3871	8	ABX97917	Abx97917 Human PRO

## ALIGNMENTS

RESULT 1  
AAH47049  
ID AAH47049 standard; DNA; 2709 BP.

AC AAH47049;

DT 29-OCT-2001 (first entry)

DE Semaphorin D cDNA sequence.

KW Drug resistance; resistance gene; semaphorin D; B94; mel-14 antigen;  
KW 24p3; proliferin; maspin; cancer; cytostatic; gene therapy; ss.

OS Homo sapiens.

PN WO200155455-A2.

PD 02-AUG-2001.

PF 31-JAN-2001; 2001WO-US003161.

PR 31-JAN-2000; 2000US-0179191P.

PA (MILL-) MILLENNIUM PHARM INC.

PI (JINS/) JIN S.

Jin S;

WPI; 2001-488799/53.

Determining if a compound modulates the drug resistance of a cell,  
comprises determining the expression or activity level of a resistance  
sequence in a cell in the presence of the test compound.

Example 1; Fig 1A-B; 79pp; English.

The invention relates to a method of determining whether a test compound  
modulates the drug resistance of a cell that comprises determining the  
expression or activity level of resistance genes (e.g. semaphorin D, B94,  
mel-14 antigen, 24p3, proliferin or maspin) in a cell in the presence of  
the test compound, and comparing its expression or activity level in a  
cell without the test compound. The drug resistant sequences are useful  
in identifying drug resistant cells, in screening methods directed to the



CC identification of compounds that can modulate the drug resistance of a  
 CC cell type or multiple cell types. An isolated resistance protein can be  
 CC used as an immunogen to generate antibodies that bind the resistance  
 CC protein. Resistance nucleic acids may be inserted into vectors and used  
 CC as gene therapy vectors. An anti-resistance protein antibody may be used  
 CC to isolate a resistance protein, or facilitate the purification of  
 CC natural resistance protein from cells and of recombinantly produced  
 CC resistance protein expressed in host cells. The methods are useful for  
 CC treating a subject having a disorder, such as a drug-resistance cancer,  
 CC characterized by aberrant resistance sequence expression or activity by  
 CC administering to the subject a resistance modulator. The present sequence  
 CC represents a semaphorin cDNA sequence, whose expression was increased in  
 CC drug resistant EMT6 tumours  
 XX  
 SQ Sequence 2709 BP; 831 A; 560 C; 620 G; 698 T; 0 U; 0 Other;

Query Match		100.0%;	Score 2709;	DB 4;	Length 2709;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 2709;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AATCTTTTATTTTATCGATGTTTAAACAAGCTTAGTAAATCGATGCCAGCTCGAGGGGTGTCG	60		
DB	1	AATCTTTTATTTTATCGATGTTTAAACAAGCTTAGTAAATCGATGCCAGCTCGAGGGGTGTCG	60		
QY	61	ACCCACGGCTCCGGGAGTAGTGTGAGCTCGCCTGTTCTCCCAATGTGACCCAGTCTATTT	120		
DB	61	ACCCACGGCTCCGGGAGTAGTGTGAGCTCGCCTGTTCTCCCAATGTGACCCAGTCTATTT	120		
QY	121	CCAGATTGTTGAATCTCTGGCGGCACAAATACAGGAAGGAAGTAAAGCAGCAAGG	180		
DB	121	CCAGATTGTTGAATCTCTGGCGGCACAAATACAGGAAGGAAGTAAAGCAGCAAGG	180		
QY	181	GACCTACAGCGTCTGAGCATGGCTGGTGTAACTAGGATGTCGTCTTTCTGGGGAGT	240		
DB	181	GACCTACAGCGTCTGAGCATGGCTGGTGTAACTAGGATGTCGTCTTTCTGGGGAGT	240		
QY	241	ATTACTTACAGCAAGCAAACTATCAGAAATGGGAAGCAAAATGTGCCAAGGCTGAAAT	300		
DB	241	ATTACTTACAGCAAGCAAACTATCAGAAATGGGAAGCAAAATGTGCCAAGGCTGAAAT	300		
QY	301	ATCCTTACAAAGAAATGTTGGAAATCAACATGTGATCATCTTCAATGGCTGGGCCAAG	360		
DB	301	ATCCTTACAAAGAAATGTTGGAAATCAACATGTGATCATCTTCAATGGCTGGGCCAAG	360		
QY	361	CTCCAGTTATCATCTCTCTTTGGATGAGGAAAGGAGTAGGCTGTATGTTGGAGCAA	420		
DB	361	CTCCAGTTATCATCTCTCTTTGGATGAGGAAAGGAGTAGGCTGTATGTTGGAGCAA	420		
QY	421	GGATCACATATTTTCAATCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCC	480		
DB	421	GGATCACATATTTTCAATCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCC	480		
QY	481	AGTATCTTACACAGAGATGAAATGCAAGTGGGCTGGAAAGACATCTCGAAGAAATG	540		
DB	481	AGTATCTTACACAGAGATGAAATGCAAGTGGGCTGGAAAGACATCTCGAAGAAATG	540		
QY	541	TGCTAAATTTTCAACAGGTAATTAAGGCATATAATCAGACTCACTTGTAGCCTGTGGAA	600		
DB	541	TGCTAAATTTTCAACAGGTAATTAAGGCATATAATCAGACTCACTTGTAGCCTGTGGAA	600		
QY	601	GGGGCTTTTTCATCAATTTGACCTTCAATTTGAAATGGACATCATCTCGAGGACAAAT	660		
DB	601	GGGGCTTTTTCATCAATTTGACCTTCAATTTGAAATGGACATCATCTCGAGGACAAAT	660		
QY	661	TTTTAAGCTGGAGACTCACATTTTGAACCGGCTGGGAGAGTCCATATGACCTTAA	720		
DB	661	TTTTAAGCTGGAGACTCACATTTTGAACCGGCTGGGAGAGTCCATATGACCTTAA	720		
QY	721	GCTGCTGACAGCATCCCTTTTAAATAGATGGAAATATACTCTGAACTGACAGCTGATTT	780		
DB	721	GCTGCTGACAGCATCCCTTTTAAATAGATGGAAATATACTCTGAACTGACAGCTGATTT	780		
QY	781	TATGGGGGAGACTTTTGCTATCTTCCGAATCTTGGGCACCAACCCCAATCAGGACAGA	840		

DB	781	TATGGGGGAGACTTTTGCTATCTTCCGAATCTTGGGCACCAACCCCAATCAGGACAGA	840
QY	841	GCAGCATGATTCAGGTGGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGA	900
DB	841	GCAGCATGATTCAGGTGGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGA	900
QY	901	GAGTGACAAATCTGAAAGTGAACAAAGTATCTTTTCTCCGTGAAATGCAATAGATGG	960
DB	901	GAGTGACAAATCTGAAAGTGAACAAAGTATCTTTTCTCCGTGAAATGCAATAGATGG	960
QY	961	AGAACACTCTCGAAAAGCTACTCAGCTAGATAGGTGAGATATCAAGAATGACTTTGG	1020
DB	961	AGAACACTCTCGAAAAGCTACTCAGCTAGATAGGTGAGATATCAAGAATGACTTTGG	1020
QY	1021	AGGGCAGAGAGTCTGGTGAATTAATGGAACAACTCTCAAGCTCGTGTGATTTGCTC	1080
DB	1021	AGGGCAGAGAGTCTGGTGAATTAATGGAACAACTCTCTCAAGCTCGTGTGATTTGCTC	1080
QY	1081	AGTGCAGGTCCAAATGCGATTGACACTCATTTTGTGATGAACTGCAAGGATGATTCCTAAT	1140
DB	1081	AGTGCAGGTCCAAATGCGATTGACACTCATTTTGTGATGAACTGCAAGGATGATTCCTAAT	1140
QY	1141	GAACTTTAAAGATCCTAAAAATCCAGTTGTATATGAGAGTGTTCAGACTTCCAGTAACAT	1200
DB	1141	GAACTTTAAAGATCCTAAAAATCCAGTTGTATATGAGAGTGTTCAGACTTCCAGTAACAT	1200
QY	1201	TTTCAAGGGATCAGCCGTGTGTATGATAGCATGATGATGAGAAAGGTTGCTTTGG	1260
DB	1201	TTTCAAGGGATCAGCCGTGTGTATGATAGCATGATGATGAGAAAGGTTGCTTTGG	1260
QY	1261	TCCATATCCACAGGGATGGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCC	1320
DB	1261	TCCATATCCACAGGGATGGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCC	1320
QY	1321	CTATCCAGCGCCAGGAACTTGTCCAGCAAAACATTTGGTGGTTTGTACTCTACAAAGGA	1380
DB	1321	CTATCCAGCGCCAGGAACTTGTCCAGCAAAACATTTGGTGGTTTGTACTCTACAAAGGA	1380
QY	1381	CTTCTCTGATGATGTTAATCTTTCAGAAAGTCAATCCAGCCATGTACAACTGATTT	1440
DB	1381	CTTCTCTGATGATGTTAATCTTTCAGAAAGTCAATCCAGCCATGTACAACTGATTT	1440
QY	1441	TCCTATGAACTCGCCCAATAGTATGATCAAAACGATGTAATTAATTAACAATTAACAAT	1500
DB	1441	TCCTATGAACTCGCCCAATAGTATGATCAAAACGATGTAATTAATTAACAATTAACAAT	1500
QY	1501	TGTCTGTAGACCGAGTGGATGAGAAAGTGGACAGTATGATGTTTATCGGAACAGA	1560
DB	1501	TGTCTGTAGACCGAGTGGATGAGAAAGTGGACAGTATGATGTTTATCGGAACAGA	1560
QY	1561	TGTTGGGACCGTCTTAAAGTATGTTTCAATTCCTAAGGAGACTGGTATGATTTAGAAGA	1620
DB	1561	TGTTGGGACCGTCTTAAAGTATGTTTCAATTCCTAAGGAGACTGGTATGATTTAGAAGA	1620
QY	1621	GGTCTGCTGGAAGAAATGACAGTTTTTCGGGAAACCGACTGTATTCAGCAATGGAGCT	1680
DB	1621	GGTCTGCTGGAAGAAATGACAGTTTTTCGGGAAACCGACTGTATTCAGCAATGGAGCT	1680
QY	1681	TTCCAATGAGCAGCAAACTATATATATGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTT	1740
DB	1681	TTCCAATGAGCAGCAAACTATATATATGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTT	1740
QY	1741	ACACGGTGTGATATTTACGGGAAAGCGTGTGAGTGTGCTCGCTCGCCCGAGACCTTTA	1800
DB	1741	ACACGGTGTGATATTTACGGGAAAGCGTGTGAGTGTGCTCGCTCGCCCGAGACCTTTA	1800
QY	1801	CTGTCTGGGATGCTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGACAAG	1860
DB	1801	CTGTCTGGGATGCTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGACAAG	1860
QY	1861	ACGACAGATATATAAATGAGAGCCCACTGATCTGATCTGCTTACACCATGATTA	1920

Db 1861 ACGACAAGATATAAGAAATGGAGACCCACTGACTCACTGTTTACAGACTTACACCATGATAA 1920  
QY 1921 TCACCATGCCCACAGCCCTGGAAGAGAGAAATCATCTATGTGTAGAGAAATAGTAGCACATT 1980  
Db 1921 TCACCATGCCCACAGCCCTGGAAGAGAGAAATCATCTATGTGTAGAGAAATAGTAGCACATT 1980  
QY 1981 TTTTGAATCGAGTCCGAACTCCGAGAGAGCGTGGTCTATTGGCAATTCAGAGGCGAAA 2040  
Db 1981 TTTTGAATCGAGTCCGAACTCCGAGAGAGCGTGGTCTATTGGCAATTCAGAGGCGAAA 2040  
QY 2041 TGAAGAGCGAAAAGAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCT 2100  
Db 2041 TGAAGAGCGAAAAGAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCT 2100  
QY 2101 TCTGCTACGTAGTCTTACAAAGAGAGATTGAGCAATTTACCTCTGCGATCGCGTGAACA 2160  
Db 2101 TCTGCTACGTAGTCTTACAAAGAGAGATTGAGCAATTTACCTCTGCGATCGCGTGAACA 2160  
QY 2161 TGGGTTTCATACAACTCTTTAAAGGTAAACCTGGGAAGTCATTTGACACAGAGCATTTGGA 2220  
Db 2161 TGGGTTTCATACAACTCTTTAAAGGTAAACCTGGGAAGTCATTTGACACAGAGCATTTGGA 2220  
QY 2221 AGAAGCTTCTTAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAG 2280  
Db 2221 AGAAGCTTCTTAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAG 2280  
QY 2281 CATGACACCTAGCCAGAGGCTCTGGTACAGAGATTTATGACAGATTCATGACGATCAACCCCAA 2340  
Db 2281 CATGACACCTAGCCAGAGGCTCTGGTACAGAGATTTATGACAGATTCATGACGATCAACCCCAA 2340  
QY 2341 TCTCAACAGATGGATGATGTTCTGTGAACAAGTTTGGAAAAGGACCGAAACCAAGCTGC 2400  
Db 2341 TCTCAACAGATGGATGATGTTCTGTGAACAAGTTTGGAAAAGGACCGAAACCAAGCTGC 2400  
QY 2401 GCAAGGCGCAGACATACCCAGGGAACAGTAACTGAAGTGAAGCTTACAGAAATAA 2460  
Db 2401 GCAAGGCGCAGACATACCCAGGGAACAGTAACTGAAGTGAAGCTTACAGAAATAA 2460  
QY 2461 GAAAGGTAGAAAACAGAGGACCCACCAATTTGAGAGGGCACCCAGAGTGTCTGAGCTGC 2520  
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Db 2521 ATTACCTCTAGAAACCTCAACAAAGTGAAGATTTGCTTGAACAATTAACCTGGAAAACAAA 2580  
QY 2581 TGCATATACATGAATCTTTTTCATGCGATTATGTGGATGTTTACAAATGGTGGAAATTC 2640  
Db 2581 TGCATATACATGAATCTTTTTCATGCGATTATGTGGATGTTTACAAATGGTGGAAATTC 2640  
QY 2641 AGCTGAGTTCCCAATTAATAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTT 2700  
Db 2641 AGCTGAGTTCCCAATTAATAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTT 2700  
QY 2701 CCTAATACC 2709  
Db 2701 CCTAATACC 2709

## RESULT 2

ADE25679

ID ADE25679 standard; cDNA; 2848 BP.

XX AC ADE25679;

XX AC ADE25679;

XX AC ADE25679;

DT 29-JAN-2004 (first entry)

DE Human cDNA differentially expressed in foam cells #83.

XX Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;

KW Cardiovascular disease; atherosclerosis.

XX Homo sapiens.

OS Homo sapiens.

XX

PN

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PD

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PF

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DR

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SQ

US2003194721-A1.

16-OCT-2003.

18-SEP-2002; 2002US-00247671.

19-SEP-2001; 2001US-0323784P.

(INCY-) INCYTE GENOMICS INC.

Mikita T, Shiffman D, Porter JG, Kaser MR;

WPI; 2003-875398/81.

P-PSDB; ADE25760.

Combination containing several polynucleotide that are differentially

expressed in foam cells and complements of the polynucleotides, useful

for diagnosing cardiovascular disease or atherosclerosis.

Claim 1; SEQ ID NO 83; 37pp; English.

The invention relates to a combination comprising several polynucleotides

having any one of 127 sequences (S1) such as the sequence of human

calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4

hydrolyase, human GGI-142 protein mRNA, human K<sup>+</sup> channel beat 2 subunit

mRNA, etc., and their complements. The cDNAs are differentially expressed

in LPS (lipopolysaccharide)-treated foam cells. Also included are

obtaining an extended or full length gene from a library of nucleic acid

sequences, an expression vector containing the nucleic acids, a host cell

containing the vector, a purified polypeptide appearing as ADE25750 and

ADE25751, producing a protein by culturing the host cell, and a

composition comprising a purified antibody that specifically binds to the

proteins. The foam cell-expressed nucleic acids are useful for a high

throughput detection of differential expression of one or more

polynucleotides in a sample. The sample is from a subject with

atherosclerosis and comparison with a standard defines early, mid or late

stages of the disorder. The foam cell-expressed nucleic acids are useful

for high throughput screening of a library of molecules or compounds to

identify a ligand which binds a polynucleotide. The library is chosen

from DNA molecules, peptides, proteins and RNA molecules. The protein is

useful for a high throughput screening of library of molecules or

compounds to identify at least one ligand which specifically binds a

protein, for purifying a ligand from a sample for making an antibody. The

foam cell-expressed nucleic acids are useful for diagnosing

cardiovascular disorder. The foam cell-expressed nucleic acids are useful

as elements on a microarray which can be used for detecting related

polynucleotide in a sample, diagnosing cardiovascular disease,

atherosclerosis. The present sequence represents a cDNA whose expression

is upregulated in LPS treated foam cells.

Sequence 2848 BP; 894 A; 569 C; 636 G; 749 T; 0 U; 0 Other;

Query Match

Best Local Similarity 92.9%; Score 2517; DB 10; Length 2848;

Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

Qy	433	TTCAATTGCAGCCTGGTTTAATATCAAGGAATTTTCAAAGAAATGTGTGGCCAGTATCTTACAC	432
Db	249	TTCAATTGCAGCCTGGTTTAATATCAAGGAATTTTCAAAGAAATGTGTGGCCAGTATCTTACAC	308
Qy	493	CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCCTGAAAGAAATGCTCAATTTTCAT	552
Db	309	CAGAAGAGATGAATGCAAGTGGGCTGGAAAGAAATCCTGAAAGAAATGTGCTCAATTTTCAT	368
Qy	553	CAAGGTACTTTAAGGCATATAATCAGACTCACTGTAGCCCTGTGGAAACGGGGCTTTTCA	612
Db	369	CAAGGTACTTTAAGGCATATAATCAGACTCACTGTGTAAGCCCTGTGGAAACGGGGCTTTTCA	428
Qy	613	TCCAAATTTGCACCTACATATTGAATTTGACATCATCTTGAGGACAATATTTTTAAGCTGGA	672
Db	429	TCCAAATTTGCACCTACATATTGAATTTGACATCATCTTGAGGACAATATTTTTAAGCTGGA	488
Qy	673	GNACTCACATTTTGAAGCGGCGTGGAGAGTCCATATGACCCCTAAGCTGCTGACAGC	732
Db	489	GAACTCACATTTTGAAGCGGCGTGGAGAGTCCATATGACCCCTAAGCTGCTGACAGC	548
Qy	733	ATCCCTTTTAAATAGATGGAGAAATATATCTCTGGAACTGCGAGCTGATTTTATGGGGCAGA	792
Db	549	ATCCCTTTTAAATAGATGGAGAAATATATCTCTGGAACTGCGAGCTGATTTTATGGGGCAGA	608
Qy	793	CTTTGCTACTCTTCCGAATCTCTTGGGCACCAACCCAAATCAGGACAGAGCATGATTC	852
Db	609	CTTTGCTACTCTTCCGAATCTCTTGGGCACCAACCCAAATCAGGACAGAGCATGATTC	668
Qy	853	CAGGTGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACATCC	912
Db	669	CAGGTGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACATCC	728
Qy	913	TGAAGATGACAAAGTATACTTTTTCTTCCTGGTGAATAAGCAATAGATGGAGAACACTCTGG	972
Db	729	TGAAGATGACAAAGTATACTTTTTCTTCCTGGTGAATAAGCAATAGATGGAGAACACTCTGG	788
Qy	973	AAAAAGTACTCAGCTAGATAGTCAAGAAATGACATTTTGGAGGGGCACAGAAG	1032
Db	789	AAAAAGTACTCAGCTAGATAGTCAAGAAATGACATTTTGGAGGGGCACAGAAG	848
Qy	1033	TCGTGTGAATAAATGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCC	1092
Db	849	TCGTGTGAATAAATGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCC	908
Qy	1093	AAATGGCAATTGACACTCATTTTGAATGAATGCGAGATGTAATTCCTAATGAACCTTTAAAGA	1152
Db	909	AAATGGCAATTGACACTCATTTTGAATGAATGCGAGATGTAATTCCTAATGAACCTTTAAAGA	968
Qy	1153	TCCTAAAAATCCAGTTGTATATGAGGTGTTTACGACTTCCAGTAACATTTTCAAGGGATC	1212
Db	969	TCCTAAAAATCCAGTTGTATATGAGGTGTTTACGACTTCCAGTAACATTTTCAAGGGATC	1028
Qy	1213	AGCCGTGTGTATGTATATGAGATGTGAGAAAGGGTGTTCCTTGGTCCATATGCCCCA	1272
Db	1029	AGCCGTGTGTATGTATATGAGATGTGAGAAAGGGTGTTCCTTGGTCCATATGCCCCA	1088
Qy	1273	CAGGGATGGACCCAACTCATCAAATGGGTGCCTTATCAAGGAGAGTGCCTTATCCAGGCC	1332
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Qy	1333	AGGAACTTGTCCCAAGCAAAACATTTGTGTGTTTTGACTCTCAAGAGGACCTTCTCATGA	1392
Db	1149	AGGAACTTGTCCCAAGCAAAACATTTGTGTGTTTTGACTCTCAAGAGGACCTTCTCATGA	1208
Qy	1393	TGTTATAACCTTTTGCAGAGAGTCAATCAGCGCATGTACAAATCCAGTGTTCCTATGAACAA	1452
Db	1209	TGTTATAACCTTTTGCAGAGAGTCAATCAGCGCATGTACAAATCCAGTGTTCCTATGAACAA	1268
Qy	1453	TCGCCCCAATAGTGAATCAAAACGGATGTAAATTTATCAATTTTACACAAATTCGTAGACCG	1512
Db	1269	TCGCCCCAATAGTGAATCAAAACGGATGTAAATTTATCAATTTTACACAAATTCGTAGACCG	1328
Qy	1513	AGTGGATGCGAAGATGGAAGATGATGTTATGTTTTATCGGAAACAGATGTGGGACCGT	1572

1329	AGTGGATGCAAGAATGGA	CAGTATGATGTTATTCGGAACAGATGTTGGGACCGGT	1388
1573	TCTTAAAGTAGTTTCAATTCCCTAAGGAGACTTGGTATGATTATGAAGAAGAGTTCTGTCTGGA	1632	
1389	TCTTAAAGTAGTTTCAATTCTCTAAGGAGACTTGGTATGATTATGAAGAAGAGTTCTGTCTGGA	1448	
1633	AGAAATGACAGTTTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCCCACTAAGCA	1692	
1449	AGAAATGACAGTTTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCCCACTAAGCA	1508	
1593	GCAACAACTATATATTGGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACGGTGTGA	1752	
1509	GCAACAACTATATATTGGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACGGTGTGA	1568	
1753	TATTTACGGGAAGCGTGTCTCAGTGTTCCTTCGCCCGAGACCTTACTGTGCTTTGGGA	1812	
1569	TATTTACGGGAAGCGTGTCTCAGTGTTCCTTCGCCCGAGACCTTACTGTGCTTTGGGA	1628	
1813	TGGTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAGACGACAAGATAT	1872	
1629	TGGTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAGACGACAAGATAT	1688	
1873	AGAAATGGAGACCCACTGACTCAGTCTTTCAGACTTTCAGCACTTACACCATGATAATCACCATGGCCA	1932	
1689	AAGAAATGGAGACCCCACTGACTCAGTCTTTCAGCACTTTCAGCACTGATAATCACCATGGCCA	1748	
1933	CAGCCTTGAAGAGAGAAATCATCTATGSGTGTAGAGAATAGTAGCACATTTTGTGAATGTCAG	1992	
1749	CAGCCTTGAAGAGAGAAATCATCTATGSGTGTAGAGAATAGTAGCACATTTTGTGAATGTCAG	1808	
1993	TCCGAACTCGCAGAGCGCTGTCTATTGGCAATTTCCAGAGGCGAAATGAAGAGCGAAA	2052	
1809	TCCGAACTCGCAGAGCGCTGTCTATTGGCAATTTCCAGAGGCGAAATGAAGAGCGAAA	1868	
2053	AGAAGAGATCAGAGTGGATGATCATATCATCATGAGACAGATCAAGAGCTTCTGCTACGTAG	2112	
1869	AGAAGAGATCAGAGTGGATGATCATATCATCATGAGACAGATCAAGAGCTTCTGCTACGTAG	1928	
2113	TCTTACAACAAAGGATTCAGGCAATTAACCTCTGCCATCGGTGCGAAACATGGGTTCAATACA	2172	
1929	TCTTACAACAAAGGATTCAGGCAATTAACCTCTGCCATCGGTGCGAAACATGGGTTCAATACA	1988	
2173	AACTCTTTTAAAGGTAAACCTCGGAAGTCATTGACACAGAGCAATTTGGAAGAACTTCTTCA	2232	
1989	AACTCTTTTAAAGGTAAACCTCGGAAGTCATTGACACAGAGCAATTTGGAAGAACTTCTTCA	2048	
2233	TAAAGATGATGAGTAGTGCTCTTAAGACCAAGAAATGTCOAATAGCATGACACCTAG	2292	
2049	TAAAGATGATGAGTAGTGCTCTTAAGACCAAGAAATGTCOAATAGCATGACACCTAG	2108	
2293	CCAGAGGTTCTGTCAGAGACTTTCATGCACTCATCAACCCCACTCTCAACACGAT	2352	
2109	CCAGAGGTTCTGTCAGAGACTTTCATGCACTCATCAACCCCACTCTCAACACGAT	2168	
2353	GGATGAGTCTGTGAAACAAGTTTTGGAAAAGGGACCGAAAACAACGCTCGGCAAGGCGCAGG	2412	
2169	GGATGAGTCTGTGAAACAAGTTTTGGAAAAGGGACCGAAAACAACGCTCGGCAAGGCGCAGG	2228	
2413	ACATACCCAGGGAACAGTAAACAAATGGAGCACTTACAAGAAAAATAAGAAAGGTAGAAA	2472	
2229	ACATACCCAGGGAACAGTAAACAAATGGAGCACTTACAAGAAAAATAAGAAAGGTAGAAA	2288	
2473	CAGGAGGCCACCAAGATTTGAGAGGGGCAACCCAGGAGTGTCTGAGCTGCATTACTCTAGA	2532	
2289	CAGGAGGCCACCAAGATTTGAGAGGGGCAACCCAGGAGTGTCTGAGCTGCATTACTCTAGA	2348	
2533	AACTCAACAAAGTAGAAACTTCGCTAGACAAATAACTGGAAAAACAATGCAATATACAT	2592	
2349	AACTCAACAAAGTAGAAACTTCGCTAGACAAATAACTGGAAAAACAATGCAATATACAT	2408	
2593	GAACTTTTTTTCATGGCAATTATGTGGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA	2652	

Db 2409 GAACTTTTTCATGGCAATATGATGGATGTTTACATGGTGGGAATTCAGCTGAGTTCA 2468

Qy 2653 CCAATTATAAATAAATCCATGAGTAACCTTCTTAATAGGCTTTTTCCTTAATACC 2709

Db 2469 CCAATTATAAATAAATCCATGAGTAACCTTCTTAATAGGCTTTTTCCTTAATACC 2525

RESULT 3

AA75767

ID AAX75767 standard; DNA; 2530 BP.

XX

AC AAX75767;

XX

DT 22-JUL-1999 (first entry)

XX

DE Human semaphorin III DNA.

XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M; neurofilament-F; presenilin I; presenilin II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A; es.

XX

OS Homo sapiens.

XX

PN WO9845322-A2.

XX

PD 15-OCT-1998.

XX

PF 02-APR-1998; 98WO-IB000705.

XX

PR 10-APR-1997; 97US-0043163P.

XX

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUT-) RIJKSUNIV UTRECHT.

XX

PI Van Leeuwen FW, Grosveld FG, Burbach JPH;

XX

DR WPI; 1998-609901/51.

XX

PT Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.

XX

PS Disclosure; Fig 16; 258pp; English.

XX

CC This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-M, neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence encodes the wild type and mutant protein fragments represented in

XX SQ Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;

Query Match 92.6%; Score 2508.4; DB 2; Length 2530;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 193 CTGAGCATGGGCTGGTAACTAGGATGCTGCTCTTTCTGGGAGTATTAATTACACG 252

Db 9 CTGAGCATGGGCTGGTAACTAGGATGCTGCTCTTTCTGGGAGTATTAATTACACG 68

Qy 253 AAGACAACTATCAGAAATGGGAAGAACAAATGTCGCAAGGCTGAAATTAATCTACAAAG 312

Db 69 AAGACAACTATCAGAAATGGGAAGAACAAATGTCGCAAGGCTGAAATTAATCTACAAAG 128

Qy 313 AATGTTGGAATCCAACTATGATCACTTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372

Db 129 AATGTTGGAATCCAACTATGATCACTTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188

Qy 373 TACCTTCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGATCACATAT 432

Db 189 TACCTTCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGATCACATAT 248

Qy 433 TTCATTGCACTGGTAAATATCAAGGATTTTCAAAAGATGTTGTCGCCAGTATCTTACAC 492

Db 249 TTCATTGCACTGGTAAATATCAAGGATTTTCAAAAGATGTTGTCGCCAGTATCTTACAC 308

Qy 493 CAGAAGAGATGAATGCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTCTAAATTCAT 552

Db 309 CAGAAGAGATGAATGCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTCTAAATTCAT 368

Qy 553 CAAGGTACTTAAGGCATATAATCAGACTCACCTGTACGCTGTGGAAACGGGGCTTTTCA 612

Db 369 CAAGGTACTTAAGGCATATAATCAGACTCACCTGTACGCTGTGGAAACGGGGCTTTTCA 428

Qy 613 TCCAAATTTGCACCTACATTAATTTGGACATCATCTGAGGACATATATTTTAAAGCTGA 672

Db 429 TCCAAATTTGCACCTACATTAATTTGGACATCATCTGAGGACATATATTTTAAAGCTGA 488

Qy 673 GAACTCACATTTTGAAGACGGCGGTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 732

Db 489 GAACTCACATTTTGAAGACGGCGGTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 548

Qy 733 ATCCCTTTTAATAGATGAGAAATTAATCTCTGAACTGCAGCTGATTTTATGGGGCAGA 792

Db 549 ATCCCTTTTAATAGATGAGAAATTAATCTCTGAACTGCAGCTGATTTTATGGGGCAGA 608

Qy 793 CTTTGCTATCTCCGAATCTTTGGGCAACCAACCAATCAGGACAGCAGCATGATTC 852

Db 609 CTTTGCTATCTCCGAATCTTTGGGCAACCAACCAATCAGGACAGCAGCATGATTC 668

Qy 853 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGACAATCC 912

Db 669 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGACAATCC 728

Qy 913 TGAAGATGACAAAGTATATCTTTTCTTCGTAAGAAATGCAATAGATGGAAGAACATCTCG 972

Db 729 TGAAGATGACAAAGTATATCTTTTCTTCGTAAGAAATGCAATAGATGGAAGAACATCTCG 788

Qy 973 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTGGAGGGCAGAGAAG 1032

Db 789 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTGGAGGGCAGAGAAG 848

Qy 1033 TCTGTGTAATTAATGAGCAACATTTCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC 1092

Db 849 TCTGTGTAATTAATGAGCAACATTTCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC 908

Qy 1093 AAATGGCATTTGACACTCAATTTTGTAGTGAATGAGGATGATTTCTTAATGAACATTTAAAGA 1152

Db 909 AAATGGCATTTGACACTCAATTTTGTAGTGAATGAGGATGATTTCTTAATGAACATTTAAAGA 968

Qy 1153 TCCTAAAAATCCAGTTGATATGAGAGTGTTTACAGACTTCCAGTAAACATTTTCAAGGGATC 1212

Db 969 TCCTAAAAATCCAGTTGTATATGAGTGTATTACGACTTCCAGTAACTTTTCAAGGATC 1028  
 QY 1213 AGCCGTGTATGTATACATGAGTGTAGAGAGGTGTCTTGTGTCATATGCCCA 1272  
 Db 1029 AGCCGTGTATGTATACATGAGTGTAGAGAGGTGTCTTGTGTCATATGCCCA 1088  
 QY 1273 CAGGATGGACCCCACTACTCAATGGGTGCTTTATCAAGGAAGAGTCCCTTATCCACGGCC 1332  
 Db 1089 CAGGATGGACCCCACTACTCAATGGGTGCTTTATCAAGGAAGAGTCCCTTATCCACGGCC 1148  
 QY 1333 AGGAATCTTCCAGCAAAACATTTGGTGGTGTGACTCTCAAGAGACCTTCTGTATGA 1392  
 Db 1149 AGGAATCTTCCAGCAAAACATTTGGTGGTGTGACTCTCAAGAGACCTTCTGTATGA 1208  
 QY 1393 TGTTATACCTTTGCAAGAGTCAATCCAGGCAATGACAAATCAAGTGTCTTCTATGAACAA 1452  
 Db 1209 TGTTATACCTTTGCAAGAGTCAATCCAGGCAATGACAAATCAAGTGTCTTCTATGAACAA 1268  
 QY 1453 TCGCCCAATAGTATCAAAACCGATGTAAATTTATCAATTTACAAAATTTGCTAGACCG 1512  
 Db 1269 TCGCCCAATAGTATCAAAACCGATGTAAATTTATCAATTTACAAAATTTGCTAGACCG 1328  
 QY 1513 AGTGATGCAAGATGACAGTATGATGTATGTTTATCGGAAACAGATGTTGGACCGT 1572  
 Db 1329 AGTGATGCAAGATGACAGTATGATGTATGTTTATCGGAAACAGATGTTGGACCGT 1388  
 QY 1573 TCTTAAAGTATGTTCAATTCCTAAGGAGACTGTTGATGATTTAGAGAGTCTCTGCTGA 1632  
 Db 1389 TCTTAAAGTATGTTCAATTCCTAAGGAGACTGTTGATGATTTAGAGAGTCTCTGCTGA 1448  
 QY 1633 AGAAATGACAGTTTTCGGGAACCGACTGCTATTTTACGCAATGGAGCTTTCACATGAACA 1692  
 Db 1449 AGAAATGACAGTTTTCGGGAACCGACTGCTATTTTACGCAATGGAGCTTTCACATGAACA 1508  
 QY 1693 GCAACAACTATATATGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTACACCGTGTGA 1752  
 Db 1509 GCAACAACTATATATGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTACACCGTGTGA 1568  
 QY 1753 TATTTACGGGAAGAGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTCTTGGGA 1812  
 Db 1569 TATTTACGGGAAGAGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTCTTGGGA 1628  
 QY 1813 TGTTTCTGATGTTCTGCTATTTTCCCACTGCAAGAGACGCAACAGCAAGATAT 1872  
 Db 1629 TGTTTCTGATGTTCTGCTATTTTCCCACTGCAAGAGACGCAACAGCAAGATAT 1688  
 QY 1873 AAGAAATGAGACCCACTGACTCTGCTTCACTGATATACCATGATATCACCATGGCCA 1932  
 Db 1689 AAGAAATGAGACCCACTGACTCTGCTTCACTGATATACCATGATATCACCATGGCCA 1748  
 QY 1933 CAGCCCTGAAGAGAGAACTCATCTATGGTGTAGAGAAATAGTACACATTTTGGAAATGCAG 1992  
 Db 1749 CAGCCCTGAAGAGAGAACTCATCTATGGTGTAGAGAAATAGTACACATTTTGGAAATGCAG 1808  
 QY 1993 TCCGAGTCCGAGAGAGCTGCTTATTTGGCAATTTCCAGAGCGCAAAATGAAGAGCGAAA 2052  
 Db 1809 TCCGAGTCCGAGAGAGCTGCTTATTTGGCAATTTCCAGAGCGCAAAATGAAGAGCGAAA 1868  
 QY 2053 AGAAGATGATGATGATGATATCATATCATAGGACAGATCAAGGCTTCTGCTAGTAG 2112  
 Db 1869 AGAAGATGATGATGATGATATCATATCATAGGACAGATCAAGGCTTCTGCTAGTAG 1928  
 QY 2113 TCTTACAAAGAGGATTCAGGCAATTTACCTCTGCCATGGGTGGAAACATGGGTTCATACA 2172  
 Db 1929 TCTTACAAAGAGGATTCAGGCAATTTACCTCTGCCATGGGTGGAAACATGGGTTCATACA 1988  
 QY 2173 AACTCTTCTTAAGGTAACCTTGAAGTCAATTTGACACAGAGCAATTTGGAAGAACTTCTTCA 2232  
 Db 1989 AACTCTTCTTAAGGTAACCTTGAAGTCAATTTGACACAGAGCAATTTGGAAGAACTTCTTCA 2048  
 QY 2233 TAAAGATGATGATGATGATGCTTGAAGCAAAAGAAATGTCGAATAGCATGACACTAG 2292  
 Db 2049 TAAAGATGATGATGATGATGCTTGAAGCAAAAGAAATGTCGAATAGCATGACACTAG 2108

QY 2293 CCAGAGGTCTGGTACAGAGACTTTCATGCGCTCATCAACCCACCAATCTCAACAGAT 2352  
 Db 2109 CCAGAGGTCTGGTACAGAGACTTTCATGCGCTCATCAACCCACCAATCTCAACAGAT 2168  
 QY 2353 GGATGAGTCTGTGAAACAGATTGGAAAAGGGACCGAAACAAAGTGGGCAAGGCCAGG 2412  
 Db 2169 GGATGAGTCTGTGAAACAGATTGGAAAAGGGACCGAAACAAAGTGGGCAAGGCCAGG 2228  
 QY 2413 ACATACCCCGAGGAAACAGTAACTTGAAGCACTTACAGAAAATTAAGAAAGGTAGAAA 2472  
 Db 2229 ACATACCCCGAGGAAACAGTAACTTGAAGCACTTACAGAAAATTAAGAAAGGTAGAAA 2288  
 QY 2473 CAGGAGACCCACCAAGTATGAGAGGACCCAGGAGTGTCTGAGCTGCATTACCTTAGA 2532  
 Db 2289 CAGGAGACCCACCAAGTATGAGAGGACCCAGGAGTGTCTGAGCTGCATTACCTTAGA 2348  
 QY 2533 AACCTCAAAACAGTATGAGAACTTGGCTAGACAAATTAACCTGGAAGAAACAAATGCAATATACAT 2592  
 Db 2349 AACCTCAAAACAGTATGAGAACTTGGCTAGACAAATTAACCTGGAAGAAACAAATGCAATATACAT 2408  
 QY 2593 GAACTTTTTCATGCGCAATTAATGATGATTTTACAAATGCTGGGAAATTCAGCTGAGTTCCA 2652  
 Db 2409 GAACTTTTTCATGCGCAATTAATGATGATTTTACAAATGCTGGGAAATTCAGCTGAGTTCCA 2468  
 QY 2653 CCAATTATATAAATAAATCCATGAGTAACTTTCTTAATAGGCTTTTTTTTC 2702  
 Db 2469 CCAATTATATAAATAAATCCATGAGTAACTTTCTTAATAGGCTTTTTTTTC 2518

RESULT 4

ABS76512  
 ID ABS76512 standard; cDNA; 2530 BP.  
 XX  
 AC ABS76512;  
 XX  
 DT 11-DEC-2002 (first entry)  
 XX  
 cDNA encoding human ovarian cancer marker M473.  
 DE  
 KW Human; ovarian cancer; marker; cancer; familial history; brain disorder;  
 central nervous system disorder; bacterial meningitis; viral meningitis;  
 Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;  
 brain herniation; inflammation; encephalitis; testicular disorder;  
 nontuberculous granulomatous orchitis; connective tissue disorder;  
 heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;  
 histological type; carcinogenic; ovarian cancer marker; gene; ss.

Homo sapiens.

WO200271928-A2.  
 19-SEP-2002.

14-MAR-2002; 2002WO-US007826.

14-MAR-2001; 2001US-0276025P.

14-MAR-2001; 2001US-0276026P.

10-AUG-2001; 2001US-0311732P.

19-SEP-2001; 2001US-0323580P.

26-SEP-2001; 2001US-0324967P.

26-SEP-2001; 2001US-0325102P.

26-SEP-2001; 2001US-0325149P.

(MILL-) MILLENNIUM PHARM INC.

Monahan JE, Gannavarapu M, Hoersch S, Kamathkar S, Kovatis SG;

Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;

Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;

WPI: 2002-723277/78.

P-PSDB; ABG96413.

XX

PT Assessing whether a patient is afflicted with ovarian cancer, useful in  
PT assessing the stage or progression of the disease, comprises comparing  
PT the expression level of a cancer marker in a sample from a patient and  
PT from a non cancer patient.

XX Disclosure; Page 400; 481pp; English.

XX The present invention relates to a new method for assessing whether a  
CC patient is afflicted with ovarian cancer. The method involves comparing  
CC the expression level of a marker in a patient sample and the normal level  
CC of expression of the marker in a control non-ovarian cancer sample, where  
CC the marker is selected from 363 cancer markers described in the  
CC specification. The method of the invention is useful in diagnosing or  
CC characterising cancer, in detecting the presence of cancer as early as  
CC possible, and the recurrence of ovarian cancer. The method may also be of  
CC particular use with patients having an enhanced risk of developing  
CC ovarian cancer (e.g. patients having a familial history of ovarian  
CC cancer). The cancer markers may be used in the management and treatment  
CC of e.g. brain and central nervous system disorders (e.g. bacterial and  
CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain  
CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),  
CC inflammations (e.g. bacterial or viral meningitis or encephalitis),  
CC testicular disorders (e.g. non-tuberculous granulomatous orchitis),  
CC connective tissue disorders, or heart disorders (e.g. ischaemic heart  
CC disease or atherosclerosis). The compositions and methods may also be  
CC used in assessing the histological type of neoplasm associated with  
CC ovarian cancer, monitoring the progression of ovarian cancer, determining  
CC whether ovarian cancer has metastasized or is likely to metastasize,  
CC selecting a composition for inhibiting ovarian cancer, assessing the  
CC ovarian carcinogenic potential of a compound, or inhibiting ovarian  
CC cancer or at risk of developing ovarian cancer. The present nucleic acid  
CC sequence encodes one of the ovarian cancer markers described in the  
CC invention

XX Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;

Query Match 92.6%; Score 2508.4; DB-6; Length 2530;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	193	CTGCACATGGGCTGTTAACTAGGATGTCCTCTTTCTGGGGAGTATTCTTACAGC	252
DB	9	CTGCACATGGGCTGTTAACTAGGATGTCCTCTTTCTGGGGAGTATTCTTACAGC	68
QY	253	AAGAGCAAACTATCAGATGGGAAGAACAAATGTCACAGGCTGAAATATTCTTACAAAGA	312
DB	69	AAGAGCAAACTATCAGATGGGAAGAACAAATGTCACAGGCTGAAATATTCTTACAAAGA	128
QY	313	AATGTTGGAATCAACAATGTGATCATCTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCA	372
DB	129	AATGTTGGAATCAACAATGTGATCATCTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCA	188
QY	373	TACCTTCTTTGGATGAGAACGGAGTAGGCTGTATGTTGGACAAAGGATCACAATTT	432
DB	189	TACCTTCTTTGGATGAGAACGGAGTAGGCTGTATGTTGGACAAAGGATCACAATTT	248
QY	433	TTCAATTCGACCTCGTTAAATCAAGGATTTTCAAAAGATTTGTGGCCAGATCTTTACAC	492
DB	249	TTCAATTCGACCTCGTTAAATCAAGGATTTTCAAAAGATTTGTGGCCAGATCTTTACAC	308
QY	493	CAGAAGAGATGAATCAAGTGGGCTCGAAAGACATCTCTGAAAGATGTCTAAATTTCAAT	552
DB	309	CAGAAGAGATGAATCAAGTGGGCTCGAAAGACATCTCTGAAAGATGTCTAAATTTCAAT	368
QY	553	CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACCGCTGTGGACCGGGGCTTTTCA	612
DB	369	CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACCGCTGTGGACCGGGGCTTTTCA	428
QY	613	TCCAAATTTGACCTACATATGAAATTTGGAATCATCATCTCTGAGGACAAATATTTAAAGCTGA	672
DB	429	TCCAAATTTGACCTACATATGAAATTTGGAATCATCATCTCTGAGGACAAATATTTAAAGCTGA	488
QY	673	GAACTCACATTTTGAACCGGCGTGGGAAGAGTCCATATGACCCCTTAAGCTGCTGACAGC	732

DB	489	GAACTCACATTTTGAACCGGCGTGGGAAGAGTCCATATGACCCCTTAAGCTGCTGACAGC	548
QY	733	ATCCCTTTTAAATAGATGGAGAATTTATCTCTGGAAGTCTGAGCTGATTTTATGGGGGAGA	792
DB	549	ATCCCTTTTAAATAGATGGAGAATTTATCTCTGGAAGTCTGAGCTGATTTTATGGGGGAGA	608
QY	793	CTTTGCTATCTTCCGAACTCTTTGGGCAACCAACCAATCAGACAGAGAGATGATTC	852
DB	609	CTTTGCTATCTTCCGAACTCTTTGGGCAACCAACCAATCAGACAGAGAGATGATTC	668
QY	853	CAGGTGGCTCAATGATCCAAAGTTCATTAAGTCCCACTCATCTCAGAGAGTACAAATCC	912
DB	669	CAGGTGGCTCAATGATCCAAAGTTCATTAAGTCCCACTCATCTCAGAGAGTACAAATCC	728
QY	913	TGAAGATGACAAAGTATATCTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTCTGG	972
DB	729	TGAAGATGACAAAGTATATCTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTCTGG	788
QY	973	AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATAGTCTTTGGAGGGCACAGAAG	1032
DB	789	AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATAGTCTTTGGAGGGCACAGAAG	848
QY	1033	TCTGTTGAATTAATGAGAACAACTTCTCAAAGTCTGCTGATTTGCTCAGTCCAGGTCC	1092
DB	849	TCTGTTGAATTAATGAGAACAACTTCTCAAAGTCTGCTGATTTGCTCAGTCCAGGTCC	908
QY	1093	AAATGGCATTTGACACTCATTTTGTGAACTGCAAGATGATTTCTTAATGAACCTTTAAAGA	1152
DB	909	AAATGGCATTTGACACTCATTTTGTGAACTGCAAGATGATTTCTTAATGAACCTTTAAAGA	968
QY	1153	TCCTAAAAATCCAGTTGTATATGGAGTGTATTACGACTCCAGTAAACATTTTCAAGGATC	1212
DB	969	TCCTAAAAATCCAGTTGTATATGGAGTGTATTACGACTCCAGTAAACATTTTCAAGGATC	1028
QY	1213	AGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTCTTGTGTCATATGCCCA	1272
DB	1029	AGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTCTTGTGTCATATGCCCA	1088
QY	1273	CAGGGATGAGCAACCACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTATCCAGGCC	1332
DB	1089	CAGGGATGAGCAACCACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTATCCAGGCC	1148
QY	1333	AGGAATCTTGTCCAGCAAAACATTTGGTGGTTTGTGACTCTCAAAAGGACCTTCTCTATGA	1392
DB	1149	AGGAATCTTGTCCAGCAAAACATTTGGTGGTTTGTGACTCTCAAAAGGACCTTCTCTATGA	1208
QY	1393	TGTTATAACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCTATGAAACA	1452
DB	1209	TGTTATAACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCTATGAAACA	1268
QY	1453	TCGCCCAATAGTGTATCAAAACCGATGTAATTTATCAATTTTACAAATTTGTCTAGACCG	1512
DB	1269	TCGCCCAATAGTGTATCAAAACCGATGTAATTTATCAATTTTACAAATTTGTCTAGACCG	1328
QY	1513	AGTGGATGCAAGAGTGGACAGTATGTTATGTTTATCGGAACAGATGTTGGGACCGT	1572
DB	1329	AGTGGATGCAAGAGTGGACAGTATGTTATGTTTATCGGAACAGATGTTGGGACCGT	1388
QY	1573	TCCTAAAGTGTGTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGA	1632
DB	1389	TCCTAAAGTGTGTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGA	1448
QY	1633	AGAAATGACAGTTCCTTCCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTTCACTAAGCA	1692
DB	1449	AGAAATGACAGTTCCTTCCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTTCACTAAGCA	1508
QY	1693	GCAACAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACGGTGTGA	1752
DB	1509	GCAACAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACGGTGTGA	1568
QY	1753	TATTTACGGGAAGCGTGTGCTGAGTGTTCCTCGCCCGAGAGCCCTTACTGTCTGTGGGA	1812



1569	Db	TATTACGGGAAGCGTGTCTGAGTGTTCCTCTGCCCGGAGACCTTACTGTGCTCTGGGA	1628
1813	Qy	TGGTTCTGCATGTTTCTCGCTATTTTTCCCACTGCAAGAGACGCAACAAGATAT	1872
1629	Db	TGGTTCTGCATGTTTCTCGCTATTTTTCCCACTGCAAGAGACGCAACAAGATAT	1688
1873	Qy	AAGAAATGGAGACCCACTGACTCACTGTTTCCAGACTTACACCATGATAATCACCATGGCCA	1932
1689	Db	AAGAAATGGAGACCCACTGACTCACTGTTTCCAGACTTACACCATGATAATCACCATGGCCA	1748
1933	Qy	CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGACACATTTTGGAAATGCAG	1992
1749	Db	CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGACACATTTTGGAAATGCAG	1808
1993	Qy	TCCGAAGTCCGAGAGCGCTGTGTTATTGGCAATTCACAGGCGAAATGAAGAGCGAAA	2052
1809	Db	TCCGAAGTCCGAGAGCGCTGTGTTATTGGCAATTCACAGGCGAAATGAAGAGCGAAA	1868
2053	Qy	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGGCCTTCTGCTACGTAG	2112
1869	Db	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGGCCTTCTGCTACGTAG	1928
2113	Qy	TCTACAAACAGAGGATTCAGGCAATTAACCTCTGCCATCGGTGGAAACATGGGTTTCAACA	2172
1929	Db	TCTACAAACAGAGGATTCAGGCAATTAACCTCTGCCATCGGTGGAAACATGGGTTTCAACA	1988
2173	Qy	AACCTCTTTTAAAGTAAACCTTGAAGTCATTGACACAGAGCATTTTGAAGAACTTTCTTCA	2232
1989	Db	AACCTCTTTTAAAGTAAACCTTGAAGTCATTGACACAGAGCATTTTGAAGAACTTTCTTCA	2048
2233	Qy	TAAAGATGATGTGGAGATGGCTCTAAGACCAAGAAATCTCCAATAGCATGACACCTAG	2292
2049	Db	TAAAGATGATGTGGAGATGGCTCTAAGACCAAGAAATCTCCAATAGCATGACACCTAG	2108
2293	Qy	CCAGAGGTCGTGTTACAGAGACTTCATGCGAGTCTCAACAACCCCAATCTCAACAGCAT	2352
2109	Db	CCAGAGGTCGTGTTACAGAGACTTCATGCGAGTCTCAACAACCCCAATCTCAACAGCAT	2168
2353	Qy	GGATGAGTCTGTGTAACAAGTTTGGAAAAGGGACCGAAAAACAGCTCGGCAAAAGGCCAGG	2412
2169	Db	GGATGAGTCTGTGTAACAAGTTTGGAAAAGGGACCGAAAAACAGCTCGGCAAAAGGCCAGG	2228
2413	Qy	ACATACCCCGGGAAACAGTAAACAAATGGAAAGCACTTACAAGAAAAATGAAGAAAGTAGAAA	2472
2229	Db	ACATACCCCGGGAAACAGTAAACAAATGGAAAGCACTTACAAGAAAAATGAAGAAAGTAGAAA	2288
2473	Qy	CAGAGGACCCACGAATTTGAGAGGGCAACCCAGAGTGTCTGAGTGCATTAACCTCTAGA	2532
2289	Db	CAGAGGACCCACGAATTTGAGAGGGCAACCCAGAGTGTCTGAGTGCATTAACCTCTAGA	2348
2533	Qy	AACCTCAAAACAAGTAGAAACTTGCTTAGACAATAACTGGHAAACAATAATGCAATATACAT	2592
2349	Db	AACCTCAAAACAAGTAGAAACTTGCTTAGACAATAACTGGHAAACAATAATGCAATATACAT	2408
2593	Qy	GAACTTTTTTTCATGGCATTAATGTGGATGTTTACAATGGTGGAAATTCAGCTGAGTTCCA	2652
2409	Db	GAACTTTTTTTCATGGCATTAATGTGGATGTTTACAATGGTGGAAATTCAGCTGAGTTCCA	2468
2653	Qy	CCAATTAAATTAATCCATGAGTAACCTTCTCAATAGGCTTTTTTTCC	2702
2469	Db	CCAATTAAATTAATCCATGAGTAACCTTCTCAATAGGCTTTTTTTTC	2518

## RESULT 5

RESULT 3  
ADD08933  
ID ADD08933 standard; cDNA; 2530 BP.

AA ADD08933;

01-JAN-2004 (first entry)

XX DE Human semaphorin 3A encoding cDNA SEQ ID NO:9.

XX

KW	screening; modulator; binding; neuropilin growth factor receptor;
KW	vascular endothelial growth factor C;
KW	vascular endothelial growth factor receptor 3; VEGF-C; VEGFR-3;
KW	neuropilin; cytosolic; neurotrophic; neuroprotective; vulnary;
KW	vasotonic; cardiac; angiogenic process; nervous system growth;
KW	nervous system function; cancer; ischaemia; cerebral infarction;
KW	cerebral bleeding; Alzheimer's disease; myocardial infarction; human;
KW	gene; ss.
XX	
XX	Homo sapiens.
XX	
XX	
EH	Key Location/Qualifiers
FT	CDS 16..2331
FT	/tag= a
FT	/product= "semaphorin 3A"
XX	
XX	WO2003029814-A2.
PN	
PD	10-APR-2003.
XX	
XX	
XX	01-OCT-2002; 2002WO-EP0111069.
PF	
XX	
XX	01-OCT-2001; 2001US-0326326P.
PR	
XX	(LUDW-) LUDWIG INST CANCER RES.
PA	(LICN ) LICENTIA LTD.
PA	
XX	
XX	Alitalo K, Karkkainen M, Karila K;
PI	
XX	WPI; 2003-381660/36.
DR	P-PSDB; ADD08934.
DR	
XX	
XX	
PT	Screening for modulators of neuropilin and vascular endothelial growth
PT	factor (VEGF)-C or VEGFR-3 interactions, comprises comparing interaction
PT	of neuropilin and VEGF-C or VEGFR-3 in the presence and absence of a
PT	modulator compound.
FT	
XX	
XX	Disclosure; SEQ ID NO 9; 181pp; English.
XX	
CC	The present invention describes a method of screening for modulators of
CC	binding between a neuropilin growth factor receptor and a vascular
CC	endothelial growth factor (VEGF)-C or VEGFR-3 polypeptide comprising
CC	comparing the binding between neuropilin and VEGF-C or VEGFR-3 in the
CC	presence and in the absence of a putative modulator compound. Also
CC	described: (1) screening for selectivity of a modulator of VEGF-C, VEGFR-
CC	3 or neuropilin biological activity; (2) modulating growth, migration or
CC	proliferation of cells in a mammalian organism; (3) a bispecific antibody
CC	which specifically binds to a neuropilin receptor and a VEGF-C or VEGFR-3
CC	polypeptide; (4) modulating neuronal growth or neuronal scarring in a
CC	mammalian organism; and (5) a polypeptide comprising a fragment of a VEGF
CC	-C that binds to a neuropilin receptor. The modulators have cytostatic,
CC	neurotropic, neuroprotective, vulnary, vasotropic and cardiant
CC	activities. The method is useful in modulating angiogenic processes and
CC	nervous system growth and function, such as in the treatment of cancer,
CC	wound, ischaemia, cerebral infarction/bleeding, Alzheimer's disease or
CC	myocardial infarction. The polypeptide comprising a fragment of a VEGF-C
CC	that binds to a neuropilin receptor, is useful for manufacturing a
CC	medicament for the treatment of diseases characterised by aberrant
CC	growth, migration or proliferation of cells that express a neuropilin
CC	receptor. The present sequence encodes human semaphorin 3A, which is used
CC	in the exemplification of the present invention.
XX	
XX	Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;
Seq	
Query Match	92.6%; Score 2508.4; DB 10; Length 2530;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2509; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	193 CTGCAGCATGGCGTGGTTAACTAGGATGTGTCCTTTCTGGGGAGCTATTACTTACAGC 252
Dd	9 CTGCAGCATGGCGTGGTTAACTAGGATGTGTCCTTTCTGGGGAGCTATTACTTACAGC 68
OY	253 AAGAGCAAACTATCAGAATGGGAAGACAATGTGCCAAGGCTGAAATATGCTTCAAAGA 312





QY 2473 CAGGAGGACCCACGAATTTGAGAGGGCCACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2532  
DB 2289 CAGGAGGACCCACGAATTTGAGAGGGCCACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2348  
QY 2533 AACCTCAACAGTAGAAGTCTGCTAGACAAATACTGGAAAAACAATGCAATATACAT 2592  
DB 2349 AACCTCAACAGTAGAAGTCTGCTAGACAAATACTGGAAAAACAATGCAATATACAT 2408  
QY 2593 GAACCTTTTTCATGCGATATATGATGTTTCAATGCTGGGAATTCAGCTGAGTTCCA 2652  
DB 2409 GAACCTTTTTCATGCGATATATGATGTTTCAATGCTGGGAATTCAGCTGAGTTCCA 2468  
QY 2653 CCAATTATATAAATAATCCATCAGTAACCTTCTTAATAGGCTTTTTCCTCC 2702  
DB 2469 CCAATTATATAAATAATCCATCAGTAACCTTCTTAATAGGCTTTTTCCTCC 2518

RESULT 6  
ADN95334  
ID ADN95334 standard; DNA; 2530 BP.  
XX AC ADN95334;  
XX DT 01-JUL-2004 (first entry)  
XX DE Human BEC/LEC-related gene sequence SeqID256.  
XX KW growth; differentiation; blood endothelial cell; BEC;  
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;  
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;  
KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;  
KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;  
KW human.  
XX OS Homo sapiens.  
XX PN WO2003080640-A1.  
XX PD 02-OCT-2003.  
XX PF 07-MAR-2003; 2003WO-US006900.  
XX PR 07-MAR-2002; 2002US-0363019P.  
XX PA (LUDW-) LUDWIG INST CANCER RES.  
XX PA (LICN) LICENTIA LTD.  
XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;  
XX WPI: 2003-876899/81.  
XX DR P-PSDB; ADN95333.  
XX PS Example 1; SEQ ID NO 256; 176pp; English.

This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a

CC medicament for the differential modulation of blood vessel endothelial cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed gene which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the CC indexer using the source data given in table 14 of the specification.

XX Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;

Query Match 92.6%; Score 2508.4; DB 11; Length 2530;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGAGCATGGCTGGTTAACTAGGATTTCTCTCTTTCTGGGAGTATTACTTACAGC 252  
DB 9 CTGAGCATGGCTGGTTAACTAGGATTTCTCTCTTTCTGGGAGTATTACTTACAGC 68  
QY 253 AAGAGCAAACTATCAGAAATGGAAACAATGTGCAAGGCTGAAATTTATCTACAAAGA 312  
DB 69 AAGAGCAAACTATCAGAAATGGAAACAATGTGCAAGGCTGAAATTTATCTACAAAGA 128  
QY 313 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 372  
DB 129 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 188  
QY 373 TACCTTCCTTTTGGATGAGGAACGGAGTAGCTGTATGTTGGAGCAAAAGGATCATAATT 432  
DB 189 TACCTTCCTTTTGGATGAGGAACGGAGTAGCTGTATGTTGGAGCAAAAGGATCATAATT 248  
QY 433 TTCAATCCACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 492  
DB 249 TTCAATCCACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 308  
QY 493 CAGAAGAGATGAATGCAAGTGGCTGGAAAGACATCTCGAAAGAAATGTGCTAAATTCAT 552  
DB 309 CAGAAGAGATGAATGCAAGTGGCTGGAAAGACATCTCGAAAGAAATGTGCTAAATTCAT 368  
QY 553 CAAGGTACTTAAGGCATATATCAGACTCACTTTGACGCTGTGGAACGGGGGCTTTTCA 612  
DB 369 CAAGGTACTTAAGGCATATATCAGACTCACTTTGACGCTGTGGAACGGGGGCTTTTCA 428  
QY 613 TCCAAATTTGCACTTAAATTTGGAACATCATCTCGAGGACAAATATTTTAAAGCTGGA 672  
DB 429 TCCAAATTTGCACTTAAATTTGGAACATCATCTCGAGGACAAATATTTTAAAGCTGGA 488  
QY 673 GAACCTCAATTTTGAACACGGCCGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 732  
DB 489 GAACCTCAATTTTGAACACGGCCGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 548  
QY 733 ATCCCTTTTAAATAGATGAGAAATTAATCTCTGGAATCTGAGTATTTTATGGGCGAGA 792  
DB 549 ATCCCTTTTAAATAGATGAGAAATTAATCTCTGGAATCTGAGTATTTTATGGGCGAGA 608  
QY 793 CTTTGCTATCTTCCGAACTCTTTGGGCACCAACCCCAATTCAGGACAGAGCATGATTC 852  
DB 609 CTTTGCTATCTTCCGAACTCTTTGGGCACCAACCCCAATTCAGGACAGAGCATGATTC 668  
QY 853 CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCCACTCATCTCAGAGAGTGACAATCC 912  
DB 669 CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCCACTCATCTCAGAGAGTGACAATCC 728  
QY 913 TGAAGTACAAAGTATATCTTTCTTCCGTGGAATCCAAATAGATGAGAGACACTCTCG 972  
DB 729 TGAAGTACAAAGTATATCTTTCTTCCGTGGAATCCAAATAGATGAGAGACACTCTCG 788  
QY 973 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTGGAGGGCACAGAAG 1032  
DB 789 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTGGAGGGCACAGAAG 848

Qy	1033	TCTGGTGAATAAATGGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC	1091
Db	849	TCTGGTGAATAAATGGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC	908
Qy	1093	AAATGGCATTTGACACTCATTTTGATGAACATGCGAGGATGTATTCCTAATGAACTTTAAAGA	1152
Db	909	AAATGGCATTTGACACTCATTTTGATGAACATGCGAGGATGTATTCCTAATGAACTTTAAAGA	968
Qy	1153	TCTTAAAAATCCAGTTGTATATGAGTGTGTTTACGACTTCACAGTAAACATTTTCAAGGGATC	1212
Db	969	TCCTAAAAATCCAGTTGTATATGAGTGTGTTTACGACTTCACAGTAAACATTTTCAAGGGATC	1028
Qy	1213	AGCCGTGTGTATGTATATGATGATGTATGTGAGAGGGTGTCTTGTTGTCATATGCCCCA	1272
Db	1029	AGCCGTGTGTATGTATATGATGATGTATGTGAGAGGGTGTCTTGTTGTCATATGCCCCA	1088
Qy	1273	CAGGGATGGACCCAACTCATCAATGGGTGCCTTATCAAGGAGAGTCCCTTATCCACGGCC	1332
Db	1089	CAGGGATGGACCCAACTCATCAATGGGTGCCTTATCAAGGAGAGTCCCTTATCCACGGCC	1148
Qy	1333	AGGAACTTGTCCACGACAAAACATTTGTTGGTGTGTTTGACTCTCAAAAGACCTTCTCTGATGA	1392
Db	1149	AGGAACTTGTCCACGACAAAACATTTGTTGGTGTGTTTGACTCTCAAAAGACCTTCTCTGATGA	1208
Qy	1393	TGTTATAACCTTTTGCAGAGAGTCAATCAGGCCATGTACAAATCCAGTGTTCCTATGAACAA	1452
Db	1209	TGTTATAACCTTTTGCAGAGAGTCAATCAGGCCATGTACAAATCCAGTGTTCCTATGAACAA	1268
Qy	1453	TGCGCCCAATAGTCAATCAAAAGGATGTAAATTTATCAATTTTACACAAATTTGTCGTAGACCG	1512
Db	1269	TGCGCCCAATAGTCAATCAAAAGGATGTAAATTTATCAATTTTACACAAATTTGTCGTAGACCG	1328
Qy	1513	AGTGGATGCGAAGATGCACATGATGATTTATGTTTATCGGAACAGATGTGCGGACCGT	1572
Db	1329	AGTGGATGCGAAGATGCACATGATGATTTATGTTTATCGGAACAGATGTGCGGACCGT	1388
Qy	1573	TCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGATGTATGATTTAGAGAGAGTTCTGCTGGA	1632
Db	1389	TCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGATGTATGATTTAGAGAGAGTTCTGCTGGA	1448
Qy	1633	AGAAATGACAGATTTTTCGGGAAACCGACTGCTATTTACGAAATCGAGCTTTCACCTAAGCA	1692
Db	1449	AGAAATGACAGATTTTTCGGGAAACCGACTGCTATTTACGAAATCGAGCTTTCACCTAAGCA	1508
Qy	1693	GCAACCACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGA	1752
Db	1509	GCAACCACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGA	1568
Qy	1753	TATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTGCTTTGGGA	1812
Db	1569	TATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTGCTTTGGGA	1628
Qy	1813	TGGTTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGACAAAGATAT	1872
Db	1629	TGGTTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGACAAAGATAT	1688
Qy	1873	AAGAAATGGAGACCCACTGACTCACTGTCAGACTTTACACCATGTATAACACCATCGGCCA	1932
Db	1689	AAGAAATGGAGACCCACTGACTCACTGTCAGACTTTACACCATGTATAACACCATCGGCCA	1748
Qy	1933	CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTACACATTTTGGAAATGCAG	1992
Db	1749	CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTACACATTTTGGAAATGCAG	1808
Qy	1993	TCCGAAGTCGAGAGACCGCTGGTCTATTTGGGCAATTTCAGAGCGGAAATGGAAGCGGAAA	2052
Db	1809	TCCGAAGTCGAGAGACCGCTGGTCTATTTGGGCAATTTCAGAGCGGAAATGGAAGCGGAAA	1868
Qy	2053	AGAAGAGATCAGAGTGCATCATATCATCAGSACAGATCAAGGCTTCTGCTGCTAGTAG	2112
Db	1869	AGAAGAGATCAGAGTGCATCATATCATCAGSACAGATCAAGGCTTCTGCTGCTAGTAG	1928
Qy	2113	TCTACAAAGAGAGGATTCAGGCAATTAACCTCTGCAATCGCGGTGGAAACATGGGTTTCATACA	2172

[illegible]

XX Example 2; SEQ ID NO 2569; 210pp; English.

PS The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual

CC and a normal soft tissue sample from the same or different individual,

CC determining the expression of a gene in both samples and comparing the

CC expression of the gene in both soft tissue samples, where a higher level

CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has

CC cytostatic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.

CC The current sequence is that of a human soft tissue sarcoma-upregulated

CC DNA of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX

SQ Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;

Query Match 92.6%; Score 2508.4; DB 12; Length 2530;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGAGCATGGCTGTTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 252

DB 9 CTGAGCATGGCTGTTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 68

QY 253 AAGAGCAACTATCAGATGGGAGGAGCAATGTCGCAAGGCTGAATATCTTACAAAGA 312

DB 69 AAGAGCAACTATCAGATGGGAGGAGCAATGTCGCAAGGCTGAATATCTTACAAAGA 128

QY 313 AATGTTGGAAATCAACAATGTGATCACTTTCAATGGCTGGCCACAGCTCCAGTTATCA 372

DB 129 AATGTTGGAAATCAACAATGTGATCACTTTCAATGGCTGGCCACAGCTCCAGTTATCA 188

QY 373 TACCTTCCCTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGACAAAGGATCAATATT 432

DB 189 TACCTTCCCTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGACAAAGGATCAATATT 248

QY 433 TTCAATCGACCTGGTTAATATCAAGATTTTCAAGAGATGTTGGCCAGTATCTTACAC 492

DB 249 TTCAATCGACCTGGTTAATATCAAGATTTTCAAGAGATGTTGGCCAGTATCTTACAC 308

QY 493 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGATGTCTAAATTTCAAT 552

DB 309 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGATGTCTAAATTTCAAT 368

QY 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGAAACGGGGCTTTTCA 612

DB 369 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGAAACGGGGCTTTTCA 428

QY 613 TCCAAATTCACCTACATGAATTTGGACATCATCTCTGAGGACATATTTTAAAGCTGA 672

DB 429 TCCAAATTCACCTACATGAATTTGGACATCATCTCTGAGGACATATTTTAAAGCTGA 488

QY 673 GAACTCACAATTTGAAACGGCGCTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGC 732

DB 489 GAACTCACAATTTGAAACGGCGCTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGC 548

QY 733 ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGAAACTGACGCTGATTTTATCGGGCGAGA 792

DB 549 ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGAAACTGACGCTGATTTTATCGGGCGAGA 608

QY 793 CTTTGTATCTTCCGACTTTGGGACCAACCAACCAATCATCAGACAGACAGCATGATTC 852

DB 609 CTTTGTATCTTCCGACTTTGGGACCAACCAACCAATCATCAGACAGACAGCATGATTC 668

QY 853 CAGGTGGCTCAATGATCCAAAGTTCAATAGTCCACCTCATCTCAGAGAGTGACAAATCC 912

DB 669 CAGGTGGCTCAATGATCCAAAGTTCAATAGTCCACCTCATCTCAGAGAGTGACAAATCC 728

QY 913 TGAAGATGACAAAGTATACCTTTTCTTCGTGAAATGCAATAGATGGAGAAACATCTGG 972

DB 729 TGAAGATGACAAAGTATACCTTTTCTCCGTGAAATGCAATAGATGAGAGAACACTCTGG 788

QY 973 AAAAGCTACTCACGCTAGAAATAGCTCAGATATGCAAGAAATGACTTTTGAGGGGCACAGAAG 1032

DB 789 AAAAGCTACTCACGCTAGAAATAGCTCAGATATGCAAGAAATGACTTTTGAGGGGCACAGAAG 848

QY 1033 TCTGGTGAATAAATGGGACAAATCTTCTCAAAAGCTCGTCTGATTTGCTCAGTGCACAGGTCC 1092

DB 849 TCTGGTGAATAAATGGGACAAATCTTCTCAAAAGCTCGTCTGATTTGCTCAGTGCACAGGTCC 908

QY 1093 AAAATGGCATTCACACTCAATTTTGAATGACGAGAGTATCTTCAATGAACTTTTAAAGA 1152

DB 909 AAAATGGCATTCACACTCAATTTTGAATGACGAGAGTATCTTCAATGAACTTTTAAAGA 968

QY 1153 TCCTAAAAATCCAGTTGTATATGAGTGTTCACGATCTTCAGTAACTATTTCAAGGGATC 1212

DB 969 TCCTAAAAATCCAGTTGTATATGAGTGTTCACGATCTTCAGTAACTATTTCAAGGGATC 1028

QY 1213 AGCCGTGTATATGATAGCATGATGTGAGAGGGTGTTCCTTGTGTCATATGCCCA 1272

DB 1029 AGCCGTGTATATGATAGCATGATGTGAGAGGGTGTTCCTTGTGTCATATGCCCA 1088

QY 1273 CAGGGATGGACCCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCACGGCC 1332

DB 1089 CAGGGATGGACCCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCACGGCC 1148

QY 1333 AGGAACCTTGTCCAGCAAAACATTTGGTGGTGTTCGACTCTACAAAGGACCTTCCTGATGA 1392

DB 1149 AGGAACCTTGTCCAGCAAAACATTTGGTGGTGTTCGACTCTACAAAGGACCTTCCTGATGA 1208

QY 1393 TGTATAAACCTTTGCAAGAGTCATCCAGCCATGTATCAATCAAGTGTTCCTATGAAACA 1452

DB 1209 TGTATAAACCTTTGCAAGAGTCATCCAGCCATGTATCAATCAAGTGTTCCTATGAAACA 1268

QY 1453 TCGCCCAATAGTGTATCAAAACGGATGTAAATTAATCAATTTTACAAATTTGTCGTAGACCG 1512

DB 1269 TCGCCCAATAGTGTATCAAAACGGATGTAAATTAATCAATTTTACAAATTTGTCGTAGACCG 1328

QY 1513 AGTGATGACGAAGATGACATGATGTATGTTTATCGGAAACAGATGTTGGACCGT 1572

DB 1329 AGTGATGACGAAGATGACATGATGTATGTTTATCGGAAACAGATGTTGGACCGT 1388

QY 1573 TCTTAAAGTATGTTCAATCTTAAAGGACATTTGGTATGATTTAGAGAGGTTCTGCTGA 1632

DB 1389 TCTTAAAGTATGTTCAATCTTAAAGGACATTTGGTATGATTTAGAGAGGTTCTGCTGA 1448

QY 1633 AGAATGACGATTTTTCGGGAACCGACTGTATTTTACGAATGGAGCTTCCACTAAGCA 1692

DB 1449 AGAATGACGATTTTTCGGGAACCGACTGTATTTTACGAATGGAGCTTCCACTAAGCA 1508

QY 1693 GCAACAACTATATTTGGTTCAACCGCTGGGGTTCGCCAGCTCCCTTTTACACCGGTGGA 1752

DB 1509 GCAACAACTATATTTGGTTCAACCGCTGGGGTTCGCCAGCTCCCTTTTACACCGGTGGA 1568

QY 1753 TATTACCGGAAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTATCTGTGCTGGGA 1812

DB 1569 TATTACCGGAAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTATCTGTGCTGGGA 1628

QY 1813 TGGTCTGCTATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAGCAGACAGATAT 1872

DB 1629 TGGTCTGCTATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAGCAGACAGATAT 1688

QY 1873 AAGAAATGGAGACCCACTGACTCACTGTTTACAGACTTTACACCATGATAATCACCATGGCCA 1932

DB 1689 AAGAAATGGAGACCCACTGACTCACTGTTTACAGACTTTACACCATGATAATCACCATGGCCA 1748

QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACACATTTTGGAAATGCG 1992

DB 1749 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACACATTTTGGAAATGCG 1808

QY 1993 TCCGAGTCCGACAGAGCGCTGTTCTATTTGGCAATTTCCAGAGCGGCAATAGAGAGCGAA 2052

DB 1809 TCCGAGTCCGACAGAGCGCTGTTCTATTTGGCAATTTCCAGAGCGGCAATAGAGAGCGAA 1868

Qy	2053	AGAAGAGATCAGAGTGGATGATCATATATCATCAGACAGATCAAGGCCCTTCTGCTACGTAG	2112
Db	1869	AGAAGAGATCAGAGTGGATGATCATATATCATCAGACAGATCAAGGCCCTTCTGCTACGTAG	1928
Qy	2113	TCTACAACAGAAAGATTTCAGGCAATTACCTTCGTCATCGCGTGGAAACATCGGGTTCATACA	2172
Db	1929	TCTACAACAGAAAGATTTCAGGCAATTACCTTCGTCATCGCGTGGAAACATCGGGTTCATACA	1988
Qy	2173	AACCTCTTTAAAGTAAACCTTGGAAATTCATGACACAGAGCATTTTGAAGAACTTCTTCA	2232
Db	1989	AACCTCTTTAAAGTAAACCTTGGAAATTCATGACACAGAGCATTTTGAAGAACTTCTTCA	2048
Qy	2233	TAAAGATGATGATGGAGATCGCTCTAAGACCAAGAAATCTCCAAATAGCATGACACCTAG	2292
Db	2049	TAAAGATGATGATGGAGATCGCTCTAAGACCAAGAAATCTCCAAATAGCATGACACCTAG	2108
Qy	2293	CCAGAAGGTCGTGTACAGAGACATTCATGCAAGCTCATCAACACCCCAATCTCAACACGAT	2352
Db	2109	CCAGAAGGTCGTGTACAGAGACATTCATGCAAGCTCATCAACACCCCAATCTCAACACGAT	2168
Qy	2353	GGATGAGTCTCTGTGAAACAAGTTTGGAAAAAGGACCGAAAAACAACGTCGGCAAAAGGCCAGG	2412
Db	2169	GGATGAGTCTCTGTGAAACAAGTTTGGAAAAAGGACCGAAAAACAACGTCGGCAAAAGGCCAGG	2228
Qy	2413	ACATACCCAGGGAAACAGTAACAAATGGAAAGCACTTACAAGAAAAATAAGAAAAAGGTAGAAA	2472
Db	2229	ACATACCCAGGGAAACAGTAACAAATGGAAAGCACTTACAAGAAAAATAAGAAAAAGGTAGAAA	2288
Qy	2473	CAGGAGACCCACGAATTTGAGAGGGGACCCAGAGGTCTGAGCTGCACTTACCTCTAGA	2532
Db	2289	CAGGAGACCCACGAATTTGAGAGGGGACCCAGAGGTCTGAGCTGCACTTACCTCTAGA	2348
Qy	2533	AACCTCAAAACAAGTAGAAAATTCGCTTAGACAATAACTTGGAAAAACAATAATCAATATACAT	2592
Db	2349	AACCTCAAAACAAGTAGAAAATTCGCTTAGACAATAACTTGGAAAAACAATAATCAATATACAT	2408
Qy	2593	GAACCTTTTTCATGGCATATGTGGATGTTTTCAATGGTGGAAAAATTCAGCTCAGTTCCA	2652
Db	2409	GAACCTTTTTCATGGCATATGTGGATGTTTTCAATGGTGGAAAAATTCAGCTCAGTTCCA	2468
Qy	2653	CCAATTATAAATTAAATCCATGAGTAACCTTCTCCTAATAGCCTTTTTTCC	2702
Db	2469	CCAATTATAAATTAAATCCATGAGTAACCTTCTCCTAATAGCCTTTTTTTC	2518

RESULT 8

RESOL 8  
AA087442AAQ87442  
IR AAQ87442 standard: cDNA: 2601 bp.

AAQ8 / 442

XX  
XC  
33087413.

AAQ8/442;

XX  
DE  
OF VXB CVC  
(continued)

25-MAR-2003 (revised)

DT 21-NOV-1995 (first entry)

1000

DE Human semaphorin III cDNA.

**XX**

KW Semaphorin; grasshopper; h

KW variola major virus; smallpox

KW modulation; nerve cell growth

KW neurological disease; neur

XX

OS Homo sapiens.

XX  
---

FH	Key	Location/Comments
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
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98	98	98
99	99	99
100	100	100

FT	CDS	16.	2331
FT	CDS	16.	2331

FT/\*tag= a

==prod/  
=test/  
=test/


XX 13  
-2222222222/

PN WO9507706-A1

PN  
yy  
MO9507706-A1.

XX  
DD  
22-MAY-1995

PD 23-MAR-1995.



PF	13-SEP-1994;	94WO-US010151.	
XX			
XX	13-SEP-1993;	93US-00121713.	
XX			
XX	(REGC ) UNIV CALIFORNIA.		
XX			
PI	Goodman CS, Kolodkin AL, Matthes D, Bentley DR, O'Connor T;		
XX			
XX	WPI; 1995-131177/17.		
DR			
DR	P-PSDB; AAR71380.		
XX			
XX			
PT	New class of semaphorin peptide(s) and polypeptide(s) - are potent		
PT	modulators of nerve cell growth and regeneration.		
XX			
XX	Example 2; Page 60-63; 101pp; English.		
XX			
CC	The sequence of the cDNA encoding the human semaphorin III protein. The		
CC	proteins encoded by the grasshopper semaphorin I (AAQ87441), human		
CC	semaphorin III, vaccinia virus semaphorin IV (AAQ87443), Drosophila		
CC	semaphorin I and II (AAQ87444-5), Tribolium semaphorin I (AAQ87446) or		
CC	varicella major (smallpox) virus semaphorin IV (AAQ87447) genes were used		
CC	to generate a series of peptides (AAR70370-R70418), which retain		
CC	semaphorin receptor binding activity. The semaphorin derived or		
CC	semaphorin receptor derived peptides are potent modulators of nerve cell		
CC	growth, immune responsiveness and viral pathogenesis. They can be used in		
CC	diagnosis and treatment of neurological disease and neuro-regeneration,		
CC	immune modulation and diagnosis and treatment of viral and oncological		
CC	infection and diseases. (Updated on 25-MAR-2003 to correct PN field.)		
XX			
XX	Sequence 2601 BP; 809 A; 533 C; 593 G; 666 T; 0 U; 0 Other;		
SQ			
	Query Match	92.6%; Score 2508.4; DB 2; Length 2601;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 2509; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	193	CTCAGCATGGGCTGGTTAACTAGGATGTCCTCTCTTTCTGGGGAGTATTACTTACAGC	252
DB	9	CTCAGCATGGGCTGGTTAACTAGGATGTCCTCTCTTTCTGGGGAGTATTACTTACAGC	68
QY	253	AAGAGCAAACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTGAATATTCTTACAAAGA	312
DB	69	AAGAGCAAACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTGAATATTCTTACAAAGA	128
QY	313	AATGTTGGAATCAACAAATGTATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA	372
DB	129	AATGTTGGAATCAACAAATGTATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA	188
QY	373	TACCTTCTTTTGGATGAGAAACGGAGTAGGCTGTATGTTGGACCAAGGATCACATATT	432
DB	189	TACCTTCTTTTGGATGAGAAACGGAGTAGGCTGTATGTTGGACCAAGGATCACATATT	248
QY	433	TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC	492
DB	249	TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC	308
QY	493	CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTCTAATTTTCA	552
DB	309	CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTCTAATTTTCA	368
QY	553	CAGAGTACTTAAGGCATATAATCAGACTCACTTGTACGCCTGTGGAAACGGGGGCTTTTCA	612
DB	369	CAAGGTACTTAAAGGCATATAATCAGACTCACTTGTACGCCTGTGGAAACGGGGGCTTTTCA	428
QY	613	TCCAAATTGACCTTACATTCGAAATGACATCATCTCTGAGGACAAATATTTTAACTGCTGA	672
DB	429	TCCAAATTGACCTTACATTCGAAATGACATCATCTCTGAGGACAAATATTTTAACTGCTGA	488
QY	673	GAACTCACATTTTGAAAACGGCCGTGGGAAGAGTCCAATGACCCCTAAGCTGTGACAGC	732
DB	489	GAACTCACATTTTGAAAACGGCCGTGGGAAGAGTCCAATGACCCCTAAGCTGTGACAGC	548
QY	733	ATCCCTTTTAAATGATCGAATAATATATCTGTGAACTGCAAGTATTTTATGGGGCGAGA	792

549	Db	ATCCCTTTTAAATAGATCGAGAAATTATTA	CTCTGGAACTGCGAGCTGATTTT	TATATGGGCGAGA	608	
793	Qy	CTTTTGTCTATCTTCCGA	ACTCTTTGGGCACCA	CCCACTCAGGACAGACAGCATGATTC	852	
609	Db	CTTTTGTCTATCTTCCGA	ACTCTTTGGGCACCA	CCCACTCAGGACAGACAGCATGATTC	668	
853	Qy	CAGTGTGCTCAATGAT	CAAAAGTTTCATTAGTGCC	CACTCATCTCAGAGAGTGACAATCC	912	
669	Db	CAGTGTGCTCAATGAT	CAAAAGTTTCATTAGTGCC	CACTCATCTCAGAGAGTGACAATCC	728	
913	Qy	TGAAGATGACAAAGTATAC	TTTTTCTTCCGTGAAATGCAATAGATGGAGAA	CACTCTGTG	972	
729	Db	TGAAGATGACAAAGTATAC	TTTTTCTTCCGTGAAATGCAATAGATGGAGAA	CACTCTGTG	788	
973	Qy	AAAAGCTACTCACGCTAGAA	TAGGT	CAGATATGCAAGAA	TGACTTTTGGAGGGGCACAGAAG	1032
789	Db	AAAAGCTACTCACGCTAGAA	TAGGT	CAGATATGCAAGAA	TGACTTTTGGAGGGGCACAGAAG	848
1033	Qy	TCTGGTGAATAAATGGACA	CAATTCCTCAAAAGCTCGTCTGATTTGCTCAGTGC	CGCCAGTCC	1092	
849	Db	TCTGGTGAATAAATGGACA	CAATTCCTCAAAAGCTCGTCTGATTTGCTCAGTGC	CGCCAGTCC	908	
1093	Qy	AAATGGCAATTGACACTCA	TTTTTGA	TGAACTGCGAGGATGTAATCCTTAATGA	ACTTTTAAAGA	1152
909	Db	AAATGGCAATTGACACTCA	TTTTTGA	TGAACTGCGAGGATGTAATCCTTAATGA	ACTTTTAAAGA	968
1153	Qy	TCCTAAAAATCCAGTCTG	TATATGAGAGT	TTTTACGACTTC	CAGTAAACATTTTCAAGGGATC	1212
969	Db	TCCTAAAAATCCAGTCTG	TATATGAGAGT	TTTTACGACTTC	CAGTAAACATTTTCAAGGGATC	1028
1213	Qy	AGCCGTGTGTATGTATAG	CTATGATGTGAGAA	GGGTGTTCTCTGGTCC	ATATGCCCCA	1272
1029	Db	AGCCGTGTGTATGTATAG	CTATGATGTGAGAA	GGGTGTTCTCTGGTCC	ATATGCCCCA	1088
1273	Qy	CAGGGATGGACCCAA	CTATCAATGGGTG	CCCTTATCAAGGAAGAGTCC	CCCTATCCAGGCC	1332
1089	Db	CAGGGATGGACCCAA	CTATCAATGGGTG	CCCTTATCAAGGAAGAGTCC	CCCTATCCAGGCC	1148
1333	Qy	AGGAACCTGTGCCAGCA	AAACATTTGGTGT	TTTTTGACTCTACAAAGAC	CTTCTCTGATGA	1392
1149	Db	AGGAACCTGTGCCAGCA	AAACATTTGGTGT	TTTTTGACTCTACAAAGAC	CTTCTCTGATGA	1208
1393	Qy	TGTTATAACCTTTGCA	AGAAAGTCATCCAGCC	ATGTACAATCCAGTGT	TTTCCCTATGAACAA	1452
1209	Db	TGTTATAACCTTTGCA	AGAAAGTCATCCAGCC	ATGTACAATCCAGTGT	TTTCCCTATGAACAA	1268
1453	Qy	TGCGCCCAATAGTGAT	CAAAA	CGGATGTAATTA	CAATTTTACACAAATGTGCTAGACCG	1512
1269	Db	TGCGCCCAATAGTGAT	CAAAA	CGGATGTAATTA	CAATTTTACACAAATGTGCTAGACCG	1328
1513	Qy	AGTGGATGCGAAGATGGA	CAGTATGATGTTATGTTTATCGGA	ACAGATGTTGGGACCGT	1572	
1329	Db	AGTGGATGCGAAGATGGA	CAGTATGATGTTATGTTTATCGGA	ACAGATGTTGGGACCGT	1388	
1573	Qy	TCCTTAAAGTAGTTTCA	ATTCTTAAAGGAC	ACTTGGTATGATTTAGAA	GAGGTTCTGTGCGGA	1632
1389	Db	TCCTTAAAGTAGTTTCA	ATTCTTAAAGGAC	ACTTGGTATGATTTAGAA	GAGGTTCTGTGCGGA	1448
1633	Qy	AGAAATGACAGTTTTTTC	GGGAA	CCGACTGCTATTTACGCA	ATGGAGCTTTCCACTAAGCA	1692
1449	Db	AGAAATGACAGTTTTTTC	GGGAA	CCGACTGCTATTTACGCA	ATGGAGCTTTCCACTAAGCA	1508
1693	Qy	GCAACACTATATATTTGG	TTTCAAGGCTGGGGTTGCC	CAGCTCCCTTTTACACCGGTGTGA	1752	
1509	Db	GCAACACTATATATTTGG	TTTCAAGGCTGGGGTTGCC	CAGCTCCCTTTTACACCGGTGTGA	1568	
1753	Qy	TATTTACGGGAAAGCG	TGCTCGT	CTGAGTGTTCCTCGCCG	GAGACCTTACTGTGCTTTGGGA	1812
1569	Db	TATTTACGGGAAAGCG	TGCTCGT	CTGAGTGTTCCTCGCCG	GAGACCTTACTGTGCTTTGGGA	1628
1813	Qy	TGTTCTGCAATGTTCTG	CTATTTTTCC	ACTGCAAAAGAGACG	CACAAAGACGACAAGATAT	1872
1629	Db	TGTTCTGCAATGTTCTG	CTATTTTTCC	ACTGCAAAAGAGACG	CACAAAGACGACAAGATAT	1688

Qy	1873	AAGAAATGGAGACCCCACTGACTCACTCTGTTGAGACTTTACACATGATTAATCAACAATGGCCCA	1932
Db	1689	AAGAAATGGAGACCCCACTGACTCACTCTGTTGAGACTTTACACATGATTAATCAACCATTGGCCCA	1748
Qy	1933	CAGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTACACATTTTGGAAATGCAG	1992
Db	1749	CAGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTACACATTTTGGAAATGCAG	1808
Qy	1993	TCCGAAGTTCGACAGAGCGCTGGTCTATTGGCAATTCACAGAGCGAAATCAAGAGAGCGAAA	2052
Db	1809	TCCGAAGTTCGACAGAGCGCTGGTCTATTGGCAATTCACAGAGCGAAATCAAGAGAGCGAAA	1868
Qy	2053	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGAGCTTCTGCTACGTAG	2112
Db	1869	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGAGCTTCTGCTACGTAG	1928
Qy	2113	TCTACAACAGAGGATTTCAGSCAATTACCTTCGCCATCGCGTGGAAATCATGGGTTCATACA	2172
Db	1929	TCTACAACAGAGGATTTCAGSCAATTACCTTCGCCATCGCGTGGAAATCATGGGTTCATACA	1988
Qy	2173	AACCTTTCTTAAAGGTAAACCTTGAAGTCAATTGAACAGAGCATTTTGGAGAACTTCTTCA	2232
Db	1989	AACCTTTCTTAAAGGTAAACCTTGAAGTCAATTGAACAGAGCATTTTGGAGAACTTCTTCA	2048
Qy	2233	TAAAGATGATGTAGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG	2292
Db	2049	TAAAGATGATGTAGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG	2108
Qy	2293	CCGAAGGCTCTGGTACAGAGACTTCATGCACTTCATCAACACCCCAATCTCAACACGAT	2352
Db	2109	CCGAAGGCTCTGGTACAGAGACTTCATGCACTTCATCAACACCCCAATCTCAACACGAT	2168
Qy	2353	GGATGATTTCTGTGAAACAAGTTTGGAAAAAGGACCGGAAAAACAACGTCGGCAAAAGGCCAGG	2412
Db	2169	GGATGATTTCTGTGAAACAAGTTTGGAAAAAGGACCGGAAAAACAACGTCGGCAAAAGGCCAGG	2228
Qy	2413	ACATACCCCAAGGAAACAGTAACAAATGGAGCACTTTACAGAAATAAAGAAAGGTAGAAA	2472
Db	2229	ACATACCCCAAGGAAACAGTAACAAATGGAGCACTTTACAGAAATAAAGAAAGGTAGAAA	2288
Qy	2473	CAGGAGGACCAACGAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCATTAACCTCTAGA	2532
Db	2289	CAGGAGGACCAACGAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCATTAACCTCTAGA	2348
Qy	2533	AACCTCAAAACAAGTAGAAAATTTCGCTAGACAATACTGGAAAAACAATAAGCAATATACAT	2592
Db	2349	AACCTCAAAACAAGTAGAAAATTTCGCTAGACAATACTGGAAAAACAATAAGCAATATACAT	2408
Qy	2593	GAACTTTTTTCATGGCAATATGTGGATGTTTTCAATGGTGGGAAATTCAGCTCAGTTCCA	2652
Db	2409	GAACTTTTTTCATGGCAATATGTGGATGTTTTCAATGGTGGGAAATTCAGCTCAGTTCCA	2468
Qy	2653	CCAATTATAAATAAATCCATGATGTAACCTTCTCTAATAGCTTTTTTTTCC	2702
Db	2469	CCAATTATAAATAAATCCATGATGTAACCTTCTCTAATAGCTTTTTTTTCC	2518

RESULT 9  
ADO23894

ADQ23894  
ID APO23894 standard: DNA: 3023 BP.

AA  
AC ADQ23894;AC XX  
ADQ23854;

DT 26-AUG-2004 (first entry)

Human soft tissue sarcoma-upregulated DNA - SEQ ID 6714.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;  
KW ds.  
KW ds.

XX Homo sapiens. OS

3 XX







1569	Db		TAATTTACGGGAAGCGGTGCTGAGTGTTCCTCGCCGACGACCTTACTGTGCTGGGA	1628
1813	Qy		TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAAGATAT	1872
1629	Db		TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAAGATAT	1688
1873	Qy		AAGAAATGGAGACCCACTGACTCTACTGTTTCAGACTTACACCATGATTAATCACCATGGCCA	1932
1689	Db		AAGAAATGGAGACCCACTGACTCTACTGTTTCAGACTTACACCATGATTAATCACCATGGCCA	1748
1933	Qy		CAGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTAGCACATTTTGGAAATCCAG	1992
1749	Db		CAGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTAGCACATTTTGGAAATCCAG	1808
1993	Qy		TCCGAAGTCGCAGAGAGCGCTGTCTTATTTGGCAATTCAGAGGCGAAATGAAGAGCGAAA	2052
1809	Db		TCCGAAGTCGCAGAGAGCGCTGTCTTATTTGGCAATTCAGAGGCGAAATGAAGAGCGAAA	1868
2053	Qy		AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGAGATCAGGCCCTTCTGCTACGTAG	2112
1869	Db		AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGAGATCAGGCCCTTCTGCTACGTAG	1928
2113	Qy		TCTACAAAGAAAGGATTCAGGCAATTACCTCTGCGCATGCGGTGGAAATCGGTTTCATACA	2172
1929	Db		TCTACAAAGAAAGGATTCAGGCAATTACCTCTGCGCATGCGGTGGAAATCGGTTTCATACA	1988
2173	Qy		AACTCTTTTAAAGTAAACCCCTGGAAGTCATTTGACACAGAGCAATTTGGAAGAACTTTCTCA	2232
1989	Db		AACTCTTTTAAAGTAAACCCCTGGAAGTCATTTGACACAGAGCAATTTGGAAGAACTTTCTCA	2048
2233	Qy		TAAAGATGATGAGATGGCTCTAGACCAAGAAATGTCCTCAATAGCATGACACCTAG	2292
2049	Db		TAAAGATGATGAGATGGCTCTAGACCAAGAAATGTCCTCAATAGCATGACACCTAG	2108
2293	Qy		CCAGAAAGTCTGGTACAGAGACTTCATGCAAGTCTCATCAACACCCCAATCTCAACACGAT	2352
2109	Db		CCAGAAAGTCTGGTACAGAGACTTCATGCAAGTCTCATCAACACCCCAATCTCAACACGAT	2168
2353	Qy		GGATGAGTTCTGTGAAACAAGTTTGGAAAAGGGACCGAAAAACAACGTCGGCAAAAGGCCAGG	2412
2169	Db		GGATGAGTTCTGTGAAACAAGTTTGGAAAAGGGACCGAAAAACAACGTCGGCAAAAGGCCAGG	2228
2413	Qy		ACATACCCAGGGAAACAGTAACTGGAAGCACTTACAGAAAAATAAGAAAGGTAGAAA	2472
2229	Db		ACATACCCAGGGAAACAGTAACTGGAAGCACTTACAGAAAAATAAGAAAGGTAGAAA	2288
2473	Qy		CAGGAGACCCACGAATTTGAGAGGGCAACCAGAGTGTCTGAGTGCATTAACCTCTAGA	2532
2289	Db		CAGGAGACCCACGAATTTGAGAGGGCAACCAGAGTGTCTGAGTGCATTAACCTCTAGA	2348
2533	Qy		AACCTCAAAACAAGTAGAAACTTCGCTAGACAAATACTGGAAAAACAATGCAATATACAT	2592
2349	Db		AACCTCAAAACAAGTAGAAACTTCGCTAGACAAATACTGGAAAAACAATGCAATATACAT	2408
2593	Qy		GAACTTTTTTTCATGGCAATTATGTGGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA	2652
2409	Db		GAACTTTTTTTCATGGCAATTATGTGGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA	2468
2653	Qy		CCAAATTAATAATTAATCCATGAGTAACTTTCTCTAATAGGCTTTTTTTTCC	2702
2469	Db		CCAAATTAATAATTAATCCATGAGTAACTTTCTCTAATAGGCTTTTTTTTCC	2518

## RESULT 10

AAO92331

AAQ92331  
ID AAQ92331 standard; cDNA; 1481 BP.XX  
XX

AC AAQ92331;

01-NOV-1995 (first entry)

XX  
 CCCT-AON-TO  
 3 38777)

DE Human collapsin cDNA.

XX		Collapsin; antibody; therapy; ds.			
KW	XX	Homo sapiens.			
OS	XX				
XX					
XX					
PH	Key	Location/Qualifiers			
FT	CDS	50..1480			
FT		/*tag= a			
XX					
PN	US5416197-A.				
XX					
PD	16-MAY-1995.				
XX					
PF	15-OCT-1993;	93US-00136922.			
XX					
PR	15-OCT-1993;	93US-00136922.			
XX					
PA	(UYPE-) UNIV PENNSYLVANIA.				
XX					
PI	Luo Y, Raper JA;				
XX					
DR	WPI; 1995-193478/25.				
DR	P-PSDB; AAR74175.				
XX					
PT	New antibody to human collapsin - used to inhibit the activity of				
PT	collapsin, to induce neurite out-growth and to treat individuals with				
PT	nerve damage.				
XX					
XX	Disclosure; Col 11-16; 11pp; English.				
CC					
CC	Human collapsin and its encoding nucleic acid may be used to identify				
CC	agents which modulate the ability of human collapsin to collapse the				
CC	growth cone of neurons. An antibody capable of specifically binding at				
CC	least a portion of the collapsin protein can be used to purify human				
CC	collapsin and to inhibit the activity of the protein. It can be used to				
CC	induce neurite outgrowth by neuronal cells and to treat individuals				
CC	suffering from nerve damage				
XX					
SQ	Sequence 1481 BP; 454 A; 299 C; 345 G; 383 T; 0 U; 0 Other;				
	Query Match	52.2%; Score 1415.2; DB 2; Length 1481;			
	Best Local Similarity	99.4%; Pred. No. 0;			
	Matches 1420; Conservative	0; Mismatches	8; Indels	0; Gaps	0;
Qy	899	GAGAGTGACAAATCCTGAAAGATGACAAAGTATACTTTTCCTCGTGAAAAATGCCAATAGAT	958		
Dd	53	GAACATGACAATCCTGAAGATGACAAAGTATACTTTTCCTCGTGAAAAATGCCAATAGAT	112		
Qy	959	GGAGAACACTCTGGAAAAGCTACTCACGGTAGAATAGGTGCAGATATGCAAGATGACTTT	1018		
Dd	113	GGAGAACACTCTGGAAAAGCTACTCACGGTAGAATAGGTGCAGATATGCAAGATGACTTT	172		
Qy	1019	GGAGGGCACAGAAGTCTGGTGAATAATGGACAACACTTCTCAAAGCTCGTCGATTGTC	1078		
Dd	173	GGAGGGCACAGAAGTCTGGTGAATAATGGACAACACTTCTCAAAGCTCGTCGATTGTC	232		
Qy	1079	TCAGTGCAGGTCCAAATGGCATTGACACTCATPTTTGTGAACCTGCAGGATGATTCCCTA	1138		
Dd	233	TCAGTGCAGGTCCAAATGGCATTGACACTCATPTTTGTGAACCTGCAGGATGATTCCCTA	292		
Qy	1139	ATGACTTTAAAGATCCTTAAATCCAGTTGTATATGGAGTGTTTTACGACTTCCAGTAAC	1198		
Dd	293	ATGACTTTAAAGATCCTTAAATCCAGTTGTATATGGAGTGTTTTACGACTTCCAGTAAC	352		
Qy	1199	ATTTTCAAGGGATCAGCCGTGTGTATGTATAGCATGAGTGCATGAGAGGGTGTTCCTT	1258		
Dd	353	ATTTTCAAGGGATCAGCCGTGTGTATGTATAGCATGAGTGCATGAGAGGGTGTTCCTT	412		
Qy	1259	GGTCCATATGCCACAGGGATGACCACCACTATCANTGGTGCCTTATCAAGGAAGTCC	1318		
Dd	413	GGTCCATATGCCACAGGGATGACCACCACTATCANTGGTGCCTTATCAAGGAAGTCC	472		
Qy	1319	CCCTATCCAGGGCCAGGAACCTTGTCGCCAGCAAAACATTTGGTGGTTTTGACTCTCAAAAG	1378		

Db 473 CCTATCCACGCGCCAGAACTTGTCCAGCAAAACATTTGGTGGTTTGACTCTCAAG 532  
 Qy 1379 GACCTTCCTGATGATGTTATACCTTTTGAAGAAGTCATCCAGCCATGTACAAATCCAGTG 1438  
 Db 533 GACCTTCCTGATGATGTTATACCTTTTGAAGAAGTCATCCAGCCATGTACAAATCCAGTG 592  
 Qy 1439 TTTCTCTATGAACAATCGCCCAATAGTGATCAAAACCGATGTAATATCAATTTACAAA 1498  
 Db 593 TTTCTCTATGAACAATCGCCCAATAGTGATCAAAACCGATGTAATATCAATTTACAAA 652  
 Qy 1499 ATTGTCGTAGACCGAGTGCATGACAGAGATGACAGTATGATGTTATGTTATCGGAACA 1558  
 Db 653 ATCGTCGTAGACCGAGTGCATGACAGAGATGACAGTATGATGTTATGTTATCGGAACA 712  
 Qy 1559 GATGTTGGGACCGCTTCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTAGAA 1618  
 Db 713 GATGTTGGGACCGCTTCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTAGAA 772  
 Qy 1619 GAGGTTCTGCTGGAAGAAATGACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAG 1678  
 Db 773 GAGGTTCTGCTGGAAGAAATGACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAG 832  
 Qy 1679 CTTTCCACTAAGCAGCAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCT 1738  
 Db 833 CTTTCCACTAAGCAGCAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCT 892  
 Qy 1739 TTACACCGGTGTGATATTACCGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTT 1798  
 Db 893 TTACACCGGTGTGATATTACCGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTT 952  
 Qy 1799 TACTGTGCTGGGATGGTTCGTGATGTTCTGCTATTTTCCACTGCAAGAGAGCGACA 1858  
 Db 953 TACTGTGCTGGGATGGTTCGTGATGTTCTGCTATTTTCCACTGCAAGAGAGCGACA 1012  
 Qy 1859 AGACGACAGATATAGAAATGGAGACCCACTGACTCTGCTGACTTACACCATGAT 1918  
 Db 1013 AGACGACAGATATAGAAATGGAGACCCACTGACTCTGCTGACTTACACCATGAT 1072  
 Qy 1919 AATCACCATTGGCCACAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACA 1978  
 Db 1073 AATCACCATTGGCCACAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACA 1132  
 Qy 1979 TTTTGGAAATGAGTCCGAGTCCGAGAGAGCGCTGCTATTTGGCAATTCAGAGGGCA 2038  
 Db 1133 TTTTGGAAATGAGTCCGAGTCCGAGAGAGCGCTGCTATTTGGCAATTCAGAGGGCA 1192  
 Qy 2039 AATGAAGCGAAAGAGAGATCAGATGAGTGCATATCATCAGGACAGATCAAGGC 2098  
 Db 1193 AATGAAGCGAAAGAGAGATCAGATGAGTGCATATCATCAGGACAGATCAAGGC 1252  
 Qy 2099 CTTCTGCTACGTAGTCTCAACAGAGAGGATTCAGGCAATTTACTCTGCCATCGGTGGAA 2158  
 Db 1253 CTTCTGCTACGTAGTCTCAACAGAGAGGATTCAGGCAATTTACTCTGCCATCGGTGGAA 1312  
 Qy 2159 CATGGGTTTCATACAAACTCTTCTTAAGGTAAACCTCGGAAGTCAATGACACAGAGATTG 2218  
 Db 1313 CATGGGTTTCATACAAACTCTTCTTAAGGTAAACCTCGGAAGTCAATGACACAGAGATTG 1372  
 Qy 2219 GAAGAACTTCTTCAATAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCAT 2278  
 Db 1373 GAAGAACTTCTTCAATAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCAT 1432  
 Qy 2279 AGCATGACACCTAGCAGAGGCTGCTGATCAGAGCTTTCATGAGCTC 2326  
 Db 1433 AGCATGACACCTAGCAGAGGCTGCTGATCAGAGCTTTCATGAGCTC 1480

RESULT 11  
 AAX89112  
 ID AAX89112 standard; DNA; 2331 BP.  
 XX  
 AC AAX89112;

XX 14-SEP-1999 (first entry)  
 DT Human brain tissue-derived polypeptide coding sequence (clone OM007).  
 XX Brain tissue; human; bone marrow; umbilical cord venous endothelial cell;  
 KW recombinant; diagnosis; treatment; ss.  
 XX Homo sapiens.  
 XX WO9933873-A1.  
 PN 08-JUL-1999.  
 PD 25-DEC-1998; 98WO-JP005952.  
 PF 26-DEC-1997; 97JP-00358811.  
 PR (ONOI) ONO PHARM CO LTD.  
 PA Fukushima D, Shibayama S, Tada H;  
 PI WPI: 1999-419088/35.  
 DR P-PSDB; AAY27127.  
 XX New adult human brain tissue-produced polypeptides useful for diagnosis  
 PT and treatment.  
 PS Claim 4; Page 39-40; 86pp; Japanese.  
 XX The invention provides polypeptides (AAY27127-27133) produced by human  
 CC adult brain tissue, human bone marrow or a human umbilical cord venous  
 CC endothelial cell. Host cells transformed with vectors comprising the  
 CC nucleic acids encoding the polypeptides are used for the recombinant  
 CC expression of the polypeptides. The polypeptides can be used in  
 CC diagnosis, treatment and basic studies, with wide applications in  
 CC treatment depending on the activity to be aimed at. Sequences AAX89112-  
 CC 125 represent nucleic acids encoding the polypeptides  
 XX  
 SQ Sequence 2331 BP; 723 A; 476 C; 529 G; 603 T; 0 U; 0 Other;  
 Query Match 26.5%; Score 718.6; DB 2; Length 2331;  
 Best Local Similarity 61.9%; Pred. No. 18-205;  
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;  
 Qy 269 AATGGAAGAAACAATGTGCCAAGGCTGAAATATCTACAAAGAAATGTGGAATCCAAAC 328  
 Db 109 ACTTTGAGCAAAATATTTCCAGACTCAAGCTAACTACAAAGACTTGTCTCTTCAAT 168  
 Qy 329 AATGTGATCATTTCATATGGCTTGGCCCAACAGCTCCAGTTATCATACCTTCTTTGGAT 388  
 Db 169 AGCTGATTCCTTTTGGGTTTCATCAGAAGGACTGGATTTCAAACTCTTCTCTTAGAT 228  
 Qy 389 GAGGAACGAGTAGCTGTATGTTGGCAAGAGATCAGATTTTTCATTCGACCTGGTT 448  
 Db 229 GAGGAAGAGGCGAGGCTGCTCTTGGGAGCCAAAGACCAATCTTCTACTAGTCTGGTT 288  
 Qy 449 AA---TATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACACCAAGAGAGATGAA 505  
 Db 289 GACTTAACAAAATTTTAAAGAAATTTATTTGGCTCTGCAAGGAACGGGTGGAATTA 348  
 Qy 506 TGCAAGTGGGCTGGAAAAGACAATCTGAAAGAAATGTGCTAAATTTTCATCAAGGTACTTAAG 565  
 Db 349 TGTAAATAGCTGGGAAAGATGCCAATACAGAATGTGCAAAATTTTCATCAGAGTACTTCAG 408  
 Qy 566 GCATATATCAGACTCATTGTACGCTGTGAAACGGGGCTTTTCATCCATTTTCACACC 625  
 Db 409 CCTATACAAAACTCACATATATGTGTGGAACCTGGAGCAATTTTCATCAATATGTGG 468  
 Qy 626 TACATTGAAATGGACATCATCTCAGGAGCAATATTTTAAAGCTGGAGAACTCACATTTT 685  
 Db 469 TATATTGATCTTGGAGTCTCAAGGAGGATATTTATTTCAAACTAGACACAGTAATTTG 528

QY 686 GAAACGGCGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAATA 745  
 Db 529 GAGTCTGGCAGACTGAAATGTCCTTTGATCCTCAGCAGCCTTTTGTTCAGTAATGACA 588  
 QY 746 GATGAGAAATTAATCTCTGGAAGTCAAGTCTGATTTTATGGGGGAGACTTTCTGCTATCTTC 805  
 Db 589 GATGAGTACTCTCTGGAAGTCAAGTCTGATTTTCTTTGGCAAGATACTGCTATCTACT 648  
 QY 806 CGAACTCTTTGGGCG-----ACCACCAACCCCAATCAGGACAGAGCAGCATGATTCAGG 856  
 Db 649 CGATCCCTTTGGGCGCTACTCATGACCAACCACTACATCAGAACTGACATTTTCAGAGCACTAC 708  
 QY 857 TGGCTCAATGATCCTAAAGTTCTATGATGCTCCACCTCATCTCAGAGAGTCAATCTGAA 916  
 Db 709 TGGCTCAATGAGGAGCAAAATTTATGGAACCTTTCTTATACACAGACACCTTCAATCCAGAT 768  
 QY 917 GATGACAAAGTATATCTTTTCTCGTGAATGCAATAGATGGAGAACACTCTGGAAA 976  
 Db 769 GATGATAAAATATATTTCTTCTTCTGTAATCATCTCAAGAGGCGAGTACCTCCGATAAA 828  
 QY 977 GCTACTCAGCTAGATAGGTGAGATATGCAAGAAATGACTTTGGAGGGGACAGAAAGTCTG 1036  
 Db 829 ACCATCCTTCTCGAGTTGGAAGAGTTTGTAGAATGATGAGGAGCAACGCGAGCCTG 888  
 QY 1037 GTGAATAAATGACAAATCTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTCCAAAT 1096  
 Db 889 ATAAACNAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTTCTGGAAGTGAT 948  
 QY 1097 GCAATGACACTCATTTTGTATGAACTGAGAGTATTTCTTAAATGAACTTTAAAGATCCT 1156  
 Db 949 GGGGCGAGATACTTCTTGTATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAA 1008  
 QY 1157 AAAATCCAGTTGTATATGAGTGTATACAGTTCAGTAAATTTTCAAGGGATCAGCC 1216  
 Db 1009 AGAATCTCTGTAGTATATGAGTCTTTACTACAAAGCTCCATCTTCAAGGCTCTGCT 1068  
 QY 1217 GTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1276  
 Db 1069 GTTGTGTGTATAGCATGCTGACATCAGAGCAGTCTTTTAAATGGTCCATATGCTCATAAG 1128  
 QY 1277 GATGACCCCACTATCAATGAGTGTCTTATCAAGAGAGTCCCTTATCCAGGGCAGGA 1336  
 Db 1129 GAAAGTGCAGACCATCGTTGGGTGAGTATGATGAGGAGAAATTCCTTATCCACGGCTGCT 1188  
 QY 1337 ACTGTGCTCCAGCAAAACATTTG---GTGGTGTGCTCTACAAAGAGCCTTCTCTGATGAT 1393  
 Db 1189 ACATGTCCAGCAAAACCTATGACCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1248  
 QY 1394 GTTATAACCTTTGCAAGAGTCAATCAGCCATGTAACATCCAGTGTCTTCTATGAACAAAT 1453  
 Db 1249 GTCATCAGTTTCAATAAGCGGCACTCTGTGATGATTAAGTCCGTATACCCAGTTGCAGGA 1308  
 QY 1454 CCCCCAATAGTATCAAAAGAGATGTAATTAATCAATTTACAAATTTGCTGAGACCGA 1513  
 Db 1309 GGACCAACGTTCAAGAGAAATCAATGTGGATTAAGTGTGATGATGATGATGATGATGATGAT 1368  
 QY 1514 GTGGATGCAAGAGATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1573  
 Db 1369 GTCAATGCAAGAGATGGCAGTACGATGTAATGTTTCTTGGAAACAGACATTTGGAATGTC 1428  
 QY 1574 CTTAAAGTATGTTCAATCTTAAGGAGACTTGGTATGATTTTGAAGAGGTTCTGCTGGA 1633  
 Db 1429 CTCAAAGTTGTGAGCATTTCAAAGGAAAGTGG---AATATGGAAGAGGAGTGTGCTGGAG 1485  
 QY 1634 GAAATGACAGTTTTCGGGAAACCGAGTCTATTTTCAAGCAATGGAGCTTTTCCACTAAGCAG 1693  
 Db 1486 GAGTTGCAGATATTCAGGACATCAATCATCTTTGAACATGGAATTTGCTCTGAAGCAG 1545  
 QY 1694 CAACAACTATATATTTGGTTTCAACGGCTGGGGTTGGCCAGCTCCCTTTACACCGGTTGAT 1753  
 Db 1546 CAACAAATGTACATTTGGTTCCCGAGATGATGATGATGATGATGATGATGATGATGATGAT 1605  
 QY 1754 ATTTACGGGAAAGCGTGTGCTGAGTGTGCTGCTGCGCCGAGACCTTTACTGTGCTTTGGGAT 1813

Db 1606 ACTTATGGAAAGCTTTGGCAGACTGTTGTCTTGGCAGAGACCCCTACTGTGCTCGGGAT 1665  
 QY 1814 GGTTCCTGATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGAGCAGCAAGATATA 1873  
 Db 1666 GGAATGATGCTCTCGATATGCTCCTACTTCTTAAGAGAGCTTAGAGCCCAAGATGTA 1725  
 QY 1874 AGAATGAGAGACCACTGACTCACTGTTTCAGACTTACACCATGATAATCACCATGGCCAC 1933  
 Db 1726 AAATATGCGACCCAATCAACCAGTGTGGGACATCGAAGACAGCATTTAGTCTATG--AA 1782  
 QY 1934 AGCCCTGAAGAGAGATCATCTATGGTGTAGAGATAGTAGCACAATTTTGGAAATGCACT 1993  
 Db 1783 ACTGCTGATGAAAGGATGATTTTGGCAATTTAACTCAACCTTTTCTGGAATGTATA 1842  
 QY 1994 CCGAAGTCGAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAA 2053  
 Db 1843 CCTAAATCCCAACAGCAACTATTAATGGTATATCCAGAGTCAAGGATGAGCATCGA 1902  
 QY 2054 GAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGTCTAGTACT 2113  
 Db 1903 GAGGATTTGAAGCCGATGAAAGAAATCATCAAAACGGAATATGGCTACTGATTCGAAGT 1962  
 QY 2114 CTACAACAGAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCATACA 2173  
 Db 1963 TTGCAGAAAGAGGATTTCTGGGATGTTTACTGCAAAAGCCAGGAGCACACTTTTCATCCAC 2022  
 QY 2174 ACTCTTCTTAAGGTAACCTCGAAGTCAATTCACACAGAGCATTTTGGAAAGAACTTCTTCTCAT 2233  
 Db 2023 ACCATGATGAGTGAAGTCACTTTGATGTCTTGAATGATGAACAGATGGAATAATACCCAGAG 2082  
 QY 2234 AAAGATGATGATG 2246  
 Db 2083 GCAGAGCATGAGG 2095

RESULT 12  
 AAA37109  
 ID AAA37109 standard; cDNA; 3871 BP.  
 XX AC AAA37109;  
 XX DT 08-AUG-2000 (first entry)  
 XX Human PRO1491 (UNQ760) cDNA sequence SEQ ID NO:309.  
 DE Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.  
 OS Homo sapiens.  
 XX PN WO200012708-A2.  
 XX PD 09-MAR-2000.  
 XX PF 01-SEP-1999; 99WO-US020111.  
 XX PR 01-SEP-1998; 98US-0098716P.  
 XX PR 01-SEP-1998; 98US-0098749P.  
 XX PR 01-SEP-1998; 98US-0098750P.  
 XX PR 02-SEP-1998; 98US-0098803P.  
 XX PR 02-SEP-1998; 98US-0098821P.  
 XX PR 02-SEP-1998; 98US-0098843P.  
 XX PR 09-SEP-1998; 98US-0099536P.  
 XX PR 09-SEP-1998; 98US-0099596P.  
 XX PR 09-SEP-1998; 98US-0099598P.  
 XX PR 09-SEP-1998; 98US-0099602P.  
 XX PR 09-SEP-1998; 98US-0099642P.  
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 XX PR 10-SEP-1998; 98US-0099754P.  
 XX PR 10-SEP-1998; 98US-0099763P.  
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 XX PR 10-SEP-1998; 98US-0099808P.

PR 10-SEP-1998; 98US-0099812P.  
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 PR 15-SEP-1998; 98US-0100385P.  
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 PR 15-SEP-1998; 98US-0100390P.  
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 PR 18-SEP-1998; 98US-0101071P.  
 PR 22-SEP-1998; 98US-0101279P.  
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 PR 23-SEP-1998; 98US-0101472P.  
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 PR 23-SEP-1998; 98US-0101474P.  
 PR 23-SEP-1998; 98US-0101475P.  
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 PR 23-SEP-1998; 98US-0101477P.  
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 PR 24-SEP-1998; 98US-0101738P.  
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 PR 20-OCT-1998; 98US-0104987P.  
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 PR 22-OCT-1998; 98US-0105169P.  
 PR 22-OCT-1998; 98US-0105266P.  
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 PR 26-OCT-1998; 98US-0105694P.  
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 PR 30-OCT-1998; 98US-0108644P.  
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 PR 03-NOV-1998; 98US-0108905P.  
 PR 03-NOV-1998; 98US-0108919P.  
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 PR 03-NOV-1998; 98US-0108934P.  
 PR 10-NOV-1998; 98US-0107783P.  
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 PR 17-NOV-1998; 98US-0108802P.  
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 PR 18-NOV-1998; 98US-0108850P.  
 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.  
 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 XX  
 XX (GETH) GENENTECH INC.  
 XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
 PI WPI; 2000-237871/20.  
 DR P-PSDB; AAY99427.  
 DR  
 XX New mammalian DNA sequences encoding transmembrane, receptor or secreted  
 PT PRO polypeptides, useful for screening of potential peptide or small  
 PT molecule inhibitors of the relevant receptor/ligand interactions.  
 XX  
 PS ClaIm 2; Fig 175; 773pp; English.  
 XX  
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane  
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding then have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
 CC primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention  
 XX  
 SQ Sequence 3871 BP; 1251 A; 704 C; 805 G; 1111 T; 0 U; 0 Other;  
 Query Match 26.5%; Score 718.6; DB 3; Length 3871;  
 Best Local Similarity 61.9%; Pred. No. 1.4e-205;  
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;  
 QY 269 AATGGAGAACAAATGTGCGAAGGCTGAATATTCACACAGAAATGTGGAAATCAAC 328  
 Db 215 ACTTTGAACAAATATTCACAGACTCAAGCTACCTACAGAGACTTGCTGCTTCAAT 274  
 QY 329 AATGTGATCATTCAATGGCTTGCCACAGCTCCAGTTATCATACCTTCCTTTGGAT 388  
 Db 275 AGCTGTATTCCCTTTTGGGTTTCATCAGAGGACTGGATTTTCAAACTCTCTCTAGAT 334  
 QY 389 GAGGACGGAGTAGGCTGTATTTGGAGCAAGGATCATATTTTCATTCGACCTGGTT 448  
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Db	335	GAGGAAGAGCGCAGGCTGCTCTTGGGAGCCAAAGACACACATCTTTCTACTCAGTCTGGTT	394
Qy	449	AA-----TATCAAGGATTTTCAAAGATTTGTGTGGCCAGTATCTTTACACCAGAAGAGATGAA	505
Db	395	GACTTAAACAAATTTTAAAGATTTTATTTGGCTGCTGCAAGGAAACGGGTGGAATTA	454
Qy	506	TGCAAGTGGGTGGAAAGACATCCTGAAAGAATGTGCTAATTTTCAACAAGGTACTTTAAG	565
Db	455	TGTAATTTAGCTGGGAAGATGCCAATACAGAAATGTGCAAAATTTTCATCAGAGTACTTCAG	514
Qy	566	GCATATAATCAGACTCACTGTAGCCCTGTGGAAACGGGGCTTTTCATCCATTTTGCACC	625
Db	515	CCCTATAACAAACCTCATATATGTGTGTGAACTGGAGCATTTTCATCCAATATGTGGG	574
Qy	626	TACATTTGAAATTTGGACATCATCTCGAGGACAATATTTTAACTGGAGAACTCACATTTT	685
Db	575	TATATTGATCTTTGGAGCTTACAGAGAGATATATATTTCAAACCTAGACACACATAATTTG	634
Qy	686	GAATAACGGCCGTGGAAAGAGTCCAATATGACCCCTAAGCTGTGACAGCATCCCTTTTAAATA	745
Db	635	GAGTCTGCAGACTGAAATGTCTTTTCGATCTCAGCAGCCCTTTGCTTCAGTAATGACA	694
Qy	746	GATGGAGAAATTATCTCTGGAACTGACAGCTGATTTTATGGGGCGAGACTTTTGCTATCTTC	805
Db	695	GATGAGTACCTCTACTCTCGAAACAGCTTCTGATTTCCCTTGGCAAGGATACTGCAATCACT	754
Qy	806	CGAACTCTTGGGC-----ACCACACCCTAATCAGGACAGAGCAGCATGATTCACGG	856
Db	755	CGATCCCTTGGGCTTACTCATGACCAACACTACATCAGAACTGACTTTTCAGAGCATCTAC	814
Qy	857	TGGCTCAATGATCCAAAGTTCAATTAGTGGCCCACTCATCTCAGAGAGTGACAATCCCTGAA	916
Db	815	TGGCTCAATGGAGCAAAATTTATTTGGAATCTTCTTCATACAGACACCTACATCCAGAT	874
Qy	917	GATGACAAAGTATACTTTTCTCCGTGAAAAATGCAATAGATGAGAGAACTCTGGAATAA	976
Db	875	GATGATAAAAATATATTTCTCTTTTCGTGTAATCATCTCAAGAAAGCAGTACCTCCGATAAA	934
Qy	977	GCTACTCACGCTAGAAATAGTFCAGATATGCAAGAAATGACTTTGAGAGGGCAGAGAGCTG	1036
Db	935	ACCATCTCTTCGAGTTTGAAGAGTTTGTAAAGAAATGATGTAGAGAGACAAACGACGCTG	994
Qy	1037	GTGTAATAAATGGACAAACATTCCTCAAAAGCTCGTCTGATTTGCTCAGTGCAGGTCCTCAAT	1096
Db	995	ATAACAAGTGGACGACTTTTCTTAAAGCCAGACTGATTTGCTCAATCTCTGGAGTGTAT	1054
Qy	1097	GGCATTGACACTCAATTTTGATGAACATCGAAGATGATTCCTAAATGAATTTTAAAGATCCT	1156
Db	1055	GGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCAAGAGAGATGAA	1114
Qy	1157	AAAAATCCAGTTGTATATGAGAGTGTTTACGACTTCAGATTAACATTTTCAAGGAGATCAGCC	1216
Db	1115	AGAAATCCTGTAGTATATGAGTCTTTTACTACAAACGAGCTCCATCTTTCAAAGGCTCTGCT	1174
Qy	1217	GTGTGTATGTATAGCATGAGTGTGAGAAAGGGTGTTCCTTGCTCCATATGCCACAGG	1276
Db	1175	GTTTGTGTGTATAGCATGGCTGACATCAGAGCAGTTTATATGTCCTCATATGCTCATAG	1234
Qy	1277	GATGGACCCAACTATCAATGGGTGCCCTTATCAAGGAAGAGTCCCTTATCAACGAGGATGAG	1336
Db	1235	GAAAGTCAGACCACTGTGGGTGCAGTATGATGGGAGAAATTCCTTTATCCAGGCGCTGGT	1294
Qy	1337	ACTTGTCCAGCAAAAACATTTG-----GTGGTTTGTGACTCTCAAGAGGACCTTCTGTGAT	1393
Db	1295	ACATGTCCAAAGCAAAACCTATGACCCCACTGATTAAGTCCACCCGAGATTTTTCAGATGAT	1354
Qy	1394	GTATAACCTTTTGCAGAAGTCACTCCAGCCATGTAACAATCCAGTGTTCCTATGAACAAT	1453
Db	1355	GTCAATCAGTTTCATAAAGCGGCCTCTGTGATGTATATAGTCCGATATACCCAGTTGCAGGA	1414
Qy	1454	CGCCCAATAGTGATCAAAACGGATGTAAATTTATCAATTTTACAAAAATTTGCTGAGACCGA	1513
Db	1415	GGACCAACGTTCAAGAGAACTAATGTGGATTTACAGACTGACACAGATAGTGGTGGATCAT	1474

Qy	1514	GTGATGCGAAGATGGACAGTAGATGTTATGTTATTCGGAACAGATGTTGGACCGGTT	1573
Db	1475	GTCATTGCGAAGAATGGCCAGTAGATGTAATGTTTCTTGGAAACAGATCTGAACTGTC	1534
Qy	1574	CTTAAAGTAGTTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGGTTCTGCTGGAA	1633
Db	1535	CTCAAGATTGTACGCAATTCAAAGGAAAAGTGG---AATATGGAAGAGGTAGTGTCTGGAG	1591
Qy	1634	GAATATGACAGTTTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCCACTAAAGCAG	1693
Db	1592	GAGTTGCGAGATATTCAGACACTCATCAATCTTGAACATGAAATGTCTCTCTGAAGCAG	1651
Qy	1694	CAACAACTATATATGTGTTCAACGGCTGGGGTGGCCAGCTCCCTTTTACACCGGTGTGAT	1753
Db	1652	CAACAAATTGTACATTTGGTTCCCGAGATGGATTAGTTCAAGCTCTCTTTCACACAGATGCGAC	1711
Qy	1754	ATTTACGGGAAGGGTGTCTGAGTGTGGCTCGCCGAGACCCCTTACTGTGCTTGGGAT	1813
Db	1712	ACTTATGGGAAAGCTTTCGCGAGACTGTGTCTTTCGCCAGAGACCCCTACTGTGCTCGGGAT	1771
Qy	1814	GGTTCTGCATGTTCTCGCTATATTTCCACCTGCAAGAGAGCGCACAAAGACAAAGATATA	1873
Db	1772	GGAATATGATGCTCTCGATATGCTCTTACTTCTTAAAGGAGAGCTAGAGCCCAAGATGTA	1831
Qy	1874	AGAAATGGAGACCCACTGACTCACTGTTACAGCTTACACCATGATTAATCACCATGCCCCAC	1933
Db	1832	AAATATGGCGACCCAAATCACCCAGTGCTGGGACATCGAAGACAGCATTAGTCA TG---AA	1888
Qy	1934	AGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGACATTTTGGGAATCGAGT	1993
Db	1889	ACTGCTGATGAAAAGGTGATTTTTTGGCAATTGAAATTTAACTCAACCTTCTTGGGAATGTATA	1948
Qy	1994	CCGAAGTCGCGAGAGAGCGCTGGTCTATTGGCAATTCAGAGGGCGAAATGAAGAGCGAAA	2053
Db	1949	CCTAAATCCCAACAAAGCAACTATTAAATGSTATATCCAGAGGTCAGGGGATGAGCATCGA	2008
Qy	2054	GAAGAGATCAGATGGATGATCATATCATCAGAGACAGATCAAGGCCTTCTGTACGTAGT	2113
Db	2009	GAGGAGTTGAAGCCCGATGAAGAATCATCAAAACGGAATATGGGCTACTGATTCCGAAGT	2068
Qy	2114	CTACAAACAGAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAACATGGTGTTCATACAA	2173
Db	2069	TTGCAGAAGAAGGAATCTCGGGATGTATTCTGCAAGCCCGAGGAGCACATTTTCATCCAC	2128
Qy	2174	ACTCTTCTTAAGGTAAACCTCGGAAGTCATTGACACAGAGCATTTTGGAAAGAACTTCTTCAT	2233
Db	2129	ACCATAGTGAAGCTGACTTTGAATGTTCATTGAGATGAACAGATGGAATAATCCAGAGG	2188
Qy	2234	AAAGATGATGATG 2246	
Db	2189	GCAGAGCATGAGG 2201	

RESULT 13	
AAFS4421	DNA encoding protein of the invention #86.
ID AAF54421	standard; DNA; 3871 BP.
XX	Secreted; transmembrane; gene therapy; ss.
AC AAF54421;	Unidentified.
XX	WO200078961-A1.
DT 02-APR-2001	(first entry)
XX	28-DEC-2000.
DE	18-FEB-2000; 2000WO-US004342.
XX	
XX	
XX	
XX	
OS	
XX	
XX	
PN	
XX	
XX	
PD	
XX	
XX	
XX	

XX 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 XX (GETH) GENENTECH INC.  
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;  
 XX WPI; 2001-071395/08.  
 DR Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 XX Claim 2; Fig 171; 787pp; English.  
 PS The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy  
 XX  
 SQ Sequence 3871 BP; 1251 A; 704 C; 805 G; 1111 T; 0 U; 0 Other;  
 Query Match 26.5%; Score 718.6; DB 4; Length 3871;  
 Best Local Similarity 61.9%; Pred. No. 1.4e-205;  
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;  
 QY 269 AATGGGAAGAACATGTGCGAAGGCTGAATATCTCTACAAAGAAATGTGGAATCCAC 328  
 DB 215 ACTTTGAACCAAAATATTCAGAGACTCAAGTAACTACAAAGACTTGTCTTTCAAAAT 274  
 QY 329 AATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATACACTTCTCTTTGGAT 388  
 DB 275 AGCTGTATTCCTTTTGGGTTTCATCAGAGAGACTGGATTTTCAAACTCTCTCTAGAT 334  
 QY 389 GAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCATATATTTTCATTCGACCTGGTT 448  
 DB 335 GAGGAAGAGGCGAGGCTGCTTGGGAGCCAAAGACCATCTTTCTACTCAGTCTGGTT 394  
 QY 449 AA---TATCAAGATTTTCAAAGATTTGTGGCCAGTATCTTACACAGAGAGATGAA 505  
 DB 395 GACTTAAACAAAATTTTAAAGATTTTATGGCTGCTGCAAGAGAACGGGTGGAATTA 454  
 QY 506 TCGAAGTGGCTGGAAAGACATCTCTGAAGAAATGTGCTGCTGCTGCAAGAGAACGGGTGGAATTA 565  
 DB 455 TGTAAATTAGCTGGGAAAGATGCCAATACAGAAATGTGCAAAATTTTATCAGAGTACTTCAG 514  
 QY 566 GCATATAATCAGACTCACTTGTACGCTGTGGAACGGGGGCTTTTTCATCCAATTTGCAACC 625  
 DB 515 CCTATAACAAAATCCACATATATGTGTGGAACCTGGAGCATTTTCATCCAATATGTGGG 574  
 QY 626 TACATTGAAATTTGGACATCATCTCTGAGGACATATTTTAAAGCTGGAGAACTCAATTTT 585  
 DB 575 TATATTGATCTTTGGAGCTTACAGAGGAGGATTTATATTCAAACCTAGACACACATATTTG 634  
 QY 686 GAAACGGCGGTGGGAGAGTCCATATGACCTTAAGCTGTCGACAGCATCCCTTTTAAATA 745  
 DB 635 GAGTCTGGCAGACTGAATGTCTCTTCGATCTCTCAGCAGCCTTTTCTTCAGTAATGACA 694

QY 746 GATGAGAAATTATCTCTGGAACCTGACAGCTGATTTTATGGGCGAGACTTTGCTATCTTC 805  
 DB 695 GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTTCTTGGCAAGACTATGCTACTCACT 754  
 QY 806 CGAAGCTCTTGGGC-----ACCACCAACCAATCAGACAGAGCAGCATGATGATCCAGG 856  
 DB 755 CGATCCCTTGGGCTTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCAGCTAC 814  
 QY 857 TGGCTCAATGATCCAAAGTTCAATAGTGCCTCACTCATCTCAGAGAGTGACAAATCTGTA 916  
 DB 815 TGGCTCAATGAGCAAAATTTTATTGAAACTTTCTTATACACAGACACCTTCAATCCAGAT 874  
 QY 917 GATGACAAAGTATATCTTTTCTTCGCTGAATGCAATAGTAGGAGAACACTCTGAAAA 976  
 DB 875 GATGATNAATATATATTTCTTCTTCGCTGAATCATCTCAAGAGGAGGAGTACCTCCGATAAA 934  
 QY 977 GCTACTCAGCTAGATAAGTGCAGATATGCAAGAAATGACTTTGGAGGGGACAGAAAGTCTG 1036  
 DB 935 ACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGTAGGAGGACACGCGCCTG 994  
 QY 1037 GTGAATAAATGGACAACTTCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCAAAAT 1096  
 DB 995 ATAAACAAGTGGAGACTTTTCTTAAGCCAGACTGATTTGCTCAATCTCTGGAAGTGT 1054  
 QY 1097 GGCATTGACACTCATTTTGTAGAACTGAGGATGTATTCTTAATGAACCTTTTAAAGATCT 1156  
 DB 1055 GGGGCGAGATATCTTACTTGTAGCTTCAAGATATTTTATTTACTCCCCCAAGAGATGAA 1114  
 QY 1157 AAAAATCCAGTTGTATATGGAGTGTTTACGACTTCCAGTAACTTTTCAAGGATCAGGC 1216  
 DB 1115 AGAAATCTGTAGTATATATGGAGTCTTTTACTACACAGCTCCATCTTCAAGGCTCTGT 1174  
 QY 1217 GTGTGTATGTATAGCATGATGATGAGAGGGTGTCTTGGTCCATATATCCCAAGG 1276  
 DB 1175 GTTGTGTGTATAGCATGCTGACATCAGAGCAGTTTTTAATGCTCCATATGCTCATAAG 1234  
 QY 1277 GATGACCAACTATCAATGGGTGCTTATCAAGAGAGTCCCTATCCAGGCCAGGA 1336  
 DB 1235 GAAAGTCAGACCACTCGTTGGTGCAGTATGATGGGAGAAATTCCTTATCCAGGGCTGT 1294  
 QY 1337 ACTTGTCCAGCAAAACATTTG---GTGGTTTTGACTCTTACAAAGAGCCTTCTCTGATGAT 1393  
 DB 1295 ACATGTCCAGCAAAACCTATGACCCACTGATTAAGTCCACCGGAGATTTTTCAGATGAT 1354  
 QY 1394 GTTATAACCTTTTGAAGAGTCAATCCAGCCATGTCAATCCAGTGTTCCTATGAACAAT 1453  
 DB 1355 GTCATCAGTTTCATAAAGCGGCACCTCTGTGATGTATAGTCCGTATATCCAGTTCGAGGA 1414  
 QY 1454 CGCCCAATAGTATCAAAACGGATGTAAATTTATCAATTTTACACAAATTTGCTAGACCGA 1513  
 DB 1415 GGACCAACGTTTCAAGAGAAATCAATGTGGATTAACAGCTGACACAGATAGTGTGGATCAT 1474  
 QY 1514 GTGGATGAGAGAGTGGACAGTATGATGTTATGTTTTATCGGAAACAGATGTTGGGACCGTT 1573  
 DB 1475 GTCAATGGAGAGATGGCCAGTACGATGTATGTTTCTTGGAAACAGACATTTGGAAGTGT 1534  
 QY 1574 CTAAAGTAGTGTCAATTTCTAAGGAGACTTGGTATGATTTTGAAGAGGTTCTGTGGAA 1633  
 DB 1535 CTCAAGTTGTGAGCATTTCAAGAGAAAGTGG---AATATGGAAGAGGAGTAGTGTGGAG 1591  
 QY 1634 GAAATGACAGTTTTCGGGAACCGATGCTATTTTCAAGCAATGAGGCTTCCATAGACAG 1693  
 DB 1592 GAGTTGCGAGATATTCAGACCTCATCAATCATCTTTGAAACATGGAATTTGCTCTGAAGCAG 1651  
 QY 1694 CAACAATATATATTTGTTTCAACGCTGGGTTGCCAGCTCCCTTACACCGTGTGAT 1753  
 DB 1652 CAACAATTTGTACATTTGGTTCCCGAGATGAGTATGTTTCACTCTCTTTCGACAGATGCGAC 1711  
 QY 1754 ATTTACGGGAAGACGCTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTCTTGGAT 1813  
 DB 1712 ACTTATGGGAAGACTTGGCAGACTGTTGTCTTTCGACAGAGACCCCTACTGTGCTGGAT 1771  
 QY 1814 GGTTCGTGATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAAGACGACAGATATA 1873

Db 1772 GGAATGCACTGCTCTCGATATGCTCTACTTCTTAAAGGAGAGCTAGACGCCAAGATGTA 1831  
Qy 1874 AGAATGGAGACCCACTGACTCACTGTTTCCAGACTTACACCATGATATCACTACCATGCCCAC 1933  
Db 1832 AAATATGGCGACCAATCAACCCAGTCTCGGACATCGAAGACAGCATTTAGTCATG---AA 1888  
Qy 1934 AGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTACACATTTTGGAAATGCACT 1993  
Db 1889 ACTGCTGTGAAGGTGATTTTGGCATTTAACTCAACCTTCTGGAATGTATA 1948  
Qy 1994 CCGAAGTCAGAGACCGCTGCTCTATTGGCAATTCAGAGCGCAAAATGAAGAGCGAATA 2053  
Db 1949 CCTAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGGTCAGGGGATGAGCATCGA 2008  
Qy 2054 GAAGATCAGATGATGATCATATCATCAGACAGATCAAGGCCCTTCTGTAGTAGT 2113  
Db 2009 GAGGAGTTGAAGCCCGCAAGAAATCATCAAAACGGAATATGGGGTACTGATTCGAAGT 2068  
Qy 2114 CTACACAGAAGATTCAAGCAATTAACCTCTGCCATGCGGTGGAAACATGGTTTCATACAA 2173  
Db 2069 TTGCAGAGAAGATTCTGGGATGTATTACTGCAAGCCAGAGGACACATTTTCATCCAC 2128  
Qy 2174 ACTCTTCTTAAGTAAACCTCGAAGTCATTTGACACAGACATTTGGAAGAACTTCTTCAT 2233  
Db 2129 ACCATAGTGAAGTGAATTTGAATGTCAATTGAGATGAACAGATGGAAATACCCAGAGG 2188  
Qy 2234 AAGATGATGATG 2246  
Db 2189 GCAGAGCATGAGG 2201

RESULT 14

AAS46098  
ID AAS46098 standard; cDNA; 3871 BP.

AC AAS46098;

XX 18-DEC-2001 (first entry)

XX Human DNA encoding PRO polypeptide sequence #174.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;  
KW PCR primer.

XX Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 06-MAR-2000; 2000US-0186968P.

XX 14-MAR-2000; 2000US-0189320P.

XX 14-MAR-2000; 2000US-0189328P.

XX 15-MAR-2000; 2000WO-US006884.

XX 21-MAR-2000; 2000US-0190828P.

XX 21-MAR-2000; 2000US-0191007P.

XX 21-MAR-2000; 2000US-0191048P.

XX 21-MAR-2000; 2000US-0191314P.

XX 28-MAR-2000; 2000US-0192655P.

XX 29-MAR-2000; 2000US-0193032P.

XX 29-MAR-2000; 2000US-0193053P.

XX 30-MAR-2000; 2000WO-US008439.

XX 04-APR-2000; 2000US-0194449P.

XX 04-APR-2000; 2000US-0194647P.

PR 11-APR-2000; 2000US-0195975P.  
PR 11-APR-2000; 2000US-0196000P.  
PR 11-APR-2000; 2000US-0196187P.  
PR 11-APR-2000; 2000US-0196690P.  
PR 11-APR-2000; 2000US-0196820P.  
PR 18-APR-2000; 2000US-0198121P.  
PR 18-APR-2000; 2000US-0198585P.  
PR 25-APR-2000; 2000US-0199397P.  
PR 25-APR-2000; 2000US-0199550P.  
PR 25-APR-2000; 2000US-0199554P.  
PR 03-MAY-2000; 2000US-0201516P.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.

XX (GETH ) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-602746/68.

XX P-PSDB; AAU29197.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.

XX Claim 2; Fig 347; 774pp; English.

XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders

XX Sequence 3871 BP; 1251 A; 704 C; 805 G; 1111 T; 0 U; 0 Other;

Query Match 26.5%; Score 718.6; DB 4; Length 3871;  
Best Local Similarity 61.9%; Pred. No. 1.4e-205;  
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

Qy 269 AATGGGAAGAACAAATGTGCCAAGGCTGAATATTCCTACAAAGAAATTTGGAATCCAAC 328

Db 215 ACTTTGAAGCAAAATATTCCAAGACTCAAGCTAACCTACAAAGACTTCTGCTTCAAAAT 274

Qy 329 AATGTGATCACTTTCATGGCTTGGCCCAAGCTCCAGTTCATCATCTTCTTTTGAT 388

Db 275 AGCTGTATTCCTTTTGGGTTTCATCAGAAGACTGGATTTTCAAACTCTTCTCTAGAT 334

Qy 389 GAGGAACCGAGTAGGCTGTATGTTGGAGCAAGAGTACATATTTTCAATCGACCTGTT 448

Db 335 GAGGAAGAGCAGGCTGCTCTTGGAGCCAAAGACACATCTTCTACTCAGTCTGTT 394

Qy 449 AA---TATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAAGAGATGAA 505



Db 395 GACTTAAACAAAATTTTAAAGAGATTATATGCGCTGCTGCAAAAGGAACGGGTGGAATTA 454  
 QY 506 TCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCATCAAGGTACTTAAG 565  
 Db 455 TGTAATTAAGCTGGGAAGATGCCAATACAGAAATGTGCAAAATTTTCATCGAGTACTTNG 514  
 QY 566 GCATATAATFAGACTCACTTTGACGCTGTGAAACGGGGCTTTTTCATCAAAATTTGCACC 625  
 Db 515 CCCTATAACAAAACCTCACATATATGTGTGGAACCTGGAGCATTTTCATCAAAATTTGGG 574  
 QY 626 FACATTAATTTGGACATCATCTCTGAGGACATATTTTAACTGGAGACTCAATTTT 685  
 Db 575 TATATTTGATCTTGGAGCTTACAAGGAGGATATATATTCAAAACCTAGACACATAATTTG 634  
 QY 686 GAAACGGCGGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAATA 745  
 Db 635 GAGTCTGGCAGACTGAAATGTCTTTCGATCTCTCAGCAGCTTTTGTCTCAGTAATGACA 694  
 QY 746 GATGAGAAATTAATCTCTGGAACCTGAGCTGATTTTATGGGCGGAGACTTTGCTATCTTC 805  
 Db 695 GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAGATATCTCAATCACT 754  
 QY 806 CGAATCTTTGGGCTACTCATGACCACTACTATCAGAACTGACATTTTCAGAGCACTAC 814  
 Db 755 CGATCCCTTTGGGCTACTCATGACCACTACTATCAGAACTGACATTTTCAGAGCACTAC 814  
 QY 857 TGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCTCATCAGAGAGTCAACATCTCTGAA 916  
 Db 815 TGGCTCAATGAGGACAAATTTATTTGAACTTTCTTCTATACCAAGACACCTTACATCAAT 874  
 QY 917 GATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGAGAGAACACTCTCGAAA 976  
 Db 875 GATGATAAATATATTTCTTCTTCTGTAATCATCTCAAGAGGCGAGTACCTCCGATAAA 934  
 QY 977 GCTACTCAGCTAGAAATAGGTGAGATATGCAAGATGCTTCTGAGAGGCGACAGAGTCTG 1036  
 Db 935 ACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGTAGGAGGACAAACGCGCCTG 994  
 QY 1037 GTGAATAATGAGCAACATCTCTCAAGCTCTGATGTTGCTCAGTGCAGCTCCAAAT 1096  
 Db 995 ATAAACAGTGGACGACTTTCTTAAAGCCAGACTGATTTGCTCAATCTCTGGAAGTAT 1054  
 QY 1097 GGCATTGACACTCACTTTTATGAACTGACAGGATGATTTCTTAATGAACTTTTAAAGATCCT 1156  
 Db 1055 GGGCGAGATACCTTTGATGAGCTTCAAGATATTTATTTACTCCCAAGAGATGAA 1114  
 QY 1157 AAAATCCAGTTGATATGAGTGTGTTTACGCTTCCAGTAAATTTTCAAGGAGTACGCC 1216  
 Db 1115 AGAAATCTCTGATATATGAGTCTTTTACTACAAACAGCTCCATCTTTCAAGGCTCTGCT 1174  
 QY 1217 GTGTGATATAGCATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCACAGG 1276  
 Db 1175 GTTTGTGTATAGCATGCTGACATCAGAGCAGTTTTTAATGGTCCATATGCTCATAG 1234  
 QY 1277 GATGAGCCCACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGCGGCAGGA 1336  
 Db 1235 GAAAGTGCAGACCATCTTTGGGTGAGTATGATGGGAGATTTCTTTATCCAGGCTGCT 1294  
 QY 1337 ACTGTGCCAGCAAAATTTG---GTGGTTTGGACTCTACAAAGAGACCTTCTCTGATGAT 1393  
 Db 1295 ACATGTCCAAAGCAAAACCTATGACCCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354  
 QY 1394 GTTATTAACCTTTGCAAGAGTATCCAGCAGTCAATCCAGTGTTCCTTATGAACAT 1453  
 Db 1355 GTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGAGGA 1414  
 QY 1454 CGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTTACAAATTTGCTGAGACCGA 1513  
 Db 1415 GGCCCAACGTTCAAGAGATCAATGTGGATTACAGACTGACACAGATAGTGTGGATCAT 1474  
 QY 1514 GTGGATGCAAGAGATCGACAGTATGATTTATGTTTATCGGAACAGATGTTGGGACCGTT 1573

Db 1475 GTCATTGCAGAGATGGCCAGTACGATGTAATGTTTCTTGGNACAGACATTTGGAACACTGTC 1534  
 QY 1574 CTTAAAGTAGTTTCAATTTCTAAGGAGACTTTGGTATGATTTTAAAGAGAGTTCTGCTGGAA 1633  
 Db 1535 CTCAAAGTTGTGAGCATTTTCAAGGAAAGTGG---AATATGGAAGAGAGTAGTCTGGAG 1591  
 QY 1634 GAAATGACAGTTTTTTCGGGAACCGAGTCTGATTTTTCAGCAATGGAGCTTTCCACTAAGCAG 1693  
 Db 1592 GAGTTGCGAGATATTTCAAGCACTCATCAATCATCTTTGAAACATGGAATTTGTCTCTGAAGCAG 1651  
 QY 1694 CAACAACATATATTTTGGTTTCAACGGCTGGGGTTCGCCAGTCCCTTTTACACCGGTGTGAT 1753  
 Db 1652 CAACAATTTGATATTTGGTTCCGAGATGATTTAGTTTCTCTTTCGACAGATGCGAC 1711  
 QY 1754 ATTTACGGGAAGCGTGTGCTGAGTGTTCCTTCGCCGAGAGCCCTTACTGTCTTGGGAT 1813  
 Db 1712 ACTTATGGGAAGCTTTGCGAGACTGTTGTCTTTCGAGAGAGCCCTACTGTCTGGGAT 1771  
 QY 1814 GGTCTGCAATGTTCTGCTATTTTCCCACTGCAAGAGAGCGCAAGAGCAGCAAGATATA 1873  
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RESULT 15

ACB89548  
 ID ACB89548 standard; cDNA; 3871 BP.

XX AC A89548;

XX AC A89548;

DT 09-JUL-2003 (first entry)

XX cDNA encoding human PRO polypeptide #174.

Human; PRO polypeptide; secreted protein; transmembrane protein;  
 chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;  
 prostate; rectal; cervical; liver; cancer; TNF-alpha;  
 tumour necrosis factor-alpha; proliferation; differentiation;  
 chondrocyte cell; bone disorder; cartilage disorder; sports injury;  
 arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;  
 ss.

XX Homo sapiens.

XX US2003036141-A1.

XX

PD 20-FEB-2003.  
XX PF  
XX XX  
XX 01-JUL-2002; 2002US-00187597.  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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SUMMARIES

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2	2508.4	92.6	2601	US-08-835-268-53	Sequence 53, Appl
3	2508.4	92.6	2601	US-09-060-692-53	Sequence 53, Appl
4	2508.4	92.6	2601	US-08-833-391-53	Sequence 53, Appl
5	2508.4	92.6	2601	US-09-060-610-53	Sequence 53, Appl
6	2508.4	92.6	2601	PCT-US94-10151A-53	Sequence 53, Appl
7	1415.2	52.2	1481	US-08-136-922-1	Sequence 1, Appl
8	596.4	22.0	2898	US-09-308-179B-2	Sequence 2, Appl
9	552.8	20.4	5177	US-09-814-915A-79	Sequence 79, Appl
10	474.8	17.5	2349	US-09-813-290-3	Sequence 3, Appl
11	474.8	17.5	2628	US-09-813-290-1	Sequence 1, Appl
12	473.6	17.5	3568	US-09-813-290-5	Sequence 5, Appl
13	138.8	5.1	229	US-09-513-999C-2555	Sequence 2555, Ap
14	125	4.6	1890	US-09-520-781-29	Sequence 29, Appl
15	125	4.6	2278	US-09-376-594-1002	Sequence 1002, Ap
16	125	4.6	3333	US-09-520-781-5	Sequence 5, Appl
17	125	4.6	3498	US-09-520-781-3	Sequence 3, Appl
18	125	4.6	4280	US-09-774-528-330	Sequence 330, App
19	95.2	3.5	3692	US-09-077-940A-1	Sequence 1, Appl
20	91.2	3.4	300	US-09-513-999C-419	Sequence 419, App
21	90.6	3.3	1923	US-09-653-274-12	Sequence 12, Appl
22	90.6	3.3	1923	US-10-461-791-12	Sequence 12, Appl
23	90.6	3.3	3261	US-09-653-274-5	Sequence 5, Appl
24	90.6	3.3	3261	US-10-461-791-5	Sequence 5, Appl
25	90.6	3.3	3694	US-09-653-274-3	Sequence 3, Appl
26	90.6	3.3	3694	US-10-461-791-3	Sequence 3, Appl
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41	60.2	2.2	2865	4	US-09-854-845-13	Sequence 13, Appl
42	60.2	2.2	3105	4	US-09-854-845-5	Sequence 5, Appl
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44	60.2	2.2	3237	4	US-09-854-845-7	Sequence 7, Appl
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ALIGNMENTS

RESULT 1  
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; Sequence 53, Application US/08121713D  
; Patent No. 5639856  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey S.  
; APPLICANT: Kolodkin, Alex L.  
; APPLICANT: Matthes, David  
; APPLICANT: Bentley, David R.  
; APPLICANT: O'Connor, Timothy  
; TITLE OF INVENTION: The Semaphorin Gene Family  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121,713D  
; FILING DATE: 13-SEP-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: B94-002-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)343-4341  
; TELEFAX: (415) 343-4342  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2601 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
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Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	493	CAGAGAGATGAATGCAAGTGGGCTGGAAAAGACATCTCTGAAAGAAATGTGCTTAATTCAT	552
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Db	1329	AGTGGATGCAGAAGATGACAGTATGATGTTATGTTATCGGAAACAGATGTTGGGACCGT	1388
QY	1573	TCCTTAAAGTATGTTCAATTCCTAAGGACATTTGGTATGATTTAGAGAGGTTCTGCTGGA	1632
Db	1389	TCCTTAAAGTATGTTCAATTCCTAAGGACATTTGGTATGATTTAGAGAGGTTCTGCTGGA	1448
QY	1633	AGAAATGACAGTCTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCACCTAAGCA	1692
Db	1449	AGAAATGACAGTCTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCACCTAAGCA	1508
QY	1693	GCAACAACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTTCCCTTTACACCGGTGGA	1752
Db	1509	GCAACAACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTTCCCTTTACACCGGTGGA	1568
QY	1753	TATTTACGGGAAGGGTGTGCTGAGTGTGCTGCTGCCCGAGACCTCTTACTGTGCTTGGGA	1812
Db	1569	TATTTACGGGAAGGGTGTGCTGAGTGTGCTGCTGCCCGAGACCTCTTACTGTGCTTGGGA	1628
QY	1813	TGGTTCTGCATGTTCTGCTTATTTTCCCACTGCAAAAGAGAGCGCAACAGCACAGATAT	1872
Db	1629	TGGTTCTGCATGTTCTGCTTATTTTCCCACTGCAAAAGAGAGCGCAACAGCACAGATAT	1688
QY	1873	AAGAAATGGAGACCCACTGACTCTGTTAGAGCTTACACCATGATAATACCATGGGCA	1932
Db	1689	AAGAAATGGAGACCCACTGACTCTGTTAGAGCTTACACCATGATAATACCATGGGCA	1748
QY	1933	CAGCCCTGAAAGAGAAATCATCTATGTTGTTAGAGATAGTAGACATTTTGGGATGAG	1992
Db	1749	CAGCCCTGAAAGAGAAATCATCTATGTTGTTAGAGATAGTAGACATTTTGGGATGAG	1808
QY	1993	TCCGAAGTCGAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGGGCGAAATGAAGCGGAAA	2052
Db	1809	TCCGAAGTCGAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGGGCGAAATGAAGCGGAAA	1868
QY	2053	AGAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTACGTAG	2112
Db	1869	AGAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTACGTAG	1928
QY	2113	TCTACAAAGAGAAATTCAGGCAATTAACCTCTGCCATGGGTGGGAACATGGGTTTCATACA	2172
Db	1929	TCTACAAAGAGAAATTCAGGCAATTAACCTCTGCCATGGGTGGGAACATGGGTTTCATACA	1988
QY	2173	AACCTTCTTAAAGGTAAACCTCGGAAGTCAATTTGACACAGAGCATTTTGGGAAGAACTTCTTCA	2232
Db	1989	AACCTTCTTAAAGGTAAACCTCGGAAGTCAATTTGACACAGAGCATTTTGGGAAGAACTTCTTCA	2048
QY	2233	TAAAGATGATGAGATGGCTCTTAAGACCAAAAGAAATGTCCAATAGATGACACCTAG	2292
Db	2049	TAAAGATGATGAGATGGCTCTTAAGACCAAAAGAAATGTCCAATAGATGACACCTAG	2108
QY	2293	CCAGAGGCTGTGGTACAGAGACTTCATGACGCTCATCAACCAACCCCAATCTCAACACCAT	2352
Db	2109	CCAGAGGCTGTGGTACAGAGACTTCATGACGCTCATCAACCAACCCCAATCTCAACACCAT	2168

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QY 2353 GGATGAGTTCTGTGAACAAGTTTGGAAAAAGGAGCCGAAAAACAGCTGGCAAGGCCAGG 2412
DB 2169 GGATGAGTTCTGTGAACAAGTTTGGAAAAAGGAGCCGAAAAACAGCTGGCAAGGCCAGG 2228
QY 2413 ACATACCCAGGGAACAGTAACAATAATGGAAGCACTTACAAAGAAATAAAGAAAGGTAGAAA 2472
DB 2229 ACATACCCAGGGAACAGTAACAATAATGGAAGCACTTACAAAGAAATAAAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGACCCAGAAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCAATTACCTCTAGA 2532
DB 2289 CAGGAGGACCCAGAAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCAATTACCTCTAGA 2348
QY 2533 AACCTCAACAAGTAGAAAACCTTGCCTTAGACAATACTGGAAGAAACAAATGCAATATACAT 2592
DB 2349 AACCTCAACAAGTAGAAAACCTTGCCTTAGACAATACTGGAAGAAACAAATGCAATATACAT 2408
QY 2593 GAACTTTTTCATGGCATTATGTGGATGTTTCAATGGTGGGAAATTCAGCTGAGTTCCA 2652
DB 2409 GAACTTTTTCATGGCATTATGTGGATGTTTCAATGGTGGGAAATTCAGCTGAGTTCCA 2468
QY 2653 CCAATTATAAATTAATCCATGAGTAACCTTCTTAATAGGCTTTTTTTTCC 2702
DB 2469 CCAATTATAAATTAATCCATGAGTAACCTTCTTAATAGGCTTTTTTTTCC 2518

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RESULT 2

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US-08-835-268-53
; Sequence 53, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS

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; LOCATION: 16...2331
US-08-835-268-53
Query Match 92.6%; Score 2508.4; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 193 CTGAGCATGGGCTGGTAACTAGGATTGTCTGTCTTTTCTGGGAGTATTATCTTACAGC 252
DB 9 CTGAGCATGGGCTGGTAACTAGGATTGTCTGTCTTTTCTGGGAGTATTATCTTACAGC 68
QY 253 AAGACAACATATCAGATGGGAAGCAATGTCGCAAGGCTGAAATTTATCTTACAAAGA 312
DB 69 AAGACAACATATCAGATGGGAAGCAATGTCGCAAGGCTGAAATTTATCTTACAAAGA 128
QY 313 AATGTTGGAATCCAAATATGATCACTTTCAATGGCTGGCCAAACAGCTCCAGTTATCA 372
DB 129 AATGTTGGAATCCAAATATGATCACTTTCAATGGCTGGCCAAACAGCTCCAGTTATCA 188
QY 373 TACCTTCCCTTTGGATGAGGAACGAGTAGGCTGTATGTTGAGCAAAAGGATCACATAT 432
DB 189 TACCTTCCCTTTGGATGAGGAACGAGTAGGCTGTATGTTGAGCAAAAGGATCACATAT 248
QY 433 TTCATTGCACTGGTAAATATCAAGGATTTTCAAAAGATTGTTGGCCAGTATCTTACAC 492
DB 249 TTCATTGCACTGGTAAATATCAAGGATTTTCAAAAGATTGTTGGCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATGCAAGTGGCTGGAAAAAGACATCTCTGAAAGAAATGTCTAAATTT 552
DB 309 CAGAAGAGATGAATGCAAGTGGCTGGAAAAAGACATCTCTGAAAGAAATGTCTAAATTT 368
QY 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACGCTGTGGAACGGGGCTTTTCA 612
DB 369 CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACGCTGTGGAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGACCTACATTTGAAATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGA 672
DB 429 TCCAAATTTGACCTACATTTGAAATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGA 488
QY 673 GAACTCACATTTTGAAAAAGCGGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 732
DB 489 GAACTCACATTTTGAAAAAGCGGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 548
QY 733 ATCCCTTTAATAGATGGAGAAATTAATCTTGAAACCTGAGCTGATTTTATGGGCGAGA 792
DB 549 ATCCCTTTAATAGATGGAGAAATTAATCTTGAAACCTGAGCTGATTTTATGGGCGAGA 608
QY 793 CTTTGCTATCTTCGAACTCTTGGGCACCAACCCCAATCAGGACAGAGCAGCATGATTC 852
DB 609 CTTTGCTATCTTCGAACTCTTGGGCACCAACCCCAATCAGGACAGAGCAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTTCATTTAGTGGCCACCTCATCTCAGAGAGTGACAATCC 912
DB 669 CAGGTGGCTCAATGATCCAAAGTTTCATTTAGTGGCCACCTCATCTCAGAGAGTGACAATCC 728
QY 913 TGAAGTACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGGAACACTCTCG 972
DB 729 TGAAGTACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGGAACACTCTCG 788
QY 973 AAAAGCTACTCAGCTAGAAATAGGTCAGATATGCAAGAAATGACTTTTGGAGGACAGAAAG 1032
DB 789 AAAAGCTACTCAGCTAGAAATAGGTCAGATATGCAAGAAATGACTTTTGGAGGACAGAAAG 848
QY 1033 TCTGGTGAATAAATGGACAACATCTCTCAAGCTCGTCTGATTTCTCAGTCCAGGTC 1092
DB 849 TCTGGTGAATAAATGGACAACATCTCTCAAGCTCGTCTGATTTCTCAGTCCAGGTC 908
QY 1093 AAATGGCAATGACACTCAATTTTGTAGTGAATGCAAGATGATTTCTTAATGAACCTTTAAAGA 1152
DB 909 AAATGGCAATGACACTCAATTTTGTAGTGAATGCAAGATGATTTCTTAATGAACCTTTAAAGA 968
QY 1153 TCCTAAAAATCCAGTTGATATGAGAGTGTATACGACTTCCAGTAACTTTTCAAGGATC 1212

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STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cdna  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 16..2331  
 US-09-060-692-53

Query Match 92.6%; Score 2508.4; DB 2; Length 2601;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	193	CTGCAGCATGGGCTGGTAACTAGGATGCTCTGCTCTTTCTGGGAGTATTAATTACAGC	252
DB	9	CTGCAGCATGGGCTGGTAACTAGGATGCTCTGCTCTTTCTGGGAGTATTAATTACAGC	68
QY	253	AAGAGCAAACTACTCAGATGGGAAGAAACAATGTGCCAAGGCTGAAATATCTTACAAGA	312
DB	69	AAGAGCAAACTACTCAGATGGGAAGAAACAATGTGCCAAGGCTGAAATATCTTACAAGA	128
QY	313	AATGTTGGAATCCAACTATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA	372
DB	129	AATGTTGGAATCCAACTATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA	188
QY	373	TACCTTCTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT	432
DB	189	TACCTTCTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT	248
QY	433	TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAGATTTTCAAGATTTGTCGCCAGTATCTTACAC	492
DB	249	TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAGATTTTCAAGATTTGTCGCCAGTATCTTACAC	308
QY	493	CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTTGAAGAAATGTCTAAATTTCAAT	552
DB	309	CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTTGAAGAAATGTCTAAATTTCAAT	368
QY	553	CAAGGTACTTAAAGGCATATAATCAGACTCACTTGTACGCTGTGGAACCGGGGCTTTTCA	612
DB	369	CAAGGTACTTAAAGGCATATAATCAGACTCACTTGTACGCTGTGGAACCGGGGCTTTTCA	428
QY	613	TCCAAATTCACCTACATTTGAATTTGGACATCATCTGAGGACAAATTTTAAAGCTGGA	672
DB	429	TCCAAATTTGACCTACATTTGAATTTGGACATCATCTGAGGACAAATTTTAAAGCTGGA	488
QY	673	GAACTCACATTTTGAAGACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC	732
DB	489	GAACTCACATTTTGAAGACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC	548
QY	733	ATCCCTTTTAAATAGATGGGAATTAATCTCTGGAACCTGAGCTGATTTTATGGGGGAGA	792
DB	549	ATCCCTTTTAAATAGATGGGAATTAATCTCTGGAACCTGAGCTGATTTTATGGGGGAGA	608
QY	793	CTTTGCTATCTTCGGAACCTTTGGGACACACCAACCAATCAGGACAGCAGATGATTC	852
DB	609	CTTTGCTATCTTCGGAACCTTTGGGACACACCAACCAATCAGGACAGCAGATGATTC	668
QY	853	CAGGTGGCTCAATGATCCAAAGTTTCAATAGTGCACCTCATCTCAGAGAGTGAACAATCC	912
DB	669	CAGGTGGCTCAATGATCCAAAGTTTCAATAGTGCACCTCATCTCAGAGAGTGAACAATCC	728
QY	913	TGAAGATGACAAAGTATACCTTTTCTCCGTGAAATGCAATAGATGGAGAACTCTCGG	972
DB	729	TGAAGATGACAAAGTATACCTTTTCTCCGTGAAATGCAATAGATGGAGAACTCTCGG	788
QY	973	AAAAGTACTCAGCTAGAAATAGGTGAGATATGCAAGAATGATTTGGAGGGGACAGAAG	1032
DB	789	AAAAGTACTCAGCTAGAAATAGGTGAGATATGCAAGAATGATTTGGAGGGGACAGAAG	848
QY	1033	TCCTGGTAAATAGTGAACACATTTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTCC	1092
DB	849	TCCTGGTAAATAGTGAACACATTTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTCC	908
QY	1093	AAATGCAATTGACACTCATTTTGTATGAACTGACAGGATGTATCTTAATGAACCTTTAAAGA	1152

DB	909	AAATGGCATTTGACACTCATTTTGTATGAACCTGCAGGATGTATCTTAATGAACCTTTAAAGA	968
QY	1153	TCCTAAAAATCCAGTTGTATATGGAGTGTTTACGACTTCCAGTAACATTTTCAAGGGATC	1212
DB	969	TCCTAAAAATCCAGTTGTATATGGAGTGTTTACGACTTCCAGTAACATTTTCAAGGGATC	1028
QY	1213	AGCCGTGTGTATGTATAGCATGAGTGTAGAAAGGGTGTCTTGTGTCATATGCCCA	1272
DB	1029	AGCCGTGTGTATGTATAGCATGAGTGTAGAAAGGGTGTCTTGTGTCATATGCCCA	1088
QY	1273	CAGGATGAGACCAACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTTATCCACGGCC	1332
DB	1089	CAGGATGAGACCAACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTTATCCACGGCC	1148
QY	1333	AGGAATCTGTCTCCAGCAAAACATTTGGTGGTTTGACTCTCAAAAGGACCTTCTCTGATGA	1392
DB	1149	AGGAATCTGTCTCCAGCAAAACATTTGGTGGTTTGACTCTCAAAAGGACCTTCTCTGATGA	1208
QY	1393	TGTTATTAACCTTTGCAAGAGTATCCAGGCAATGTAACATCCAGTGTCTTCTATGAACAA	1452
DB	1209	TGTTATTAACCTTTGCAAGAGTATCCAGGCAATGTAACATCCAGTGTCTTCTATGAACAA	1268
QY	1453	TCGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTTACAAATTTGTCTAGACCG	1512
DB	1269	TCGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTTACAAATTTGTCTAGACCG	1328
QY	1513	AGTGGATGAGAAAGATGACAGTATGATGTATGTTATTCGGAACAGAGTGTGGGACCGT	1572
DB	1329	AGTGGATGAGAAAGATGACAGTATGATGTATGTTATTCGGAACAGAGTGTGGGACCGT	1388
QY	1573	TCCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTTGGTATGATTTAGAAAGAGTGTCTGGA	1632
DB	1389	TCCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTTGGTATGATTTAGAAAGAGTGTCTGGA	1448
QY	1633	AGAAATGACAGTGTTCGGGAACCGACTGCTATTTTCGCAATGGAGCTTTTCCACTAAGCA	1692
DB	1449	AGAAATGACAGTGTTCGGGAACCGACTGCTATTTTCGCAATGGAGCTTTTCCACTAAGCA	1508
QY	1693	GCAACAACTATATTTGTTTCAACGGCTGGGGTGTCCAGCTCCCTTTTACACGGTGTGA	1752
DB	1509	GCAACAACTATATTTGTTTCAACGGCTGGGGTGTCCAGCTCCCTTTTACACGGTGTGA	1568
QY	1753	TATTTACGGGAAGCGTGTGTGAGTGTTCCTCCGCGGAGACCTTTACTGTCTGGGA	1812
DB	1569	TATTTACGGGAAGCGTGTGTGAGTGTTCCTCCGCGGAGACCTTTACTGTCTGGGA	1628
QY	1813	TGTTTTCTGCTATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAACAGACGACAGATAT	1872
DB	1629	TGTTTTCTGCTATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAACAGACGACAGATAT	1688
QY	1873	AAGAAATGGAGACCACTGACTCAGCTTTCAGACTTACACCATGATAATCACCATGGCCA	1932
DB	1689	AAGAAATGGAGACCACTGACTCAGCTTTCAGACTTACACCATGATAATCACCATGGCCA	1748
QY	1933	CAGCCCTGAAGAGAGAACTCATCTATGGTGTAGAGAAATAGTAGCACAATTTTGGAAATGACG	1992
DB	1749	CAGCCCTGAAGAGAGAACTCATCTATGGTGTAGAGAAATAGTAGCACAATTTTGGAAATGACG	1808
QY	1993	TCCGAAGTGCAGAGAGCGCTGCTATTTGGCAATTTCCAGAGCGCAATTAAGAGCGGAAA	2052
DB	1809	TCCGAAGTGCAGAGAGCGCTGCTATTTGGCAATTTCCAGAGCGCAATTAAGAGCGGAAA	1868
QY	2053	AGAAGAGATCAGAGTGGATGATCATATCATAGGACAGATCAAGGCTTCTGCTAGCTAG	2112
DB	1869	AGAAGAGATCAGAGTGGATGATCATATCATAGGACAGATCAAGGCTTCTGCTAGCTAG	1928
QY	2113	TCCTAACACAGAAAGGATTCAGGCAATTTACCTCTGCCATCGGTGGGAACATGGGTTCATACA	2172
DB	1929	TCCTAACACAGAAAGGATTCAGGCAATTTACCTCTGCCATCGGTGGGAACATGGGTTCATACA	1988
QY	2173	AACTCTTCTTAAGGTAACCTCGAAGTCAATTCACACAGAGCAATTTGGGAAGAACTTCTTCA	2232

1989	Db	AACTCTTCTTAAGGTAACCTCGGAGTCATTGACACAGAGCATTTTGGAAAGCACTTCTTCA	2048
2233	Qy	TAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG	2292
2049	Db	TAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG	2108
2293	Qy	CCAGAGGTCCTGGTACAGAGACTTTCATGCGAGCTCATCAACCAACCCCAATCTCAACAGCAT	2352
2109	Db	CCAGAGAGGTCCTGGTACAGAGACTTTCATGCGAGCTCATCAACCAACCCCAATCTCAACAGCAT	2168
2353	Qy	GGATGAGTCTCTGTGAACAAGCTTTTGGAAAAAGGACCGGAAAAACAACGTGCGCAAAAGGCCAGG	2412
2169	Db	GGATGAGTCTCTGTGAACAAGCTTTTGGAAAAAGGACCGGAAAAACAACGTGCGCAAAAGGCCAGG	2228
2413	Qy	ACATACCCCAAGGGAACAGTAAACAAATGGAGAGCACTTACAAGAAAAATAGAAAAAGGTAGAAA	2472
2229	Db	ACATACCCCAAGGGAACAGTAAACAAATGGAGAGCACTTACAAGAAAAATAGAAAAAGGTAGAAA	2288
2473	Qy	CAGGAGGACCCACAAGAAATTTGAGAGGGGACCCAGGAGTGTCTGAGCTGTGCACTTACTCTAGA	2532
2289	Db	CAGGAGGACCCACAAGAAATTTGAGAGGGGACCCAGGAGTGTCTGAGCTGTGCACTTACTCTAGA	2348
2533	Qy	AACTCTAAAACAAGTAGAAAATCTTGCTTAGACAATAACTGGAAAAACAATGCAATATACAT	2592
2349	Db	AACTCTAAAACAAGTAGAAAATCTTGCTTAGACAATAACTGGAAAAACAATGCAATATACAT	2408
2593	Qy	GAACCTTTTTTCATGGCAATATGTGGATGTTTTACAATGGTGGGAAATTCAGCTCAGTTTCCA	2652
2409	Db	GAACCTTTTTTCATGGCAATATGTGGATGTTTTACAATGGTGGGAAATTCAGCTCAGTTTCCA	2468
2653	Qy	CCAATTATAAATAAATCCCATGAGTAACCTTCCTTAATAGAGCTTTTTTTTCC	2702
2469	Db	CCAATTATAAATAAATCCCATGAGTAACCTTCCTTAATAGAGCTTTTTTTTCC	2518

## RESULT 4

US-08-833-391-53  
; Sequence 53, Application US/08833391  
; Patent No. 6013781  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey S.  
; APPLICANT: Kolodkin, Alex L.  
; APPLICANT: Matthes, David  
; APPLICANT: Bentley, David R.  
; APPLICANT: O'Connor, Timothy  
; TITLE OF INVENTION: The Semaphorin Gene Family  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,391  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/121,713  
; FILING DATE: 13-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: B94-002-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)343-4341  
; TELEFAX: (415) 343-4342

1033 TCTGGTGAATAAATGAGCAACATTCTCAAGCTGCTGATTTGCTCAGTGCCAGGTCC 1092  
 849 TCTGGTGAATAAATGAGCAACATTCTCAAGCTGCTGATTTGCTCAGTGCCAGGTCC 908  
 1093 AAATGSCATTGACACTCATTTTGTGATGAACTGCGAGGATGATTTCCTAATCAATTTAAAGA 1152  
 909 AAATGSCATTGACACTCATTTTGTGATGAACTGCGAGGATGATTTCCTAATCAATTTAAAGA 968  
 1153 TCTAAAAATCCAGTTGTATATGAGATGTTTACGACTTCCAGTAAACATTTTCAAGGGATC 1212  
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 1089 CAGGGATGACCAACTATCAATGGGTGCTTATCAAGGAAGATGCCCTTATCCAGGCC 1148  
 1333 AGGAACCTTGTCCAGCAAAACATTTTGGTGTGTTTGACTCTCAAAAGGACCTTCTCTGATGA 1392  
 1149 AGGAACCTTGTCCAGCAAAACATTTTGGTGTGTTTGACTCTCAAAAGGACCTTCTCTGATGA 1208  
 1393 TGTATTAACCTTGTCAAGAGTATCCAGGCATGTACATCAGTGTTCCTATGAACAA 1452  
 1209 TGTATTAACCTTGTCAAGAGTATCCAGGCATGTACATCAGTGTTCCTATGAACAA 1268  
 1453 TCGCCCAATAGTATCAAAACCGATGTAATTTATCAATTTTACAAATTTGCTGAGACCG 1512  
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 1513 AGTGAATGAGAGATGAGACAGTATGATGTTTATGTTTATCGGAACAGATGTTGGGACCGT 1572  
 1329 AGTGAATGAGAGATGAGACAGTATGATGTTTATGTTTATCGGAACAGATGTTGGGACCGT 1388  
 1573 TCTTAAAGTAGTTTCAATTTCTTAAAGGAGACTGTTGATGATTTAGAGAGGTTCTGCTGGA 1632  
 1389 TCTTAAAGTAGTTTCAATTTCTTAAAGGAGACTGTTGATGATTTAGAGAGGTTCTGCTGGA 1448  
 1633 AGAATGACAGTTTTCGGGAACCGACTGCTATTTTCCAGCAATGAGCTTTCACATGAACA 1692  
 1449 AGAATGACAGTTTTCGGGAACCGACTGCTATTTTCCAGCAATGAGCTTTCACATGAACA 1508  
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 1753 TATTTACGGGAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTCTTGGGA 1812  
 1569 TATTTACGGGAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTCTTGGGA 1628  
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 1873 AGAATGAGAGACCCACTGACTCAGCTCAGCTTACACTTACCAATCAATCAATGCGCA 1932  
 1689 AGAATGAGAGACCCACTGACTCAGCTTACACTTACCAATCAATCAATGCGCA 1748  
 1933 CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGAAATAGTAGACACATTTTGGAAATGACAG 1992  
 1749 CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGAAATAGTAGACACATTTTGGAAATGACAG 1808  
 1993 TCGGAATGCGAGAGCGTGTGCTATTTGGCAATTTCCAGAGCGGAAATGAGAGCGAAA 2052  
 1809 TCGGAATGCGAGAGCGTGTGCTATTTGGCAATTTCCAGAGCGGAAATGAGAGCGAAA 1868  
 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGTAG 2112  
 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGTAG 1928  
 2113 TCTAACACAGAGGATTCAGGCAATTTACCTCTGCCATGGGTGGAACATGGGTTTCATACA 2172

1929 TCTAACACAGAGGATTCAGGCAATTTACCTCTGCCATGGGTGGAACATGGGTTTCATACA 1988  
 2173 AACTCTTCTTAAAGGTAAACCTCTGGAAGTCAATTCACACAGAGCAATTTGGGAAGAACTTCTTCA 2232  
 1989 AACTCTTCTTAAAGGTAAACCTCTGGAAGTCAATTCACACAGAGCAATTTGGGAAGAACTTCTTCA 2048  
 2233 TAAAGATGATGATGAGATGGCTTAAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2292  
 2049 TAAAGATGATGATGAGATGGCTTAAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2108  
 2293 CCAGAGGCTCTGCTACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACACGAT 2352  
 2109 CCAGAGGCTCTGCTACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACACGAT 2168  
 2353 GGATGAGTCTCTGTAACCAAGTTTGGAAAGGAGCCGAAACCAACCGTCGCAAGGCGCAGG 2412  
 2169 GGATGAGTCTCTGTAACCAAGTTTGGAAAGGAGCCGAAACCAACCGTCGCAAGGCGCAGG 2228  
 2413 ACATACCCAGGGAACAGTAAACAATGGAAGCACTTACGAAGAAATTAAGAAAGGTAGAAA 2472  
 2229 ACATACCCAGGGAACAGTAAACAATGGAAGCACTTACGAAGAAATTAAGAAAGGTAGAAA 2288  
 2473 CAGGAGGACCCAGATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCAATTTACCTCTAGA 2532  
 2289 CAGGAGGACCCAGATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCAATTTACCTCTAGA 2348  
 2533 AACCTCAACCAAGTAGAAAACCTTGCCTTAGACAATACTGGAAGAAACAAATGCAATATACAT 2592  
 2349 AACCTCAACCAAGTAGAAAACCTTGCCTTAGACAATACTGGAAGAAACAAATGCAATATACAT 2408  
 2593 GAACCTTTTTCATGCGATTTATGAGTGTGTTTCAATGTTGGGAAATTCAGCTGAGTTCCA 2652  
 2409 GAACCTTTTTCATGCGATTTATGAGTGTGTTTCAATGTTGGGAAATTCAGCTGAGTTCCA 2468  
 2653 CCAATATAAATAAATCCATGAGTAACTTCTTCTAATAGGCTTTTTCCTCC 2702  
 2469 CCAATATAAATAAATCCATGAGTAACTTCTTCTAATAGGCTTTTTCCTCC 2518

RESULT 5  
 US-09-060-610-53  
 ; Sequence 53, Application US/09060610  
 ; Patent No. 6344544  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodman, Corey S.  
 ; APPLICANT: Kolodkin, Alex L.  
 ; APPLICANT: Matthes, David  
 ; APPLICANT: Bentley, David R.  
 ; APPLICANT: O'Connor, Timothy  
 ; TITLE OF INVENTION: The Semaphorin Gene Family  
 ; NUMBER OF SEQUENCES: 100  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP  
 ; STREET: 268 Bush Street, Suite 3200  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/060,610  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/835,268  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Osman, Richard A.

REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: B94-002-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)343-4341  
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2601 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 16..2331  
US-09-060-610-553

Query Match 92.6%; Score 2508.4; DB 3; Length 2601;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	193	CTGCAGCATGGCTGGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGC	252
DB	9	CTGCAGCATGGCTGGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGC	68
QY	253	AGAGCAACTATCAGATGGGAGGAGCAATCTGCCMAGGCTGAAATTCCTACAGAGA	312
DB	69	AGAGCAAACTATCAGATGGGAGGAGCAATCTGCCMAGGCTGAAATTCCTACAGAGA	128
QY	313	AATGTTGGAATCCAACTATGTCATCTTCAATGGCTTGGCCAAAGCTCCAGTTATCA	372
DB	129	AATGTTGGAATCCAACTATGTCATCTTCAATGGCTTGGCCAAAGCTCCAGTTATCA	188
QY	373	TACCTTCCTTTGGATGAGGAAACGGAGTAGGCTGATGTTGGAGCAAGGATCACATAT	432
DB	189	TACCTTCCTTTGGATGAGGAAACGGAGTAGGCTGATGTTGGAGCAAGGATCACATAT	248
QY	433	TTCAATCGACCTGGTTAATATCAAGGATTTTCAAAAGATGTTGGCCAGTATCTTACAC	492
DB	249	TTCAATCGACCTGGTTAATATCAAGGATTTTCAAAAGATGTTGGCCAGTATCTTACAC	308
QY	493	CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTTCAAAAGATGTTGCTAAATTCAT	552
DB	309	CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTTCAAAAGATGTTGCTAAATTCAT	368
QY	553	CAAGGTACTTAAGGCATATAATCAGACTCCTTGTACGCTGTGGAAACGGGGCTTTTCA	612
DB	369	CAAGGTACTTAAGGCATATAATCAGACTCCTTGTACGCTGTGGAAACGGGGCTTTTCA	428
QY	613	TCCAAATTCACCTACATTTGAATGGACATCATCTGAGGACATATTTTAAAGCTGGA	672
DB	429	TCCAAATTCACCTACATTTGAATGGACATCATCTGAGGACATATTTTAAAGCTGGA	488
QY	673	GAACTCACATTTTGAAGACGGCGTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGC	732
DB	489	GAACTCACATTTTGAAGACGGCGTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGC	548
QY	733	ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGGAACCTGAGCTGATTTTATGGGGAGA	792
DB	549	ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGGAACCTGAGCTGATTTTATGGGGAGA	608
QY	793	CTTTCGTATCTTCGGAACCTTTGGGACCAACCAACCAATCAGGACAGACGACATGATTC	852
DB	609	CTTTCGTATCTTCGGAACCTTTGGGACCAACCAACCAATCAGGACAGACGACATGATTC	668
QY	853	CAGGTGGCTCAATGATCCAAAGTTCAATTAGTCCCACTCATCTCAGAGAGTGACAAATCC	912
DB	669	CAGGTGGCTCAATGATCCAAAGTTCAATTAGTCCCACTCATCTCAGAGAGTGACAAATCC	728
QY	913	TGAAGATGACAAAGTATATCTTTTCTCCGTGGAATGCAATAGATGGAGAACATCTCTGG	972
DB	729	TGAAGATGACAAAGTATATCTTTTCTCCGTGGAATGCAATAGATGGAGAACATCTCTGG	788

QY	973	AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTTGGAGGSCACAGAG	1032
DB	789	AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTTGGAGGSCACAGAG	848
QY	1033	TCCTGTGAATAAATGAGCAAACTTCTCAAAGCTCGTCTGATTTCCTCAGTCCAGGTC	1092
DB	849	TCCTGTGAATAAATGAGCAAACTTCTCAAAGCTCGTCTGATTTCCTCAGTCCAGGTC	908
QY	1093	AAATGGCAATTGACACTCATTTTGTATGAATCGCAGAGATGTTTCTTAATGAATTTAAAGA	1152
DB	909	AAATGGCAATTGACACTCATTTTGTATGAATCGCAGAGATGTTTCTTAATGAATTTAAAGA	968
QY	1153	TCCTAAATAATCCAGTTGTATATGAGAGTGTTCACGACTTCCAGTACATTTTCAAGGATC	1212
DB	969	TCCTAAATAATCCAGTTGTATATGAGAGTGTTCACGACTTCCAGTACATTTTCAAGGATC	1028
QY	1213	AGCCGTGTATGTATAGCATGAGTGTGAGAAAGGTTTCTTGGTCCATATGCCCA	1272
DB	1029	AGCCGTGTATGTATAGCATGAGTGTGAGAAAGGTTTCTTGGTCCATATGCCCA	1088
QY	1273	CAGGATGAGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCT	1332
DB	1089	CAGGATGAGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCT	1148
QY	1333	AGGAACTTGTCCAGCAAAACATTTTGGTGGTTTTCACCTCAAAAGGACCTTCTCTGATGA	1392
DB	1149	AGGAACTTGTCCAGCAAAACATTTTGGTGGTTTTCACCTCAAAAGGACCTTCTCTGATGA	1208
QY	1393	TGTTATAACCTTTGCAAGAAGTCATCCAGCCATGTACAAATCAGTGTCTTCTATGAACAA	1452
DB	1209	TGTTATAACCTTTGCAAGAAGTCATCCAGCCATGTACAAATCAGTGTCTTCTATGAACAA	1268
QY	1453	TGCCCCAATAGTGTACAAACCGGATGTAAATTTATCAATTTACACAAATTTGCTGAGACCG	1512
DB	1269	TGCCCCAATAGTGTACAAACCGGATGTAAATTTATCAATTTACACAAATTTGCTGAGACCG	1328
QY	1513	AGTGTATGACAGAAAGTGGACAGTATGTTTATGTTTATCGGAAACAGATTTGGGACCGT	1572
DB	1329	AGTGTATGACAGAAAGTGGACAGTATGTTTATGTTTATCGGAAACAGATTTGGGACCGT	1388
QY	1573	TCCTAAAGTAGTTCCTCAATTTCTTAAGGAGACTTTGGTATGATTTTGAAGAGGTTCTCTGGA	1632
DB	1389	TCCTAAAGTAGTTCCTCAATTTCTTAAGGAGACTTTGGTATGATTTTGAAGAGGTTCTCTGGA	1448
QY	1633	AGAAATGACAGTTTTTTCGGAAACCGACTGTATTTTTCAGCAATGGAGCTTTCACCTAAGCA	1692
DB	1449	AGAAATGACAGTTTTTTCGGAAACCGACTGTATTTTTCAGCAATGGAGCTTTCACCTAAGCA	1508
QY	1693	GCAACAACTATATATTTTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGGA	1752
DB	1509	GCAACAACTATATATTTTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGGA	1568
QY	1753	TATTTTACGGGAAAGCGTGTGCTGAGTGTTCCTCCCGGAGACCTTACTTGTCTGGGA	1812
DB	1569	TATTTTACGGGAAAGCGTGTGCTGAGTGTTCCTCCCGGAGACCTTACTTGTCTGGGA	1628
QY	1813	TGGTCTGCAATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAAAGACGACATAT	1872
DB	1629	TGGTCTGCAATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAAAGACGACATAT	1688
QY	1873	AAGAAATGGAGACCCACTGACTCTGTTTTCAGCTTACACCTATGATTAATCACCATGGCCA	1932
DB	1689	AAGAAATGGAGACCCACTGACTCTGTTTTCAGCTTACACCTATGATTAATCACCATGGCCA	1748
QY	1933	CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGCAATTTTGGAAATGCGAG	1992
DB	1749	CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGCAATTTTGGAAATGCGAG	1808
QY	1993	TCCGAAGTCCGACAGAGCGCTGCTTATTTGGCAATTCAGAGGCGCAAAATGAGAGCGAAA	2052
DB	1809	TCCGAAGTCCGACAGAGCGCTGCTTATTTGGCAATTCAGAGGCGCAAAATGAGAGCGAAA	1868

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QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAG 2112
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAG 1928
QY 2113 TCTCAACACAGAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTTATACA 2172
Db 1929 TCTCAACACAGAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTTATACA 1988
QY 2173 AACTCTTCTTAAGGTAACCTCGAAGTCAATGACACAGAGCAATTTGGAGAACTTCTTCA 2232
Db 1989 AACTCTTCTTAAGGTAACCTCGAAGTCAATGACACAGAGCAATTTGGAGAACTTCTTCA 2048
QY 2233 TAAAGATGATGAGAGTGGCTCTAAGACCAAGAAATGTCCAATAGGATGACACCTAG 2292
Db 2049 TAAAGATGATGAGAGTGGCTCTAAGACCAAGAAATGTCCAATAGGATGACACCTAG 2108
QY 2293 CCAGAAAGGTCGTGACAGAGACTTCATGAGCTCATCAACCAACCCCAATCTCAACAGAT 2352
Db 2109 CCAGAAAGGTCGTGACAGAGACTTCATGAGCTCATCAACCAACCCCAATCTCAACAGAT 2168
QY 2353 GGATGAGTCTGTGAACAAAGTTTGGAAAGGGAACCAACCAACCAAGGCCAGG 2412
Db 2169 GGATGAGTCTGTGAACAAAGTTTGGAAAGGGAACCAACCAACCAAGGCCAGG 2228
QY 2413 ACATACCCAGGAGACAGTAAACAAATGGAAGCACTTACAGAAATAGAAAGGTAGAAA 2472
Db 2229 ACATACCCAGGAGACAGTAAACAAATGGAAGCACTTACAGAAATAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGACCCAGAAATTTGAGAGGACCCAGGAGTGTCTGAGCTGCAATACCTTAGA 2532
Db 2289 CAGGAGGACCCAGAAATTTGAGAGGACCCAGGAGTGTCTGAGCTGCAATACCTTAGA 2348
QY 2533 AACCTCAACAAAGTAAAGTTCCTTAGAACAATACTGGAAACCAAAATGCAATATACAT 2592
Db 2349 AACCTCAACAAAGTAAAGTTCCTTAGAACAATACTGGAAACCAAAATGCAATATACAT 2408
QY 2593 GAACTTTTTCATGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2652
Db 2409 GAACTTTTTCATGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2468
QY 2653 CCAATTTATAAATTAATCATCAGTAACTTCTCTAATAGGCTTTTTC 2702
Db 2469 CCAATTTATAAATTAATCATCAGTAACTTCTCTAATAGGCTTTTTC 2518

```

RESULT 6

PCT-US94-10151A-53

Sequence 53, Application PC/TUS9410151A

GENERAL INFORMATION:

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR HOEBACH TEST ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/10151A

FILING DATE: 13-SEP-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A.

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299 FHT UR

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 2601 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 16...2331

PCT-US94-10151A-53

Query Match

Best Local Similarity 92.6%; Score 2508.4; DB 5; Length 2601;

Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 133 CTGACGATGGGCTGGTTAACTAGGATTGTCTCTTTCTGGGAGTATTACTTACAGC 252

Db 9 CTGACGATGGGCTGGTTAACTAGGATTGTCTCTTTCTGGGAGTATTACTTACAGC 68

QY 253 AAGACCAACTATCAGAAATGGGAACAACAATGTGCCAAGGCTGAAATATCTCTACAAAGA 312

Db 69 AAGACCAACTATCAGAAATGGGAACAACAATGTGCCAAGGCTGAAATATCTCTACAAAGA 128

QY 313 AATGTTGGAATCCCAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCA 372

Db 129 AATGTTGGAATCCCAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCA 188

QY 373 TACCTTCCTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCAATATT 432

Db 189 TACCTTCCTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCAATATT 248

QY 433 TTCATTGCACTGGTTTAAATATCAAGGATTTTCAAAAGATTTGTTGGCCAGTATCTTACAC 492

Db 249 TTCATTGCACTGGTTTAAATATCAAGGATTTTCAAAAGATTTGTTGGCCAGTATCTTACAC 308

QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCAAT 552

Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCAAT 368

QY 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGAAACGGGGGCTTTTCA 612

Db 369 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGAAACGGGGGCTTTTCA 428

QY 613 TCCAAATTTGCACTACATTTGAAATTTGGACATCATCTGAGGACATATATTTTAAAGCTGA 672

Db 459 TCCAAATTTGCACTACATTTGAAATTTGGACATCATCTGAGGACATATATTTTAAAGCTGA 488

QY 673 GAACTCACAATTTTGAACCGGCGGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 732

Db 489 GAACTCACAATTTTGAACCGGCGGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 548

QY 733 ATCCCTTTTAATAGATGGAGAAATATATCTCTGAACTGCACTGATTTTATGGGGGAGAG 792

Db 549 ATCCCTTTTAATAGATGGAGAAATATATCTCTGAACTGCACTGATTTTATGGGGGAGAG 608

QY 793 CTTTGCTATCTTCGAACTCTTGGGACACCAACCAATCAGGACAGAGCAGCATGATTC 852

Db 609 CTTTGCTATCTTCGAACTCTTGGGACACCAACCAATCAGGACAGAGCAGCATGATTC 668

QY 853 CAGGTGGCTCAATGATCCAAAGTTTCATTTAGTGGCCACCTCTCTCAGAGAGTGACAATCC 912

Db 669 CAGGTGGCTCAATGATCCAAAGTTTCATTTAGTGGCCACCTCTCTCAGAGAGTGACAATCC 728

QY 913 TGAAGATGACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGAGAGAACATCTCTGG 972

Db 729 TGAAGATGACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGAGAGAACATCTCTGG 788

QY 973 AAAAGCTACTCAGCTAGAAATAGGTGACATATGCAAGATGACTTTGGAGGACAGAG 1032









Query Match		22.0%;	Score 596.4;	DB 3;	Length 2898;
Best Local Similarity		56.3%;	Pred. No. 2.4e-176;		
Matches 1229;		Conservative	0;	Mismatches 931;	Indels 24; Gaps 5;
QY	223	CTGTCTTTTCTGGGAGTATTA	CTTACAGCAAGAGCAAACTATCAGAATGGGAAGCAAA	282	
DB	396	CTTGCTGCTCTGGGTCACCTGCTGGAAC	CTCTGGACCCCGAGTCACTCGCGGAACCCCTC	455	
QY	283	TGTGCCAAGGCTGAATTA	CTCTACAAAGAAATGTTGGNAATCCAACTATGATCACTTT	342	
DB	456	CTACCCCAAGGCTACGCTGTCTACATAAAGAACTTTTGGAACTGAATAGGACTTTCAATATT	515		
QY	343	CAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTCTTTTGGATGAGGAACGGAGTAG	402		
DB	516	TCAAAGCCCCCTTGGATTTCTTGATCTCATACAAATGCTGCTGGATGAGTATCAAGAAG	575		
QY	403	GCTGTATGTTGGACAAAGGATCA	CATATTTTCATTCGACCTGGTTAATATCA---AGGA	459	
DB	576	GCTCTTTGGGAGGCAGAGACCTTGTCTATTCCCTGAACTTTGGAACGAGTCAGTGACGG	635		
QY	460	TTTTCAAAGATTGTGTGCCAGTATCTTACACGAGAGAGATGAATGCAAGTGGCTGG	519		
DB	636	CTACAGAGAGATATATCGCCGAGCACAGCAGTAAAGGTAGAAGATGCATTAATGAAAGG	695		
QY	520	AAAGACATCCTGAAAGAAATGTGCTAAATTTTCATCAAGGTACTTTAAGGCATATAATCAGAC	579		
DB	696	AAAGAA---CGCAATGAGTGTGCCATTTATATCCGGGTTTGCATCACTACAAACAGAC	752		
QY	580	TCACTTGTAACGCTGTGGAACGGGGCTTTTCATCAATTTTCACCTACATTTGAAATGG	639		
DB	753	ACAACCTTCTGACCTGTCTACTGAGCTTTTTCATCCACTGTGCTTTCATCAGAGTCGG	812		
QY	640	ACATCATCTGAGGACATATTTTAAAGCTGAGAACTCACATTTTGAAGCGGCGTGG	699		
DB	813	GCACCAATTCAGAGAAACCCCTGTTTCACTGGAGTCCACACAGATCTGAGAGAGGAAGGG	872		
QY	700	GAAAGATCCATATGACCCCTTAAGCTGTGACAGCATCCCTTTTAAATAGATGGAGAAATATA	759		
DB	873	CAGATGTCTTTTGAACCCCACTCTCTCTTGTGTCCAGCTAGTTGGGAATGACTGTT	932		
QY	760	CTCTGGAATCGAGCTGATTTTATGGGCGAGACTTTGCTATCTTCCGAACCTCTTTGGGA	819		
DB	933	TGCTGGAATCTACAGTGAATTTGGGCGAGAGACTCGGCGATCTTCCGACAGCATGGGAA	992		
QY	820	CCACCACCAATCAGACAGACAGCATGATTTCCAGGTGGCTCAATGATCCAAAGTTCAT	879		
DB	993	GTTAGGCCATATTCGCATCGACATGACGATGAGCGGCTCCTGAAAGAAACCAAAATTTGT	1052		
QY	880	TAGTGCCCACTCATCTCAGAGAGTGACAAATCCTGAAGATGACAAAGTATATCTTTTCTT	939		
DB	1053	AGGTTTCATATGATTCCTGTATAACGAAGACCGAGATGACACAAATGATCTTTTCTT	1112		
QY	940	CCGTGAAATGCAATAGATGGAGAACATCTCTGGAAAGCTACTCGTGTAGAAATAGGTCA	999		
DB	1113	TACTGAGAAGGGCTGGAGGCGGAGAACAAACGCCACACAGATCTACACCCGAGTGGGCG	1172		
QY	1000	GATATGCAAGATGATTTGGAGGCGACAGAGATCTGGTGAATAAATGGACACAACTCT	1059		
DB	1173	GCTGTGCGTGAATGACATGGGAGGACAGAGAAATCTCTGGTGAACAAGTGGAGCACCTTCT	1232		
QY	1060	CAAAGCTCTCTGATTTGCTCAGTGCAGGTCCTGAAAGTGAACATTTGATGA	1119		
DB	1233	TAAAGCGGCTGGTTGCTCAGTGCAGGGAATGAATGGAATCGACACATCTTTGACGA	1292		
QY	1120	ACTGAGAGATGATTCCTTAATGAACTTTAAAGATCCTTAAATCCAGTTGTATATGAGT	1179		
DB	1293	ACTAGAGATGATGTTTTTACTCCGACACAGATCCTAAGATCCAGTGAATATTTGGACT	1352		
QY	1180	GTTTACGACTTCCAGTAAATTTTCAAGGATCAGCGGTGTGTATGATAGCATGATGA	1239		
DB	1353	GTTTAAATCTACAGCAATATATTTAGAGGCCATGCTGTATGTGTATCATATGTCAAG	1412		

QY	1240	TGTGAGAAAGGTTGTTCTTGTTCATATGCCCACAGGATGAGCCAACTATCAATGGGT	1299		
DB	1413	TATCGGGAAGCTTTAATTTGCCCCATATGCTCATAAAGAGCCCTGAATACCACTGGTC	1472		
QY	1300	GCCTTATCAAGAGAGTCCCTATCCAGGCGAGAACTTGTCCAGCAAAACATTTGG	1359		
DB	1473	ACTATATGAAGGAAAGTCCCTACCAAGGCTGGTTCTGTGCGCAGCAAGATAACGG	1532		
QY	1360	TGG---TTTTGACTCTACAAAGGACCTTCTGTATGATGTTATAAACCCTTTGCAAGAAGTCA	1416		
DB	1533	AGGCAAGTATGGAACCAACCAAGATTACCCGATGACCCATCCGGTTCGCAAGATGCA	1592		
QY	1417	TCCAGCCATGACAAATCCAGTGTTCATGAACAATCGCCCAATAGTATGATCAAAACGGA	1476		
DB	1593	TCCTCTAATGATCAGCCCATAAACCTGTTTCATAAAAAACCAATACTGGTAAAAACAGA	1652		
QY	1477	TGTAATATCAATTTTACAAATTTGTCGTAGACCGAGTGGATGAGAGATGGAAGTCA	1536		
DB	1653	TGMAAATACAACTTGAGGCAACTTGGCGTGGATCGGGTGGAGCGGAGGATGGCAGTA	1712		
QY	1537	TGATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTTAAAGTAGTTTCAATTTCTAA	1596		
DB	1713	TGACGCTCTTATTTATTTGGGACAGACACAGGAATTTGCTGAAAGTAATCAACAATTTACA	1772		
QY	1597	GGAGACTTTGGTATGATTTTAGAAGAGGTTCTGCTGGAAGAAATGACAGATTTTTCGGGAACC	1656		
DB	1773	CCAGAAACAGAGTGGATGGAGGAAGTCAATTTCTAGAGGAACCTTCAATATTTCAAGATCC	1832		
QY	1657	GACTGCTATTTACGCAATGGAGCTTTCCATTAAGCAGCAACAACTATATATTTGGTTCAAC	1716		
DB	1833	AGCCCTATCATTTCTATGSAATTTCTTCAAGAGACACACAGCTTTTACATTTGGATCAGC	1892		
QY	1717	GGCTGGGCTGCCAGCTCCCTTTACACGGTGTGATATTTACGGGAAAGCGTGTCTGA	1776		
DB	1893	CTCTCTGTGGACAAAGTCAGATTCATCTAGTCCGACATGTATGCGAGTCTTGTGCTGA	1952		
QY	1777	GTGTGCTCCCGCAGACCCCTTACTGTGCTTTGGAGTGGTTCTGATGTTCTCGCTATTT	1836		
DB	1953	CTGCTGCTGCTCGAGACCCGTAATGCTGCTGGGATGGCATATCTGCTCCAGGTACTA	2012		
QY	1837	TCCAC-----TGCAAGAGAGCACAAGACGACAGCAAGATATAAGAAATGGAGACCC	1887		
DB	2013	CCCAACAGGTGCACACGCAAGAGAGGTTCCGAGGAGGACGTTCCGCGATGGCAACGC	2072		
QY	1888	ACTGACTCACTGTTTACAGACTTACCATGATAATCACCATGCGCCACAGCCCTGGAAGAG	1947		
DB	2073	CGCCCAACAGTCTTTTGGACAGCAATTTTGGAGACCGGTTGGACAGACCTGAAGAG	2132		
QY	1948	AATCATCTATGTTGATAGAGATAGTACACATTTTGGAAATGCAAGTCCGAAATGCGAG	2007		
DB	2133	GCTGGCTTATGGCATAGAGAGCAACAGTACTCTGTTGGAATGCACCCCGGATCACTACA	2192		
QY	2008	AGCGTGTCTATTTGGCAATTTCCAGAGCGGAAATGAAGAGGAAAGAGATCAGAGT	2067		
DB	2193	AGCAAAAGTCTATGTTTGTACAGAGGGAACGACGCTTAAGAAAGAGAGGTGAAGAC	2252		
QY	2068	GGATCATCATATCATCAGACAGATCAAGGCTTCTGCTAGCTAGTCTACAAACAGAGGA	2127		
DB	2253	GGATGACAGATTTGATAGATGGACTTGGGCTTGTCTCTCTCAGAGTACGCAAGTCA	2312		
QY	2128	TTCAGGCAATTAACCTCTGCCATGCGGTGGAAATGCGGTTTCATACAACTCTTTTAAAGT	2187		
DB	2313	TGAGGGACCTTATTTTGGCAGACAGTAGAAACACAAATTTTGTCCATCTGTGCGTAAAT	2372		
QY	2188	AACCTCGAAGTCTTGGACAGACATTTGGAGAACTTCTTCAATAAGATGATGATG-	2246		
DB	2373	CACCTTGAAGTGTGCGAAGAGCATAAAGTGGAGGCGATGTTTCAATAGGACCATGAAGA	2432		
QY	2247	-----GAGATGGCTCTAAGAACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAGGT	2301		
DB	2433	GGAAAGACATCAAGATGCGCTCCCTTAAAGCGGTATGTCTCAGGGGACAAAACC	2492		
QY	2302	CTGGTACAGAGACTTTCATGCGCTCATCAACCAACCCCAATCTCAACACGATGGATGATT	2361		

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Db 2493 GTGGTCAAGGAATCTTGAGCTGATGGCTACAGCAACTCCAGAGAGTGGAGAAATA 2552
Qy 2362 CTGTGAACAAGTTTGGAAAAGGGA 2385
Db 2553 CTGCGAAGAGTCTGGGTACAGA 2576

RESULT 9
US-09-814-915A-79
; Sequence 79, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
; TITLE OF INVENTION: Thoreto
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 79
; LENGTH: 5177
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-915A-79

Query Match 20.4%; Score 552.8; DB 4; Length 5177;
Best Local Similarity 57.5%; Pred. No. 1.9e-162;
Matches 1115; Conservative 0; Mismatches 802; Indels 21; Gaps 6;

Qy 288 CAAGGCTGAATATCTTACAAAGAAATGTTGGAATCCAAATGATGATCACTTTCAATG 347
Db 642 CAAGAGTTTATTAAATTTGATGAATCTCGAAGAACCAAGACCTCTGAATACCTTCAGCC 701

Qy 348 GCTTGCCCAACAGCTCCAGTTATCATACCTTCCCTTTGGATGAGGAACGGAGTAGGCTGT 407
Db 702 TTTCCACCATCTTTAGACTACAGGATTTTATTAAATGATGAAGTACAGGACCGGATAT 761

Qy 408 ATGTTGGGCAAGGATCAATATTTTCAATTTGACCTGTTTAAATCA---AGGATTTTC 464
Db 762 ATGTGGGAAGCAAGATCAATCTTCTCCCTGAATTAATCAATATAAAGTCAAGAAGCTT 821

Qy 465 AAAAGATTTGTGGCCAGTATCTTACACCAAGAGATGAATGCAAGTGGGCTGGAAAG 524
Db 822 TGAGTGTCTTGTGGCCAGCATCTACAATCAAAGTTGAAGATGCAAAATGGGCTGGCAAG 881

Qy 525 ACATCTGAAAGAAATGTGCTAATTTTCAAGTACTTAAAGCATATAATCAGACTCACT 584
Db 882 ATCCCAACACCGCTGTGGAACTTTGTCCGTGTAATTCAGACTTCAATCGCACATTT 941

Qy 585 TGTACGCTGTGGAACGGGGCTTTTCATCCAAATTTGACCTACATTTGAAATTTGACATC 644
Db 942 TGTATGCTGTGGAGTGGGCTTTTCAGTCTCTGTCTGTACTTGAACAGAGGAGGA 1001

Qy 645 ATCTGTGAGACATATTTTAAAGCTGGAGAACTCACTATTTTGAACCGCCGTGGGAAGA 704
Db 1002 GATCAGAGGACCAAGTTTTTTCATGATTG---ACTCCAAAGTGTGAATCTGGAAAAGGACGCT 1058

Qy 705 GTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAAATAGATGGAGAAATTATCTGT 764
Db 1059 GCTCTTTCAACCCCAACGTGAACACGGTGTCTGTTATGATCAATGAGGAGCTTTTCTGT 1118

Qy 765 GAACTGACGCTGATTTTATGGGCGGAGACTTTTGCTATCTTCGAACTCTTGGGCCACC 824
Db 1119 GAATGTATATAGATTTTATGGGAGACAGATGCTGCTATTTTTCGAAGTTTAAACCAAGAGGA 1178

Qy 825 ACCAATCAGGACAGAGCAGATGATTCAGGTGGCTCAATGATCCAAAGTTTCATATG 884
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Qy 885 CCCACTCATCTCAGAGAGTGCAATCTCTGAAGATGACAAAGTATATCTTTTCTTCCTG 944
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Qy 1005 GCAAGAAATGACTTTTGGAGGGCACAAGAGTCTGGTGAATAAATGGAACAAATCTCTCAAAG 1064
Db 1359 GTCTTAATGACACTGGTGGACTGCGTAGCTTGTCAAAGTGGACCACTTTCTTAAAGG 1418

Qy 1065 CTCGCTGATTTGCTCAGTGCAGGTCGAGTCCAAATGGGATTCACACTCAATTTTGTGAACTGC 1124
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Qy 1125 AGGATGTATTCTTAATGAACCTTTAAAGATCCCTAAAATCCAGTTGTATATGANGTCTTAA 1184
Db 1479 AGGATGTGTTCTGCTGGAACTGATAACCCGAGGACAACTAGTGTATGGAATTTTAA 1538

Qy 1185 CGACTTCCAGTAACATTTTCAAGGATCAGCCGCTGTGTATGTATAGCATGATGATGTA 1244
Db 1539 CAACATCAAGCTCAGTTTCAAGAGTCAAGCCGCTGTGTGTATCATTTATCTGATATAC 1598

Qy 1245 GAAAGGTGTTCTTGGTCCATATGCCACAGGATGGACCCAACTATCAATGGGTGCCCT 1304
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Qy 1305 ATCAGGAAGAGTCCCTTATCCAGCCGAGGAACCTTGTCCAGCAAAACATTT---GGTG 1361
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Qy 1362 GTTTTGACTCTCAAAAGGACCTTCTGATGATGTTTATAACCTTTGCAAGAAGTCATCCAG 1421
Db 1719 ATATCGGAACCAAGAGGTTCCAGATGATGTTGTCACTTTTATTCGGAACCATCTCTC 1778

Qy 1422 CCATGTACAATCAGTGTGTTCTTGAACAAATCGCCCAATAGTGTATCAAAACGGATGTAA 1481
Db 1779 TCATGTACAAATTCATCTACCCAAATCCCAAAAGGCTTTGATTTGTTGTTGGCACTG 1838

Qy 1482 ATTTATCAATTTACAAATTTGCTAGACCGAGTGGATGCAAGAATGACAGATGATGATG 1541
Db 1839 ACTACAAGTACAAAGAATAGCTGTGGATCGAGTGAACCTGCTGATGGAGATACCTG 1898

Qy 1542 TTATGTTTATCGGAACAGATGTTGGGACCGTTCTTAAAGTAGTGTTCATTTCTCTAAGGAGA 1601
Db 1899 TCCTGTTTCTCGGAACAGATCGGGGTACTGTGCAAAAGTGGTGTGTTCTTCTCTACTAACA 1958

Qy 1602 CTTGGTATGATTTAGAAGAGTTCCTGTGGAAAGAAATGACAGTTTTCGGGAACCGACTG 1661
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Qy 1662 CTATTTTACGAATGAGCTTTTCCATAGCAGCAACAACTATATATTTGTTTCAACGGCTG 1721
Db 2016 CTATAACAACTAAGAAATTTTCATCTAAAAGCAACAGTTGTATGTAGTTCCTAATGAAG 2075

Qy 1722 GGGTTGCCAGCTCCCTTTTACACCGGTGTGATATTTACGGGAAAGCGTGTGCTGAGTGT 1781
Db 2076 GGGTTTCCCAAGTATCTCTGACCGCTGCGCAATCTATGGTACAGCTGTGCTGACTGCT 2135

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Db 2136 GCTCGCGCGGACCTTATTCGCTGGATGGCAATCTCTGTTCCAGATTTCTACCCAA 2195

Qy 1842 CTGCAAGAGAGCACAAGACGACAGATATAAGAAATGGAGACCCACTGACTCACTGTT 1901
Db 2196 CTGGGAAAACGGAGGAGCGGAGACAGATGTGAGACATGGAAACCCCACTGACTCAATGCA 2255

Qy 1902 CAGACTTACACCATGATTAATCACCATGCGCCACAGCCCTGGAAGAGAGAATCACTATGTTG 1961
Db 2256 GAGGATTT-----TAATCTAAAGCATACAGAAATGCACTGAAATTTGTGAGTATGGAG 2309

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QY 1962 TAGAGATAGTACGACATTTTGGATGCAAGTCCGAAGTCGAGAGAGCGCTGTATT 2021  
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 QY 2370 GGCTGTATACAGA---AAGACAAGACAGGAGGAAAGAGGTTAAGCTGATGAACGAATAA 2426  
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 QY 2142 TCTGCCATCGGTGGAACTATGTTTCAATAAACTCTTCTTAAGGTAAACCTCGGAAGTCA 2201  
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 QY 2547 TAGATTCAGAAATGGTG 2564  
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 ; Sequence 3, Application US/09813290  
 ; Patent No. 6815538  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Wilganowski, Nathaniel L.  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Hilbun, Erin  
 ; APPLICANT: Wang, Xiaoming  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Scoville, John  
 ; TITLE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encodin  
 ; FILE REFERENCE: LEX-0151-USA  
 ; CURRENT APPLICATION NUMBER: US/09/813,290  
 ; CURRENT FILING DATE: 2001-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/190,638  
 ; PRIOR FILING DATE: 2000-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/191,188  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: US 60/193,639  
 ; PRIOR FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2349  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-09-813-290-3  
 Query Match 17.5%; Score 474.8; DB 3; Length 2349;  
 Best Local Similarity 53.9%; Pred. No. 3.9e-138;  
 Matches 1146; Conservative 1; Mismatches 948; Indels 33; Gaps 7;  
 QY 280 CAATGTGCCAAGGCTCAATTTATCTTACAAAGAAATGTTGGAATCCAAATGTGATCAC 339  
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 QY 144 CTTTCTGGGCCCCCGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTACCGAGA 203  
 QY 400 TAGGCTGTATGTTGGAGCAAGAGATACATATTTTCATTCGACCTGGTTAATATCAAG-- 457  
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 QY 204 CCGCTCTTTCTGGGTGGCTGGAGCGCCCTCTACTCTTCGGCTGGACAGGCAATGGCC 263  
 QY 458 -GATTTTCAAAGATTTGTGGCCAGATATCTTACACCAAGAGAGATGAATGCAAGTGGGC 516  
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 QY 264 AGATCCCGGGAGGCTCTGTGGCCACCGCAGCAGACAGAGGGAGGAGTGTGTTCGAA 323  
 QY 517 TGGAAAGACATCCTGGAAGATGTGCTAATTTTCAAGGTACTTAAGGCATATAATCA 576  
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Db 324 GGGAGAGATCCTTTTACAGAGTGCGCCAACTTCTGTGGGGTGTCTACAGCCTCACAACCG 383  
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 Db 384 GACCACCTGTAGCTGTGGACCTTGGGGCTTTCCAGCCACCTGTGCCCTCATCACAGT 443  
 QY 637 TGGACATCATCTCGAGGCAATATTTTAAAGCTGGAGAACTCACATTTTGAAGAAACGGCG 696  
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 Db 444 TGGCCACG---TGGGAGCATGTCTCCACTTGGAGCTGGCAGTGTGGAAGTGGCG 500  
 QY 697 TGGGAAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAAATAGATGGAATTT 756  
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 Db 501 GGGGGCTGTCCCTTCACAGAGCCAGCCGTCCCTTTTCCAGACACTTCATAGACGGGAGCT 560  
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 Db |||||  
 Db 678 TGTGATGGCCCGCGGATCCCTGAGAACTCTGACCAAGCAATGACAAAGGTGTACTTCTT 737  
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 Db 858 TTTCTCAAGGCCAGGCTGCTGCTGGTGGCCCGGCTGTGGTGGCCGAGACCCACTT 917  
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 QY 1294 ATGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGCCAGGAATCTTGTCCAGCAAAA- 1352  
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 QY 1582 AGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAGGCTTCTGCTGGGAAGATGAC 1641  
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1642 AGTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGAGCTTTCCACTAAGCAGCAACAAT 1701
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1702 ATATATATGCTTCAACGGCTGGGGTGGCCAGCTCCCTTTACACGGTGTGATATTACGG 1761
1518 ATACGTGGGCTCTCGGCTGGGTGGCCAGCTGGCGCTGCACCAATGTGAGACTTACGG 1577
1762 GAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTTGGGATGGTTCTGC 1821
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1822 ATGTTCTCCTATTTTCCCA---CTGCAAGAGAGCGCAACAGCAGCAAGATATAGAAA 1878
1638 CTGTACCCACTACCGCCCGAGCGCTTGGCAAGCGCGGTTCCCGCGGAGGACATCCGGCA 1697
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1698 CGGCAACCTGCGCTGCACTGCTGGGCCAGAGCCAGGAGGAGGAGGAGTGGGACTTGT 1757
1939 TGAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTAGCAATTTTGGAAATGCAAGTCCGAA 1998
1758 GCGACCCACCATGCTTACGCGACGAGCAGATAGCACTTCTCTGGAGTGTGCTGCCAA 1817
1999 GTGCGAGAGAGCGCTGCTCTATTGGCAATTCAGAGCGGAAATGAGAGCGGAAAGAA 2058
1818 GTCTCCCAAGCTGTGCTGCTGCTGCTTTCAGAGCGGCGGCTGCTTCCGAGGCTGACCA 1877
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2179 TCTTAAGGTAACCTCGAAGTCAATTGACACAGAGCAATTTGGAAGAACTTCTTATAAAGA 2238
1998 GGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2057
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2058 GCCAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2111
2299 GGTCTGTGACAGAGCTTCACTGAGCTCATCAACCAACCACTCAACCAACCACTCAACCA 2358
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2359 GTTCTGTGAACAAGTTTGGAAAGGAG 2386
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RESULT 11
US-09-813-290-1
; Sequence 1, Application US/09813290
; Patent No. 6815538
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hilbun, Erin
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; PRIOR APPLICATION NUMBER: 2001-03-20
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188

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; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-813-290-1

Query Match      17.5%; Score 474.8; DB 4; Length 2628;
Best Local Similarity 53.9%; Pred. No. 4.3e-138;
Matches 1146; Conservative 1; Mismatches 948; Indels 33; Gaps 7;

QY 280 CAATGTGCCAAGGCTGAAATTTATCTCAAAAGAAATGTTTGGAAATCCAAACAATGTGATCAC 339
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QY 340 TTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTCTTTTGGATGAGAAACGAG 399
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QY 400 TAGGCTGTATGTGGAGCAAAAGGATCATATTTTTCATTCGACCTGTTTAAATATCAAG-- 457
DB 483 CCGCCTCTTTCTGGGTGGCTGGACCGCTCTACTCTCTGCGGCTGGACCGGCAATGGCC 542
QY 458 -GATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGAATGCAAGTGGGC 516
DB 543 AGATCCCGGAGGCTCTGTGGCCACCGCAGCAGCAGAGAGGAGGTGTGTTGAAA 602
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QY 577 GACTCATTGTAGCTGTGGAAACGGGGCTTTTTCATCCAAATTTGCACTACATTTGAAT 636
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Db 1197 TGACAGCTAGAGGATGTGTTCTCTGTGTGGCCCAAGGCCGGAGAGCGCTCGAGGTGA 1256  
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 Qy 1582 AGTTTCAATCTTAAGGAGCTTGTATGATTTAGAGAGGTTCCTGTGGAGAAATGAC 1641  
 Db 1677 CATCGCTCTCCAGGAGGGGCTCAGCTGAACTGAGGAGTGTCTGGAGAGCTCCA 1736  
 Qy 1642 AGTTTTTCGGGAACGATGTATTTTCAAGATGAGCTTTCCATTAAGCAGCAACAAT 1701  
 Db 1737 GGTGTTAAGGTGCCAACACCTATCACGGAATGAGATCTCTGTCAAAAGGCAATGCT 1796  
 Qy 1702 ATATATTGTTCAACGGCTGGGGTTGCCAGCTCTTACACCGGTGTGATTTACGG 1761  
 Db 1797 ATACGTGGGCTCTCGGCTGGGTGTGGCCAGCTGGGCTGACCAATGTGAGACTTACG 1856  
 Qy 1762 GAAAGCGTGTGTGAGTGTGCTCGCCGAGACCTTACTGTGCTTGGAGTGTCTGTC 1821  
 Db 1857 CACTGCTGTGAGAGTGTGCTGCGCGGGACCATATCTGTGCTTGGAGTGTGCTC 1916  
 Qy 1822 ATGTTCTCGTATTTTCCCA-----CTGCAAGAGACGCAACAGCAAGATTAAGAAA 1878  
 Db 1917 CTGTACCCACTACCGCCCGAGCTTTGGCAAGCGCGGTTCCGCGCGCAGGACATCCGCA 1976  
 Qy 1879 TGGAGACCCACTGACTCTGTTTCAGACTTACCATGATATACCATGGCCACAGCCC 1938  
 Db 1977 CGGCAACCTGCGCTGCTGCTGGCCAGAGCCAGGAGGAGGAGGAGGAGGAGGAGG 2036  
 Qy 1939 TGAAGAGAGAAATCATCTATGTGTAGAGAAATAGTACCAATTTTGGAAATGCAAT 1998  
 Db 2037 GGCAGCCCATGCTTACCGGACGAGCAGCAATAGCACTTCTTGGAGTGTCTGCCCAA 2096  
 Qy 1999 GTCCAGAGAGCGCTGTCTATTTGGCAATTCAGAGGGGAAATGAAGAGCGGAAAGAGA 2058  
 Db 2097 GTCTCCCAAGTGTGTGTGCGTGTGCTTGTGAGAGGCGCAGGGGATGAGGGGCTGACCA 2156  
 Qy 2059 GATCAGAGTGAATGATATATCATCAGGACAGATCAAGGCTTCTGCTACGTFAGTCTACA 2118  
 Db 2157 GGTGAAGACGACGAGCGTGTGCAACGGAGCGGGGCTGTGTTCCGAGCGCTTAG 2216  
 Qy 2119 ACAGAGAGATTCAGGCAATTAATCTCTGCGCATGCGGTGGAAATGAGGTTTATCAAACTCT 2178  
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 Qy 2179 TCTTAAGGTAACTTGAAGTCAATTTGAACAGAGATTTTGAAGAACTTCTTCAATAAGA 2238  
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Qy 2239 TGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAA 2298  
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 Db 2391 GGCCTGGTACAGAGACATCTCTGAGCTCATTTGGCTTGCCTCAACCTGCCCCGGGTGATGA 2450  
 Qy 2359 GTTCTGTGAACAAGTTTGGAAAAGGGAC 2386  
 Db 2451 GTACTGTAGCGCGTGTGTGTCAGGGC 2478  
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 US-09-813-290-5  
 ; Sequence 5, Application US/09813290  
 ; Patent No. 6815538  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walke, D. Wade  
 ; APPLICANT: Wilganowski, Nathaniel L.  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Hilbun, Erin  
 ; APPLICANT: Wang, Xiaoming  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Scoville, John  
 ; TITLE OF INVENTION: No. 681538el Human Secreted Proteins and Polynucleotides Encodir  
 ; FILE REFERENCE: LEX-0151-USA  
 ; CURRENT APPLICATION NUMBER: US/09/813,290  
 ; PRIOR FILING DATE: 2001-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/190,638  
 ; PRIOR FILING DATE: 2000-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/191,188  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: US 60/193,639  
 ; PRIOR FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 3568  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-813-290-5  
 Query Match 17.5%; Score 473.6; DB 4; Length 3568;  
 Best Local Similarity 53.9%; Pred No. 1.3e-137;  
 Matches 1146; Conservative 0; Mismatches 949; Indels 33; Gaps 7;  
 Qy 280 CAATGTGCCAAGGCTGAAATTTATCTACAAAGAAATGTTGGAATCCAAATGTGATCAC 339  
 Db 917 CAGTGTGCCCCGCTCGGGCTCTCTACCGAGACCTCTCTGTCTGCAACCGCTCTGCCAT 976  
 Qy 340 TTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTTTTGGATGAGAACGGAG 399  
 Db 977 CTTTCTGGGCCCCCAGGGCTCTCTGAACTCCAGGCCATGTACTAGATGATACCGAGA 1036  
 Qy 400 TAGGCTGTATGTGGAGCAAGAGATCATATTTTTCATTCGACCTGGTTAATATCAAG-- 457  
 Db 1037 CGGCTCTTTCTGGTGGCTTGGAGCCCTCTACTCTCTGGCGGTGGACCGCATGGCC 1096  
 Qy 458 -GATTTTCAAGAGTGTGTGGCCAGTATCTTACACAGAGAGATGAATGCAATGGGCG 516  
 Db 1097 AGATCCCGGAGGTCTGTGGCCACCGCAGCAGGAGGAGGAGTGTGTTCGAAA 1156  
 Qy 517 TGGAAAACATCTTGAAGATGTCTTAATTTTCATCAAGGTACTTAAGGCATATAACA 576  
 Db 1157 GGAAGAGATCTTTTGACAGAGTGGCCAACTTCGTGGGGTGTCTACAGCCTCACACCG 1216  
 Qy 577 GACTCATTGTACGCTGTGGAACCGGGGCTTTTTCATCCAATTTGCACCTACATTGAAT 636  
 Db 1217 GACCCACCTGTAGCTGTGCACTGGGGCCCTTCCAGCCCACTGTGCCCTCATCACAGT 1276  
 Qy 637 TGGACATCATCTGTAGGACAATATTTTAAAGCTGGAGAACTCACATTTTGAAGAACGGCG 696



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 QY 937 CTTCCGTGAAATG---CAATAGATGGAGAACACTCTGGAAAGCTACTCAAGCTAGAAAT 993  
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 Db 1691 TTTCTCTAAGGCAGAGCTGTCTGCTCGGTGCGCGCCCTGTGGTGGCCGAGACCCACTT 1750  
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 QY 1234 GAGTGTATGTGAAGAGGTGTTCTGCTCATATGCCACAGGATGGAGCCCAACTATCA 1293  
 Db 1871 GGCAGACATCTGGAGGTTTTCAACGGGCCCTTTGCCACCGAGATGGCCCTCAGACCA 1930  
 QY 1294 ATGGGTGCTTTATCAAGGAGAGTCCCTATCAGCGCCAGGAACTTTGCCAGCAAAA- 1352  
 Db 1931 GTGGGGCCCTATGGGGGCAAGTGGCTTCCCTCGCCCTGGCGTGTGCCCCAGCAAGAT 1990  
 QY 1353 -----CATTTGGTGGTTTGACTCTCAAAAGGACCTTCCTGATGATGTATATAC 1401  
 Db 1991 GACCGCACAGCCAGGACGGCCCTTTTGGCAGCACCAAGGACTACCCAGATGAGGTGCTGCA 2050  
 QY 1402 CTTTGAAGAAGTCAATCCAGCCATGTACAATCCAGTGTTCCTATCAACAATCGCCCAAT 1461  
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 Db 2171 AGAGGATGGACCTACGATGTCTATTTTCTCGGGGACTGACTCAGGGTCTGTGCTCAAAGT 2230  
 QY 1582 AGTTTCAATTTCAAGAGACTTGGTATGATTTTGAAGAGGTTCTGCTGAAGAAATGAC 1641  
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 QY 1642 AGTTTTTCGGGAACCGAGTCTATTTTCAAGATGGAGCTTTTCCACTAAGCAGCAACAAT 1701  
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Db 2351 ATACGTGGGCTCTCGCTGGGTGTGGCCAGCTGGCGCTGCACCAATGTGAGACTTACGG 2410  
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 Db 2411 CACTGCTGTGAGAGTGTGCTGGCCGGGACCCATACTGTGCTGGGATGGTGCCTC 2470  
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 QY 1999 GTGCGAGAGAGCGCTGGTCTATTGGCAATTCAGAGGCGAATGAAGAGGAAAGAAAGA 2058  
 Db 2651 GTCTCCCCAGGCTGTGTGCTGCTCTTTGAGAGGCGCAGGGGATGAGGGGCGCTGACCA 2710  
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 QY 2239 TGATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGCA 2298  
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 QY 2299 GGTCTGTTACAGAGACTTCATGAGCTCATCAACCAACCCCAATCTCAACACGATGATGA 2358  
 Db 2945 GCGCTGTTACAAGGACATCTGCAGCTCATTTGGCTTTCGCCAACCTGCCCGGGTGGATGA 3004  
 QY 2359 GTTCTGTGAACAGTTTGGAAAGGGAC 2386  
 Db 3005 GTACTGTGAGCGCTGTGGTGCAGGGGC 3032

RESULT 13

US-09-513-999C-2555  
 ; Sequence 2555, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; FILE REFERENCE: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/122,487  
 ; PRIOR FILING DATE: 1999-02-26  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 2555  
 ; LENGTH: 229  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 29..229  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature



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; LOCATION: 110
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 113
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: w=a or t
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; NAME/KEY: misc_feature
; LOCATION: 122
; OTHER INFORMATION: r=a or g
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; NAME/KEY: UNSURE
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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 29
; OTHER INFORMATION: Xaa=Ala or Thr
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; NAME/KEY: UNSURE
; LOCATION: 30
; OTHER INFORMATION: Xaa= * or Lys
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 32
; OTHER INFORMATION: Xaa=Gly or Ser
; OTHER INFORMATION: Xaa=Gly or Ser
US-09-513-999C-2555

Query Match 5.1%; Score 138.8; DB 4; Length 229;
Best Local Similarity 97.0%; Pred. No. 4.6e-33; Mismatches 0; Indels 2; Gaps 2;
Matches 159; Conservative 3;

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QY 177 AAGGACCTACAGCGTCTCAGCATGGCTGTTAACTAGGATTGCTCTTTCTGGG 236
DB 126 AAGGACCTACAGCGTCTCAGCATGGCTGTTAACTAGGATTGCTCTTTCT-GG 184
QY 237 GAGTATTACTTACAGCAAGCAAACTATCAGAAATGGGAAGAAC 280
DB 185 GAGTATTACTTACAGCAAGCAAACTATCAGAAATGGGAAGAAC 228

RESULT 14
US-09-520-781-29
; Sequence 29, Application US/09520781
; Patent No. 6689866
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN.60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1890)
US-09-520-781-29

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Query Match

4.6%; Score 125; DB 4; Length 1890;

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Best Local Similarity 50.5%; Pred. No. 4.3e-28;
Matches 488; Conservative 0; Mismatches 440; Indels 39; Gaps 6;

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DB 490 GGAAAACTATCTCTAGCCACAGTGACTTCTTGGCAATTGACGAGTCAATTTACCGG 549
QY 809 ACTCTTGGGCACCAACCCCAATCAGGACAGCATGATTCAGGTGGCTCAATGAT 868
DB 550 AGTCTTGGAGAAAGCCCTACCTCGGACCGTCAAGCAGCATTCAAAATGGTTGAAGAA 609
QY 869 CCAAGTTTCATTAGTGCCCACTCATCTCAGAGTGAATCTCTGAAGATGACAAAGTA 928
DB 610 CCATACCTTTTCAAGCCGTGA-----TTACGGAGATTATATC 648
QY 929 TACTTTTTCTTCGTAAGAAATGCAATAGATGGAGAACACTCTGGAAGAGCTACTCAGCT 988
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QY 989 AGAATAGTCAAGATATGCAAGAATGACTTTTGAGG---GCAAGAGTCTGGTGAATAAA 1045
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QY 1046 TGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAATGGCATGAC 1105
DB 769 TGGACGCTGTTCTGGAAGCGCTTGAACCTGCTCAGTTCCTGG-----AGACTCTCAT 822
QY 1106 ACTCATTTTGTGATGAATCAGAGTGTATTCCTAATGAACCTTTAAAGATCTCTAAATCCA 1165
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QY 1640 ACAGTTT 1646
DB 1360 AGTGTTT 1366

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RESULT 15

US-09-976-594-1002  
; Sequence 1002, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; APPLICANT: Buchbinder, Jenny  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 1002  
; LENGTH: 2278  
; TYPE: DNA  
; ORGANISM: Homo sapiens.  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6673549 411373.7  
US-09-976-594-1002

Query Match 4.6%; Score 125; DB 4; Length 2278;  
Best Local Similarity 50.5%; Pred. No. 4.9e-28;  
Matches 488; Conservative 0; Mismatches 440; Indels 39; Gaps 6;  
  
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DB 758 AGCGGNAATGCCAGATGCCATATGATGCCAACATGCCCAAGTTCACATGTTGCAGAT 817  
  
QY 749 GGAGAAATATATCTCTGGAACTGCGACTGATTTTATGGGCGGAGACTTTGCTATCTTCCGA 808  
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DB 878 AGTCTTGGAGAAAGCCCTACCTCGGGACCGTCAAGCAGCATTCATAAATGGTTGAAGAA 937  
  
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- 6: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
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- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
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- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
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- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2709	100.0	2709	9	US-09-774-490-1
2	2517	92.9	2848	16	US-10-247-671-83
3	2508.4	92.6	2530	14	US-10-097-340-283
4	2508.4	92.6	2530	15	US-10-262-538-9
5	2508.4	92.6	2530	18	US-10-669-176-9
6	2508.4	92.6	2530	18	US-10-723-860-2569
7	2508.4	92.6	2501	16	US-10-067-632-53
8	2508.4	92.6	3023	18	US-10-723-860-6714
9	718.6	26.5	2331	17	US-10-404-438-2
10	718.6	26.5	3871	10	US-09-946-374-309
11	718.6	26.5	3871	13	US-10-052-586-347

12	718.6	26.5	3871	14	US-10-174-590-347	Sequence 347, App
13	718.6	26.5	3871	14	US-10-176-758-347	Sequence 347, App
14	718.6	26.5	3871	14	US-10-175-737-347	Sequence 347, App
15	718.6	26.5	3871	14	US-10-174-581-347	Sequence 347, App
16	718.6	26.5	3871	14	US-10-176-483-347	Sequence 347, App
17	718.6	26.5	3871	14	US-10-176-749-347	Sequence 347, App
18	718.6	26.5	3871	14	US-10-176-914-347	Sequence 347, App
19	718.6	26.5	3871	14	US-10-176-915-347	Sequence 347, App
20	718.6	26.5	3871	14	US-10-173-706-347	Sequence 347, App
21	718.6	26.5	3871	14	US-10-175-738-347	Sequence 347, App
22	718.6	26.5	3871	14	US-10-175-752-347	Sequence 347, App
23	718.6	26.5	3871	14	US-10-176-482-347	Sequence 347, App
24	718.6	26.5	3871	14	US-10-176-757-347	Sequence 347, App
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44	718.6	26.5	3871	14	US-10-184-658-347	Sequence 347, App
45	718.6	26.5	3871	14	US-10-176-991-347	Sequence 347, App

## ALIGNMENTS

RESULT 1  
US-09-774-490-1  
; Sequence 1, Application US/09774490  
; Patent No. US2001003432A1  
; GENERAL INFORMATION:  
; APPLICANT: Jin, Shengfang  
; TITLE OF INVENTION: RESISTANCE SEQUENCES AND USES THEREOF  
; FILE REFERENCE: 07334-138001  
; CURRENT APPLICATION NUMBER: US/09/774,490  
; CURRENT FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: US 60/179,191  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-774-490-1

Query Match	100.0%;	Score 2709;	DB 9;	Length 2709;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2709;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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Qy	61	ACCCACGCGTCGGGAGTAGGTTGAGCTCGCCTGTTCTCCCATTTGTCCACGAGTCTATTT	120	
Db	61	ACCCACGCGTCGGGAGTAGGTTGAGCTCGCCTGTTCTCCCATTTGTCCACGAGTCTATTT	120	
Qy	121	CCAGATTGTTGAACCTTCTCTGGCCGCAACAATACAGGAAGAGACTAAAGCAGCAAGG	180	

Db 121 CCAGATTGTTGAACCTCTCTGCGCGCACATAACAGGAAGAGACTAAAGCAGCAAGG 180  
 Qy 181 GACCTACAGGCTCTGAGCATGGCTGGTTAACTAGGATTGCTGCTTTCTGGGAGT 240  
 Db 181 GACCTACAGGCTCTGAGCATGGCTGGTTAACTAGGATTGCTGCTTTCTGGGAGT 240  
 Qy 241 ATTACTTACAGCAAGAGCAAACTATCAGAAATGGGAAGAACAAATGTCACAGGCTGAAAT 300  
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 Db 301 ATCTTACAAAGAAATGTTGGAAATCCAAATGTGATCACTTTCAATGGCTGGCCAAACAG 360  
 Qy 361 CTCCAGTTATCATACCTCTCTTTGGATGAGAAACGGAGTGGCTGTATGTTGGAGCAAA 420  
 Db 361 CTCCAGTTATCATACCTCTCTTTGGATGAGAAACGGAGTGGCTGTATGTTGGAGCAAA 420  
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 Db 421 GGATCACATATTTTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTGTGGCC 480  
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 Db 481 AGTATCTTACACAGAGAGATGAATGCAAGTGGCTGGAAAGACATCTCGAAAGATG 540  
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 Db 601 GGGGCTTTTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTGTGGCC 660  
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 Db 721 GCTGCTGACAGCATCCCTTTTAAATAGATGGAAATTTATCTCTGAACTGCACTGATTT 780  
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RESULT 2

US-10-247-671-83  
 ; Sequence 83, Application US/10247671  
 ; Publication No. US20030194721A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mikita, Thomas  
 ; APPLICANT: Shiffman, Dov  
 ; APPLICANT: Porter, Gordon, J.  
 ; APPLICANT: Kaser, Matthew R.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS  
 ; FILE REFERENCE: PA-0050 US  
 ; CURRENT APPLICATION NUMBER: US/10/247,671  
 ; CURRENT FILING DATE: 2002-09-18  
 ; PRIOR APPLICATION NUMBER: 60/323,784  
 ; PRIOR FILING DATE: 2001-09-19  
 ; NUMBER OF SEQ ID NOS: 186  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 83  
 ; LENGTH: 2848  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CB1  
 US-10-247-671-83

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 253 AAGAGCAAACTACTAGAAATGGAAGAAACAATGCGCAAGGCTGAAATATCTTACAAAGA 312  
 Db 69 AAGAGCAAACTACTAGAAATGGAAGAAACAATGCGCAAGGCTGAAATATCTTACAAAGA 128  
 QY 313 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372  
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 QY 373 TACCTTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGAGCAAGGATCAATATT 432

Db 189 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248  
 QY 433 TTTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTTACAC 492  
 Db 249 TTTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTTACAC 308  
 QY 493 CAGAGAGATGAATCGAATGGGCTGGAAAGACATCTCTGAAAGATGTGCTAAATTTTCAT 552  
 Db 309 CAGAGAGATGAATCGAATGGGCTGGAAAGACATCTCTGAAAGATGTGCTAAATTTTCAT 368  
 QY 553 CAAAGTACTTAAAGGACATAAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCA 612  
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 QY 673 GAACTCACAATTTTGAAGCGGCGGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 732  
 Db 489 GAACTCACAATTTTGAAGCGGCGGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 548  
 QY 733 ATCCCTTTTAAATAGATGGAGAATTAATCTCTGAACTGCGAGCTGATTTTTATGGGGCGAGA 792  
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 QY 793 CTTTGTCTATCTTCGAACTCTTTGGGACCAACCAATCAGGACAGAGCAGCATGATTC 852  
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 QY 853 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTCCCAACCTCATCTCAGAGAGTGACAAATCC 912  
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 QY 913 TGAAGATGACAAAGTATACCTTTTCTCGTCAAAATGCAATAGATGGAAGAACACTCTCG 972  
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 Db 849 TCTGTGTAATAATGGAACAATTTCTCAAGCTGCTGTGATTTGCTCAGTGGCAGGTCC 908  
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1329 AGTGGATGCGAAGATGGACAGTATGATGTTATGTTATCGAAGACAGATGTTGGACCGT 1388  
Qy |||||||  
1573 TCTTAAAGTAGTTTCAATTCCTAAGAGACCTGGTATGATGTTAGAAAGAGTTCTGCTGA 1632  
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1633 AGAATACAGTTTTCGGGACCCAGCTGCTATTTTCAGCAATGGAGCTTCCACTAAGCA 1692  
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1689 AAGAAATGGAGACCCCACTGACTCACTGTTTCCAGCTTACACCATGATAATCACCATGGCA 1748  
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1933 CAGCCTCGAAGAGAGATCATCTATGTTGGTGTAGAGATAGTAGACATTTTGGATGCG 1992  
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1749 CAGCCTCGAAGAGAGATCATCTATGTTGGTGTAGAGATAGTAGACATTTTGGATGCG 1808  
Qy |||||||  
1993 TCCGAAGTCGACAGAGCGCTGCTTATTGGCAATTCAGAGCGCAATGAAGCGGAA 2052  
Db |||||||  
1809 TCCGAAGTCGACAGAGCGCTGCTTATTGGCAATTCAGAGCGCAATGAAGCGGAA 1868  
Qy |||||||  
2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG 2112  
Db |||||||  
1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG 1928  
Qy |||||||  
2113 TCTACACAGAGAGATTCGGCAATTCCTGTCGATCGGTTGGAACATGGGTTTATACA 2172  
Db |||||||  
1929 TCTACACAGAGAGATTCAGGCAATTCCTGTCGATCGGTTGGAACATGGGTTTATACA 1988  
Qy |||||||  
2173 AACTCTTCTTAAGTAAACCTGGAAGTCAATTCACACAGAGCATTTGGAAGAACTTCTTCA 2232  
Db |||||||  
1989 AACTCTTCTTAAGTAAACCTGGAAGTCAATTCACACAGAGCATTTGGAAGAACTTCTTCA 2048  
Qy |||||||  
2233 TAAAGATGATGATGAGATGGCTTAAAGACCAAGAAATGTCCTAATAGCATGACACCTAG 2292  
Db |||||||  
2049 TAAAGATGATGATGAGATGGCTTAAAGACCAAGAAATGTCCTAATAGCATGACACCTAG 2108  
Qy |||||||  
2293 CCAAGAGTCTGTTACAGAGCTTCATGAGCTCATCAACACCCCATCTCAACAGCAT 2352  
Db |||||||  
2109 CCAAGAGTCTGTTACAGAGCTTCATGAGCTCATCAACACCCCATCTCAACAGCAT 2168  
Qy |||||||  
2353 GATCAGTCTCTGAACAAAGTTTGAAGAGGACCGAAGAAACAGCTCGCAAGGCCAGG 2412  
Db |||||||  
2169 GATCAGTCTCTGAACAAAGTTTGAAGAGGACCGAAGAAACAGCTCGCAAGGCCAGG 2228  
Qy |||||||  
2413 ACATACCCCGAGGAAACAGTAAACAAATGGAAGCACTTACAGAAAAATAAGAAAGGTAGAAA 2472  
Db |||||||  
2229 ACATACCCCGAGGAAACAGTAAACAAATGGAAGCACTTACAGAAAAATAAGAAAGGTAGAAA 2288  
Qy |||||||  
2473 CAGGAGGACCCAGATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCATTTACCTCTAGA 2532  
Db |||||||  
2289 CAGGAGGACCCAGATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCATTTACCTCTAGA 2348  
Qy |||||||  
2533 AACCTCAACAGTAGTAACCTTGCCTAGACATAAATCGGAAAAACAAATGCAATATACAT 2592  
Db |||||||  
2349 AACCTCAACAGTAGTAACCTTGCCTAGACATAAATCGGAAAAACAAATGCAATATACAT 2408

2593 GAACCTTTTTCATGGCATTTATGATGTTTACAAATGTTGGGAAATTCAGCTGAGTTCA 2652  
Db |||||||  
2409 GAACCTTTTTCATGGCATTTATGATGTTTACAAATGTTGGGAAATTCAGCTGAGTTCA 2468  
Qy |||||||  
2653 CCAATTAATAAATCAATCATGAGTAACTTTTCTTAATAGGCTTTTCTTCTTAATACC 2709  
Db |||||||  
2469 CCAATTAATAAATCAATCATGAGTAACTTTTCTTAATAGGCTTTTCTTCTTAATACC 2525

RESULT 3  
US-10-097-340-283  
; Sequence 283, Application US/10097340  
; Publication No. US20030087250A1  
; GENERAL INFORMATION:  
; APPLICANT: John MONAHAN  
; APPLICANT: Manjula GANNAVAPU  
; APPLICANT: Sebastian HOERSCH  
; APPLICANT: Shubhangi KAMATKAR  
; APPLICANT: Steve G. KOVATS  
; APPLICANT: Rachel E. MEYERS  
; APPLICANT: Michael MORRISEY  
; APPLICANT: Peter OLANDT  
; APPLICANT: Ami SEN  
; APPLICANT: Peter VEIBY  
; APPLICANT: Gordon B. MILLS  
; APPLICANT: Robert C. EAST, Jr.  
; APPLICANT: Karen LU  
; APPLICANT: Rosemarie SCHMANDT  
; APPLICANT: Xumei ZHAO  
; APPLICANT: Karen GLATT  
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
; FILE REFERENCE: MRI-030  
; CURRENT APPLICATION NUMBER: US/10/097,340  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 60/276,025  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/325,149  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/276,026  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/324,967  
; PRIOR FILING DATE: 2001/09/26  
; PRIOR APPLICATION NUMBER: 60/311,732  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,102  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/323,580  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 363  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 283  
; LENGTH: 2530  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-097-340-283

Query Match 92.6%; Score 2508.4; DB 14; Length 2530;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 193 CTGCAGCATGGCTGGTTAACTAGGATTTGCTGCTTTTCTGGGAGTATTACTTTACAGC 252  
Db |||||||  
9 CTGCAGCATGGCTGGTTAACTAGGATTTGCTGCTTTTCTGGGAGTATTACTTTACAGC 68

Qy 253 AAGACCAACTCATCAGATGGGAACAATGTGCAAGGCTGAATTTCTTACAAAGA 312  
Db |||||||  
69 AAGACCAACTCATCAGATGGGAACAATGTGCAAGGCTGAATTTCTTACAAAGA 128

Qy 313 AATGTTGGAATCCCAACAAATGTGATCCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372  
Db |||||||  
129 AATGTTGGAATCCCAACAAATGTGATCCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188



QY 373 TACCTTCCTTTTGGATGAGGACCGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432  
Db 189 TACCTTCCTTTTGGATGAGGAAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248  
QY 433 TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTGTGTGGCCAGATCTTACAC 492  
Db 249 TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTGTGTGGCCAGATCTTACAC 308  
QY 493 CAGAAGAGATGAATCAAGTGGGCTGGAAAAGACATCTCTGAAGAATGTGCTAAATTTCA 552  
Db 309 CAGAAGAGATGAATCAAGTGGGCTGGAAAAGACATCTCTGAAGAATGTGCTAAATTTCA 368  
QY 553 CAGAGTACTTAAGGCATATAATCAGACTCACTGTGTAGGCTGTGGAAACGGGGCTTTTCA 612  
Db 369 CAGAGTACTTAAGGCATATAATCAGACTCACTGTGTAGGCTGTGGAAACGGGGCTTTTCA 428  
QY 613 TCCAAATTCGACCTCAATTTGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGA 672  
Db 429 TCCAAATTCGACCTCAATTTGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGA 488  
QY 673 GAACTCACATTTTGA AAAACGGCGGTGGGAAGAGTCATATGACCCCTTAAGCTGTCGACAGC 732  
Db 489 GAACTCACATTTTGA AAAACGGCGGTGGGAAGAGTCATATGACCCCTTAAGCTGTCGACAGC 548  
QY 733 ATCCCTTTTAATAGATGGAGAAATATATCTCTGGAACCTGAGCTGATTTTATGGGGGAGA 792  
Db 549 ATCCCTTTTAATAGATGGAGAAATATATCTCTGGAACCTGAGCTGATTTTATGGGGGAGA 608  
QY 793 CTTTGTCTATCTCCGAACTCTTGGGCACCAACCAATCAGGACAGACAGCATGATTC 852  
Db 609 CTTTGTCTATCTCCGAACTCTTGGGCACCAACCAATCAGGACAGACAGCATGATTC 668  
QY 853 CAGGTGGCTCAATGATCCAAAGTTCAATGATGCGCACCTCATCTCAGAGAGTGACAATCC 912  
Db 669 CAGGTGGCTCAATGATCCAAAGTTCAATGATGCGCACCTCATCTCAGAGAGTGACAATCC 728  
QY 913 TGAAGATGACAAAGTATATCTTTTCCGTGAAATGCAATAGATGGAGAACATCTCTGG 972  
Db 729 TGAAGATGACAAAGTATATCTTTTCCGTGAAATGCAATAGATGGAGAACATCTCTGG 788  
QY 973 AAAAGCTACTCAGCTAGAAATAGGTCAGATATGCAAGATGATTTTGGAGGGCACAGAAG 1032  
Db 789 AAAAGCTACTCAGCTAGAAATAGGTCAGATATGCAAGATGATTTTGGAGGGCACAGAAG 848  
QY 1033 TCTGTGTAAATAATGAGCAACATCTCTCAAAGCTGCTGATTTGCTCAGTGCCAGGTCC 1092  
Db 849 TCTGTGTAAATAATGAGCAACATCTCTCAAAGCTGCTGATTTGCTCAGTGCCAGGTCC 908  
QY 1093 AAATGGCATTGACATCTATTTTGAATGAACTGCAAGGATGATTCCTTAATGAACTTTAAAGA 1152  
Db 909 AAATGGCATTGACATCTATTTTGAATGAACTGCAAGGATGATTCCTTAATGAACTTTAAAGA 968  
QY 1153 TCCTAAAAATCCAGTTGTATATGAGGTGTTACGACTTCCAGTTACAGATTTTCAAGGGATC 1212  
Db 969 TCCTAAAAATCCAGTTGTATATGAGGTGTTACGACTTCCAGTTACAGATTTTCAAGGGATC 1028  
QY 1213 AGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTCTTGGTCCATATGCCCCA 1272  
Db 1029 AGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTCTTGGTCCATATGCCCCA 1088  
QY 1273 CAGGATGAGCCCAACTATCAATGAGGTGCTTATCAAGGAAGATGCCCTTATCCAGGGCC 1332  
Db 1089 CAGGATGAGCCCAACTATCAATGAGGTGCTTATCAAGGAAGATGCCCTTATCCAGGGCC 1148  
QY 1333 AGGAACTTCTCCAGCAAAACATTTGGTGTGTTGACTCTCAAAAGGACCTTCTGTATGA 1392  
Db 1149 AGGAACTTCTCCAGCAAAACATTTGGTGTGTTGACTCTCAAAAGGACCTTCTGTATGA 1208  
QY 1393 TGTATAACTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAA 1452  
Db 1209 TGTATAACTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTCTTCTATGNACAA 1268  
QY 1453 TCGCCCAATPAGTATCAAAAACGGATGTAAATTTATCAAAATTTTACAAATTTGTCGTAGACCG 1512

Db 1269 TCGCCCAATPAGTATCAAAAACGGATGTAAATTTATCAAAATTTGTCGTAGACCG 1328  
QY 1513 AGTGGATGCAAGAAGTGGACAGTATGATGTTATGTTATCGGAAACAGATGTTGGGACCGT 1572  
Db 1329 AGTGGATGCAAGAAGTGGACAGTATGATGTTATGTTATCGGAAACAGATGTTGGGACCGT 1388  
QY 1573 TCTTAAAGTAGTATTTCAATTTCTTAAGGAGACTTGGTATGATTTAGAAAGAGGTTCTGCTGA 1632  
Db 1389 TCTTAAAGTAGTATTTCAATTTCTTAAGGAGACTTGGTATGATTTAGAAAGAGGTTCTGCTGA 1448  
QY 1633 AGAAATGACAGTTTTTTCGGGAACCGACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1692  
Db 1449 AGAAATGACAGTTTTTTCGGGAACCGACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1508  
QY 1693 GCACAAACTATATATTTGGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACGGTGTGA 1752  
Db 1509 GCACAACTATATATTTGGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACGGTGTGA 1568  
QY 1753 TATTTTACGGGAAGGCTGTGCTGAGTGTGGCTTCGCCCGAGACCTTTACTGTCTTGGGA 1812  
Db 1569 TATTTTACGGGAAGGCTGTGCTGAGTGTGGCTTCGCCCGAGACCTTTACTGTCTTGGGA 1628  
QY 1813 TGGTTCTGCTGCTCTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGACAATAT 1872  
Db 1629 TGGTTCTGCTGCTCTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGACAATAT 1688  
QY 1873 AAGAAATGGAGACCCCACTGACTCACTGTTTTCAGACTTTTACACCATGATAATCACCATGGCCA 1932  
Db 1689 AAGAAATGGAGACCCCACTGACTCACTGTTTTCAGACTTTTACACCATGATAATCACCATGGCCA 1748  
QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCAATTTTGGAAATGCGAG 1992  
Db 1749 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCAATTTTGGAAATGCGAG 1808  
QY 1993 TCCGAAGTGCAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGAAATGGAAGAGCGAAA 2052  
Db 1809 TCCGAAGTGCAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGAAATGGAAGAGCGAAA 1868  
QY 2053 AGAAGAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG 2112  
Db 1869 AGAAGAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG 1928  
QY 2113 TCTTCAACAGAAAGATTCAGGCAATTAATCTCTGCCATGCGGTGGAAACATGGGTTCATACA 2172  
Db 1929 TCTTCAACAGAAAGATTCAGGCAATTAATCTCTGCCATGCGGTGGAAACATGGGTTCATACA 1988  
QY 2173 AACTCTTCTTAAGGTAAACCTTGGAAAGTCATTTGACACAGAGCATTTGGAAAGAACTTCTTCA 2232  
Db 1989 AACTCTTCTTAAGGTAAACCTTGGAAAGTCATTTGACACAGAGCATTTGGAAAGAACTTCTTCA 2048  
QY 2233 TAAAGATGATGATGAGATGGCTCTTAAAGACCAAGAAATGTCCAATAGCATGACACTAG 2292  
Db 2049 TAAAGATGATGATGAGATGGCTCTTAAAGACCAAGAAATGTCCAATAGCATGACACTAG 2108  
QY 2293 CCAGAAGGTCTGGTACAGAGACTTTCATGAGCTCATCAACCAACCCCAATCTCAACACGAT 2352  
Db 2109 CCAGAAGGTCTGGTACAGAGACTTTCATGAGCTCATCAACCAACCCCAATCTCAACACGAT 2168  
QY 2353 GATGAGTCTGTGAACAAAGTTTGGAAAGGGACCGAAACAAACGTCGCGCAAGGCCAGG 2412  
Db 2169 GATGAGTCTGTGAACAAAGTTTGGAAAGGGACCGAAACAAACGTCGCGCAAGGCCAGG 2228  
QY 2413 ACATACCCCAAGGAAACAGTAAACAAATGGAAGCACTTACAAAGAAATTAAGAAAGGTAGAAA 2472  
Db 2229 ACATACCCCAAGGAAACAGTAAACAAATGGAAGCACTTACAAAGAAATTAAGAAAGGTAGAAA 2288  
QY 2473 CAGGAGGACCCCAAGTATTTGAGAGGGACCCAGGAGTGTCTGAGCTGCAATTAACCTTAGA 2532  
Db 2289 CAGGAGGACCCCAAGTATTTGAGAGGGACCCAGGAGTGTCTGAGCTGCAATTAACCTTAGA 2348  
QY 2533 AACCTCAAAACAGATGAGAAACCTTGGCTTAGCAATTAAGTGAAGAAACAAATTAACATATACAT 2592

Db 2349 AACCTCAAACTAGTAACTTGCCTAGACAAATACTGGAACAAATAATCAATATACAT 2408  
 QY 2593 GAACCTTTTTCATGCGATTTATGCGATTTTACAAATGTTGGAAATTCAGCTGAGTTCCA 2652  
 Db 2409 GAACCTTTTTCATGCGATTTATGCGATTTTACAAATGTTGGAAATTCAGCTGAGTTCCA 2468  
 QY 2653 CCAATTATAAATTAATCAATGAGTAACTTTCTTAATAGCTTTTTCCTCC 2702  
 Db 2469 CCAATTATAAATTAATCAATGAGTAACTTTCTTAATAGCTTTTTCCTCC 2518

RESULT 4  
 US-10-262-538-9  
 ; Sequence 9, Application US/10262538  
 ; Publication No. US20030113324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alitalo et al  
 ; TITLE OF INVENTION: NEUROFILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS  
 ; FILE REFERENCE: 28967/37564  
 ; CURRENT APPLICATION NUMBER: US/10/262,538  
 ; CURRENT FILING DATE: 2002-09-30  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 2530  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (16)..(2331)  
 US-10-262-538-9

Query Match 92.6%; Score 2508.4; DB 15; Length 2530;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 193 CTCGAGCATGGGCTGGTTAACTAGGATTTCTGTCTTTCTGGGAGTATTACTTACAGC 252  
 Db 9 CTCGAGCATGGGCTGGTTAACTAGGATTTCTGTCTTTCTGGGAGTATTACTTACAGC 68  
 QY 253 AGAGCAAACTATCAGATGGGAAGAACTATGCGCAAGCTGGAATTAATCTCAAGA 312  
 Db 69 AGAGCAAACTATCAGATGGGAAGAACTATGCGCAAGCTGGAATTAATCTCAAGA 128  
 QY 313 AATGTTGGAATCAACAATGTGATCATCTTTCAATGCTTGGCCCAACAGCTCCAGTTATCA 372  
 Db 129 AATGTTGGAATCAACAATGTGATCATCTTTCAATGCTTGGCCCAACAGCTCCAGTTATCA 188  
 QY 373 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATAT 432  
 Db 189 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATAT 248  
 QY 433 TTCACTCGACCTGGTTAATATCAAGATTTTCAAAAGATTTGTGGCCAGATCTTACAC 492  
 Db 249 TTCACTCGACCTGGTTAATATCAAGATTTTCAAAAGATTTGTGGCCAGATCTTACAC 308  
 QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTTGAAGAAATGTGCTAAATTTTCA 552  
 Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTTGAAGAAATGTGCTAAATTTTCA 368  
 QY 553 CAAGGTACTTAAGGCATATAATCAGATCTACCTTGTACGCTGTGGAACGGGGCTTTTCA 612  
 Db 369 CAAGGTACTTAAGGCATATAATCAGATCTACCTTGTACGCTGTGGAACGGGGCTTTTCA 428  
 QY 613 TCCAAATTCACCTACATTAATTTGGACATCATCTTGAGGACATATTTTAACTGGA 672  
 Db 429 TCCAAATTCACCTACATTAATTTGGACATCATCTTGAGGACATATTTTAACTGGA 488  
 QY 673 GAACCTCACATTTTGAACCGGCGGTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 732  
 Db 489 GAACCTCACATTTTGAACCGGCGGTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 548  
 QY 733 ATCCCTTTTAAATAGATGGGAATTAATCTCTGGAACCTGAGCTGATTTTATGGGGCGAGA 792

Db 549 ATCCCTTTTAAATAGATGAGAAATATATCTTGGAACTGCGAGTGAATTTTATGGGGCGAGA 608  
 QY 793 CTTTGCTATCTTTCCGAACTCTTTGGGCAACAACAACCAATCAGGACAGAGCATGATTC 852  
 Db 609 CTTTGCTATCTTTCCGAACTCTTTGGGCAACAACAACCAATCAGGACAGAGCATGATTC 668  
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 Db 669 CAGGTGGCTCAATGATCCAAAGTTTCATTTAGTGGCCACCTCATCTCAGAGAGTGACATCC 728  
 QY 913 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAAATGCAATAGATGAGAACTCTCTGG 972  
 Db 729 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAAATGCAATAGATGAGAACTCTCTGG 788  
 QY 973 AAAAGCTACTCACGCTAGATAGTTCAGATATGCAAGAAATGACTTTGGAGGGGCAAGAAG 1032  
 Db 789 AAAAGCTACTCACGCTAGATAGTTCAGATATGCAAGAAATGACTTTGGAGGGGCAAGAAG 848  
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 Db 849 TCTGGTGAATAAATGAGCAACAATTCCTCAAGCTCGTCTGATTTGCTCAGTCCAGAGTCC 908  
 QY 1093 AAATGGCATTTGACACTCAATTTTGTATGAATGCAAGATGTATTTCTTAATCAACTTTAAAGA 1152  
 Db 909 AAATGGCATTTGACACTCAATTTTGTATGAATGCAAGATGTATTTCTTAATCAACTTTAAAGA 968  
 QY 1153 TCCTAAATAATCGAGTTGATATGAGAGTGTATGAGCTTCCAGTAACTTTCAAGGGATC 1212  
 Db 969 TCCTAAATAATCGAGTTGATATGAGAGTGTATGAGCTTCCAGTAACTTTCAAGGGATC 1028  
 QY 1213 AGCGTGTGATGATATAGCATGATGATGAGAGGTTTCTTGTGTCATATGCCCA 1272  
 Db 1029 AGCGTGTGATGATATAGCATGATGATGAGAGGTTTCTTGTGTCATATGCCCA 1088  
 QY 1273 CAGGATGGAACCCAACTATCAATGGTGCTCTTATCAAGGAAGAGTCCCTTATCCAGGCC 1332  
 Db 1089 CAGGATGGAACCCAACTATCAATGGTGCTCTTATCAAGGAAGAGTCCCTTATCCAGGCC 1148  
 QY 1333 AGGAATCTGTCAGCAAAACAATTTGGTGGTGTGACTCTCAAGAGGACCTTCTGATGA 1392  
 Db 1149 AGGAATCTGTCAGCAAAACAATTTGGTGGTGTGACTCTCAAGAGGACCTTCTGATGA 1208  
 QY 1393 TGTATAAATCTTTCAGCAAAACAATTTGGTGGTGTGACTCTCAAGAGGACCTTCTGATGA 1452  
 Db 1209 TGTATAAATCTTTCAGCAAAACAATTTGGTGGTGTGACTCTCAAGAGGACCTTCTGATGA 1268  
 QY 1453 TCGCCCAATAGTGTATCAAAACGGATGTAATTAATCAATTTTACAAATTTGCTAGACCG 1512  
 Db 1269 TCGCCCAATAGTGTATCAAAACGGATGTAATTAATCAATTTTACAAATTTGCTAGACCG 1328  
 QY 1513 AGTGGATCGAAGATGAGACATGATGATGTTTATCGGAAACAGATTTGGGACCGT 1572  
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 Db 1389 TCTTAAAGTGTCTTCAATTTCTAAGGACCTTGGTGTATGATTTAGAGAGGTTCTGCTGA 1448  
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 Db 1449 AGAAATGACGTTTTTTCGGGAAACCGACCTGTATTTTACAGCAATGAGGCTTTTCACTAAGCA 1508  
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 QY 1753 TATTTACGGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTTACTGTGCTGGGA 1812  
 Db 1569 TATTTACGGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTTACTGTGCTGGGA 1628  
 QY 1813 TGGTTTGCATGTTCTGCTATTTTCCACATGCGAAAGAGACGCAACAGCAAGATAT 1872

Db 1629 TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAACAGACGACATAT 1688  
Qy 1873 AAGAAATGGAGACCCACCTGACTCAGTGTTCAGACTTTACACCATGATTAATCACCATGGCCA 1932  
Db 1689 AAGAAATGGAGACCCACCTGACTCAGTGTTCAGACTTTACACCATGATTAATCACCATGGCCA 1748  
Qy 1933 CAGCCCTGAGAGAGAAATCATCTATGTTGTAGAGATAGTAGACATATTTTGGATGCG 1992  
Db 1749 CAGCCCTGAGAGAGAAATCATCTATGTTGTAGAGATAGTAGACATATTTTGGATGCG 1808  
Qy 1993 TCCGAAGTCGACAGAGCCCTGCTTATTTGGCAATTTCCAGAGCGGAGAAATGAAGAGCGAAA 2052  
Db 1809 TCCGAAGTCGACAGAGCCCTGCTTATTTGGCAATTTCCAGAGCGGAGAAATGAAGAGCGAAA 1868  
Qy 2053 AGAAGAGATCAGAGTGGATGATCATATCATATCAGGACAGATCAAGGCTTCTCTACGTAG 2112  
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATATCAGGACAGATCAAGGCTTCTCTACGTAG 1928  
Qy 2113 TCTACAAAGAGAGATTTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTTCATACA 2172  
Db 1929 TCTACAAAGAGAGATTTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTTCATACA 1988  
Qy 2173 AACTCTTCTTAAGTTAACTGGAAGTCAATGACACAGAGCATTTTGGAAAGAACTTCTTCA 2232  
Db 1989 AACTCTTCTTAAGTTAACTGGAAGTCAATGACACAGAGCATTTTGGAAAGAACTTCTTCA 2048  
Qy 2233 TAAAGATGATGAGAGATGGCTCTAAGACCAAGAAATGTCCAAATAGCATGACACCTAG 2292  
Db 2049 TAAAGATGATGAGAGATGGCTCTAAGACCAAGAAATGTCCAAATAGCATGACACCTAG 2108  
Qy 2293 CCAGAGGTCGTGACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACACGAT 2352  
Db 2109 CCAGAGGTCGTGACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACACGAT 2168  
Qy 2353 GGATGAGTTCTGTGAACAGTTTGGAAAGGGACCGGAAACAACTCGGCAAGGCCAGG 2412  
Db 2169 GGATGAGTTCTGTGAACAGTTTGGAAAGGGACCGGAAACAACTCGGCAAGGCCAGG 2228  
Qy 2413 ACATACCCCGAGGAAACAGTAACAAATGGAAGCAGCTTACAGAAATTAAGAAAGGTAGAAA 2472  
Db 2229 ACATACCCCGAGGAAACAGTAACAAATGGAAGCAGCTTACAGAAATTAAGAAAGGTAGAAA 2288  
Qy 2473 CAGGAGGCCACGAAATTTGAGAGGCCACCCAGGAGTGTCTGAGCTGCATTAACCTCTAGA 2532  
Db 2289 CAGGAGGCCACGAAATTTGAGAGGCCACCCAGGAGTGTCTGAGCTGCATTAACCTCTAGA 2348  
Qy 2533 AACCTCAACAAAGTAGAAGTGTGCTTAGACAATTAAGTGAAGAAACAAATGCAATATACAT 2592  
Db 2349 AACCTCAACAAAGTAGAAGTGTGCTTAGACAATTAAGTGAAGAAACAAATGCAATATACAT 2408  
Qy 2593 GAACTTTTTCATGGCATTATGTGGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA 2652  
Db 2409 GAACTTTTTCATGGCATTATGTGGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA 2468  
Qy 2653 CCAATTAATAATTAATCAATGAGTAACCTTCTTAATAGGCTTTTTTCC 2702  
Db 2469 CCAATTAATAATTAATCAATGAGTAACCTTCTTAATAGGCTTTTTTTC 2518

RESULT 5

US-10-669-176-9  
; Sequence 9, Application US/10669176  
; Publication No. US20040214766A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: VEGF-C OR VEGF-D MATERIALS AND METHODS FOR TREATMENT OF  
; FILE REFERENCE: 28967/37564B  
; CURRENT APPLICATION NUMBER: US/10/669,176  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 9

; LENGTH: 2530  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (16)..(2331)  
US-10-669-176-9  
  
Query Match 92.6%; Score 2508.4; DB 18; Length 2530;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 193 CTGACGATGGCTGGTTAACTAGCATGTCTGTCTTTTCTGGGAGTATTACTTACAGC 252  
Db 9 CTGACGATGGCTGGTTAACTAGCATGTCTGTCTTTTCTGGGAGTATTACTTACAGC 68  
Qy 253 AAGAGCAAACTATCAGAAATGGGAAGAAACAATCTGCAAGGCTGAAATTAATCTTACAAAGA 312  
Db 69 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTGCGAGGCTGAAATTAATCTTACAAAGA 128  
Qy 313 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTTGGCCAAACAGCTCCAGTTATCA 372  
Db 129 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTTGGCCAAACAGCTCCAGTTATCA 188  
Qy 373 TACCTTCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGAGCAAGGATCACAATTT 432  
Db 189 TACCTTCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGAGCAAGGATCACAATTT 248  
Qy 433 TTCTATTCGACCTGGTTTAATATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACAC 492  
Db 249 TTCTATTCGACCTGGTTTAATATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACAC 308  
Qy 493 CAGAAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTCA 552  
Db 309 CAGAAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTCA 368  
Qy 553 CAGGTACTTAAGGATTAATATCAGATCTCATCTGAGGACATCTCTGAGGACAAATTTTAAAGCTGA 672  
Db 369 CAGGTACTTAAGGATTAATATCAGATCTCATCTGAGGACATCTCTGAGGACAAATTTTAAAGCTGA 428  
Qy 613 TCCAAATTTGCACTACATTTGAAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGA 672  
Db 429 TCCAAATTTGCACTACATTTGAAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGA 488  
Qy 673 GAACTCACAATTTTGAAGACGGCCGTGGGAAGAGTCCATATGACCCCTCAAGCTGCTGACAGC 732  
Db 489 GAACTCACAATTTTGAAGACGGCCGTGGGAAGAGTCCATATGACCCCTCAAGCTGCTGACAGC 548  
Qy 733 ATCCCTTTTAATAGATGAGAAATTAATCTCTGGAATCTGCAAGCTGATTTTATGGGGGAGA 792  
Db 549 ATCCCTTTTAATAGATGAGAAATTAATCTCTGGAATCTGCAAGCTGATTTTATGGGGGAGA 608  
Qy 793 CTTTGCTATCTTCGAACTCTTTGGGACCCACCAATTCAGGACAGACAGCATGATTC 852  
Db 609 CTTTGCTATCTTCGAACTCTTTGGGACCCACCAATTCAGGACAGACAGCATGATTC 668  
Qy 853 CAGGTGGCTCAATGATCCAAAGTTCATTTAGTCCCACTCATCTCTCAGAGAGTGACAATCC 912  
Db 669 CAGGTGGCTCAATGATCCAAAGTTCATTTAGTCCCACTCATCTCTCAGAGAGTGACAATCC 728  
Qy 913 TGAAGATGACAAAGTATATCTTTTCTCGTGAATAATGCAATAGATGGAGAACACTCTCG 972  
Db 729 TGAAGATGACAAAGTATATCTTTTCTCGTGAATAATGCAATAGATGGAGAACACTCTCG 788  
Qy 973 AAAAGCTACTCAGCTAGAAATAGTATGCAAGATGACTTTGGAGGCGACAGAG 1032  
Db 789 AAAAGCTACTCAGCTAGAAATAGTATGCAAGATGACTTTGGAGGCGACAGAG 848  
Qy 1033 TCTGCTGAATAAATGGACAAATCTCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGCTCC 1092  
Db 849 TCTGCTGAATAAATGGACAAATCTCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGCTCC 908  
Qy 1093 AAAAGCTACTCAGCTAGAAATAGTATGCAAGATGACTTTGCTTAATGAACACTTTTAAAGA 1152

Db	909	AAATGGGCATTGACACTCATTTTGATGAACATGTCAGATGTATTTCTTAATGAACCTTTAAAGA	968
Qy	1153	TCCTAAAAATCCAGTTGTATATGAGAGTGTTTACGACTTCCAGTAACATATTTTCAAGGGATC	1212
Db	969	TCCTAAAAATCCAGTTGTATATGAGTGTTTACGACTTCCAGTAACATTTTCAAGGGATC	1028
Qy	1213	AGCCGTGTGTATGTATATGACATGAGTGATGTGAGAAGGGTGTTCCTTGCTCCATATGCCCA	1272
Db	1029	AGCCGTGTGTATGTATATGACATGAGTGATGTGAGAAGGGTGTTCCTTGCTCCATATGCCCA	1088
Qy	1273	CAGGGAATGGACCCCAACTATCAATCGGTGCCTTTATCAAGGAAGAGTCCCTTATCCACGGCC	1332
Db	1089	CAGGGAATGGACCCCAACTATCAATCGGTGCCTTTATCAAGGAAGAGTCCCTTATCCACGGCC	1148
Qy	1333	AGGAACCTTGCCCAAGCAAAACATTTTGTGTGTTTTGACTCTACAAAGACCTTCTGTATGA	1392
Db	1149	AGGAACCTTGCCCAAGCAAAACATTTTGTGTGTTTTGACTCTACAAAGACCTTCTGTATGA	1208
Qy	1393	TGTTATTAACCTTTGCAAGAGTCAATCAGCCATGTACAAATCCAGTGTTCCTATGAACAA	1452
Db	1209	TGTTATTAACCTTTGCAAGAGTCAATCAGCCATGTACAAATCCAGTGTTCCTATGAACAA	1268
Qy	1453	TCGCCCAATAGTGATCAAAACCGATGTAAATTTATCAATTTTACACAAATTTGCTGTAGACCG	1512
Db	1269	TCGCCCAATAGTGATCAAAACCGATGTAAATTTATCAATTTTACACAAATTTGCTGTAGACCG	1328
Qy	1513	AGTGGATGCAGAGATGCAGATGATGTTATGTTTTATCGGAACAGATGTTGGGACCGT	1572
Db	1329	AGTGGATGCAGAGATGCAGATGATGTTATGTTTTATCGGAACAGATGTTGGGACCGT	1388
Qy	1573	TCCTTAAAGTAGTTTCAATTCCTTAAGGAGACTTGGTATGATTTAGAAGAGGTTCTGCTGGA	1632
Db	1389	TCCTTAAAGTAGTTTCAATTCCTTAAGGAGACTTGGTATGATTTAGAAGAGGTTCTGCTGGA	1448
Qy	1633	AGAAATGACAGTTTTTTCGGGAAACCGACTGTATTTACAGAAATGGAGCTTTCCACTAAGCA	1692
Db	1449	AGAAATGACAGTTTTTTCGGGAAACCGACTGTATTTACAGAAATGGAGCTTTCCACTAAGCA	1508
Qy	1693	GCAACACTATATATGTTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACCGTGTGA	1752
Db	1509	GCAACACTATATATGTTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACCGTGTGA	1568
Qy	1753	TATTTACGGGAAAGCGTGTCTGAGTGTTCCTCGCCCGGAGACCTTACTGTGCTTTGGGA	1812
Db	1569	TATTTACGGGAAAGCGTGTCTGAGTGTTCCTCGCCCGGAGACCTTACTGTGCTTTGGGA	1628
Qy	1813	TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAGAGAGACGACACAGACGACAAGATAT	1872
Db	1629	TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAGAGAGACGACACAGAGACGACAAGATAT	1688
Qy	1873	AAGAAATGGAGACCCACTGACTCACTGTTTCAGAGCTTACACCATGATAATCACCATGGCCA	1932
Db	1689	AAGAAATGGAGACCCACTGACTCACTGTTTCAGAGCTTACACCATGATAATCACCATGGCCA	1748
Qy	1933	CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACATATTTTGGAAATGCAG	1992
Db	1749	CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACATATTTTGGAAATGCAG	1808
Qy	1993	TCCGAAGTCCGAGAGACGCTGGTCTATTTGCGCAATTCAGAGGCGAAATGAAGAGCGAAA	2052
Db	1809	TCCGAAGTCCGAGAGACGCTGGTCTATTTGGCAATTCAGAGGCGAAATGAAGAGCGAAA	1868
Qy	2053	AGAAGAGATCAGAGTGGATGATCATATCATCATGAGACAGATCAAGGCTTCTGTCATGTAG	2112
Db	1869	AGAAGAGATCAGAGTGGATGATCATATCATCATGAGACAGATCAAGGCTTCTGTCATGTAG	1928
Qy	2113	TCTACAAACAAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGACATGGGTTCAACA	2172
Db	1929	TCTACAAACAAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGACATGGGTTCAACA	1988
Qy	2173	AACCTCTTTAAAGGTAAACCTTGAAGTTCATTTGACACAGAGCAATTTGGAAGAACTTCTTCA	2232

Db	1989	AACTCTCTTTAAGGTAAACCCCTGGGAAGTCATTGACACAGAGCATTTGGAGAAGAACTTCTTCA	2048
Qy	2233	TAAAGATGATGATGAGGATGGCTCTTAAGAGACCAAGAAATGTCCAAATAGCATGACACCTAG	2292
Db	2049	TAAAGATGATGATGAGGATGGCTCTTAAGAGACCAAGAAATGTCCAAATAGCATGACACCTAG	2108
Qy	2293	CCAGAAGGCTCTGGTACAGAGACTTTCATGCGAGCTCATCAACACCCCAATCTTCAACACGAT	2352
Db	2109	CCAGAAGGCTCTGGTACAGAGACTTTCATGCGAGCTCATCAACACCCCAATCTTCAACACGAT	2168
Qy	2353	GGATGAGTCTTGTCGAAACAAGTTTGGAAAAAGGACCGGAAAAACAACGTCGGCAAAAGGCCAGG	2412
Db	2169	GGATGAGTCTTGTCGAAACAAGTTTGGAAAAAGGACCGGAAAAACAACGTCGGCAAAAGGCCAGG	2228
Qy	2413	ACATACCCCGAGGAACAGTACAATAATGGAAGCACTTACAAGAAAAATGAAGGATAGAAA	2472
Db	2229	ACATACCCCGAGGAACAGTACAATAATGGAAGCACTTACAAGAAAAATGAAGGATAGAAA	2288
Qy	2473	CAGGAGGACCCACGAATTTGAGAGGGGACCCAGAGAGTGTCTGAGCTGCATTTACCTCTAGA	2532
Db	2289	CAGGAGGACCCACGAATTTGAGAGGGGACCCAGAGAGTGTCTGAGCTGCATTTACCTCTAGA	2348
Qy	2533	AACCTCAAAACAAGTAGAAAACTTGCTGTAGACAATAAATCTGGAAAAACAATAATGCAATATACAT	2592
Db	2349	AACCTCAAAACAAGTAGAAAACTTGCTGTAGACAATAAATCTGGAAAAACAATAATGCAATATACAT	2408
Qy	2593	GAACCTTTTTCATGCGCAATATATGTGGATGTTTTCAATGGTGGAAAAATTCAGCTGAGTTCCA	2652
Db	2409	GAACCTTTTTCATGCGCAATATATGTGGATGTTTTCAATGGTGGAAAAATTCAGCTGAGTTCCA	2468
Qy	2653	CCAATTATAAATAAATCCATGAGTAACTTTTCCTAATAGGCTTTTTTTTC	2702
Db	2469	CCAATTATAAATAAATCCATGAGTAACTTTTCCTAATAGGCTTTTTTTTC	2518
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US-10-723-860-2569			
; Sequence 2569, Application US/10723860			
; Publication No. US20040253606A1			
; GENERAL INFORMATION:			
; APPLICANT: Aziz, Natasha			
; APPLICANT: Ginsburg, Wendy M.			
; APPLICANT: Zlotnik, Albert			
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions			
; FILE REFERENCE: 05882.0193.NPUS01			
; CURRENT APPLICATION NUMBER: US/10/723,860			
; PRIOR FILING DATE: 2003-11-26			
; PRIOR FILING DATE: 2002-11-26			
; NUMBER OF SEQ ID NOS: 8393			
; SOFTWARE: Patent in version 3.2			
; SEQ ID NO 2569			
; LENGTH: 2530			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-723-860-2569			

	Query Match	92.6%	Score 2508.4	DB 18	Length 2530	
	Best Local Similarity	100.0%	Pred. No. 0			
	Matches 2509	Conservative 0	Mismatches 1	Indels 0	Gaps 0	
Qy	193	CTGCAGCATGGCTGGTTAACTAGGATGTCTGTCTTTCTGGGGAGTATTACTTTACAGC	252			
Db	9	CTGCAGCATGGCTGGTTAACTAGGATGTCTGTCTTTCTGGGGAGTATTACTTTACAGC	68			
Qy	253	AAGAGCAAACTATCAGAAATGGGAAGAACAAATGTCCAGGCTGAAATTTATCTCTCAAAAGA	312			
Db	69	AAGAGCAAACTATCAGAAATGGGAAGAACAAATGTCCAGGCTGAAATTTATCTCTCAAAAGA	128			
Qy	313	AATGTTGGAATCCAAACATGTGATPCATTTTCAATGGCTTGCCCAACAGCTCAAGTTATCA	372			
Db	129	AATGTTGGAATCCAAACATGTGATPCATTTTCAATGGCTTGCCCAACAGCTCAAGTTATCA	188			

QY 373 TACCTTCCCTTTTGGATGAGGACCGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432  
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 QY 433 TTCAATTCGACCTGGTTAAATCAAGGATTTCAAAGATTTGTTGGCCAGTATCTTACAC 492  
 DB 249 TTCAATTCGACCTGGTTAAATCAAGGATTTCAAAGATTTGTTGGCCAGTATCTTACAC 308  
 QY 493 CAGAAGAGATGAATCAAGTGGGCTCGAAAAGACATCTCGAAAAGATGTCTAAATTTCA 552  
 DB 309 CAGAAGAGATGAATCAAGTGGGCTCGAAAAGACATCTCGAAAAGATGTCTAAATTTCA 368  
 QY 553 CAAAGTACTTAAGGCATATAATCAGACTCACTTGTAGGCTGTGGAAACCGGGGCTTTTCA 612  
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 QY 613 TCCAAATTCGACCTCAATTTGAATTTGAGCATCATCTGAGGACAAATTTTAAAGCTGA 672  
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 DB 549 ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGAACTGAGCTGATTTTATGGGGGAGA 608  
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 QY 853 CAGGTGGCTCAATGATCCAAAGTTCAATAGTGCCCACTCATCTCAGAGAGTGACAATCC 912  
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 QY 1033 TCTGGTGAATAAATGACAAACATCTCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCC 1092  
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 QY 1153 TCCATAAATCCAGTTGTATATGAGGTGTTACGACTTCCAGTAACTTTCAAGGGATC 1212  
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 QY 1213 AGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTCTTGGTCCATATGCCCA 1272  
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QY 1453 TCGCCCAATAGTGTATCAAAACCGGATGTAAATTTATCAATTTTACAAATTTGCTGTAGACCG 1512  
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 QY 1513 AGTGGATGAGAGATGAGACAGTATGATTTATCGGAAACAGATGTTGGGACCGT 1572  
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 QY 1633 AGAAATGACAGTTTTTCGGGAAACCGACTCTATTTTTCAGCAATGGAGCTTTCCACTAAGCA 1692  
 DB 1449 AGAAATGACAGTTTTTCGGGAAACCGACTCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1508  
 QY 1693 GCAACAACTATATATTTGGTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACCCGGTGTGA 1752  
 DB 1509 GCAACAACTATATATTTGGTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACCCGGTGTGA 1568  
 QY 1753 TATTTACCGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTGCTTTGGGA 1812  
 DB 1569 TATTTACCGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTGCTTTGGGA 1628  
 QY 1813 TGGTTCTGCTGCTTCTGCTATTTTCCCACTGCAAAAGACAGCGCAAGAGCAAGATAT 1872  
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 QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACATTTTGGAAATGCGAG 1992  
 DB 1749 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACATTTTGGAAATGCGAG 1808  
 QY 1993 TCCGAAGTGCAGAGAGCGCTGCTATTTGGGCAATTCAGAGCGGAAATAGAGAGCGAAA 2052  
 DB 1809 TCCGAAGTGCAGAGAGCGCTGCTATTTGGGCAATTCAGAGCGGCGAAATAGAGAGCGAAA 1868  
 QY 2053 AAGAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTTCTGTACGTAG 2112  
 DB 1869 AAGAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTTCTGTACGTAG 1928  
 QY 2113 TCTCAACACAGAGAGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCATACA 2172  
 DB 1929 TCTCAACACAGAGAGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCATACA 1988  
 QY 2173 AACTCTTTTAAAGGTAAACCTCGAAGTCAATTGACACAGAGCATTTTGGAAAGAACTTCTTCA 2232  
 DB 1989 AACTCTTTTAAAGGTAAACCTCGAAGTCAATTGACACAGAGCATTTTGGAAAGAACTTCTTCA 2048  
 QY 2233 TAAAGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACTAG 2292  
 DB 2049 TAAAGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACTAG 2108  
 QY 2293 CCAGAGGCTCTGCTCAGAGACTTCATGAGCTCATCAACCCCACTTCAACACGAT 2352  
 DB 2109 CCAGAGGCTCTGCTCAGAGACTTCATGAGCTCATCAACCCCACTTCAACACGAT 2168  
 QY 2353 GATGAGTCTGTGTAAACAAATTTTGGAAAGGAGCGGAAACAAAGTTCGGCAAGGCGCAGG 2412  
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 QY 2413 ACATACCCAGGAAACAGTAAACAAATTTGGAAGCAGCTTACAGAAATAAAGAAAGGTAGAAA 2472  
 DB 2229 ACATACCCAGGAAACAGTAAACAAATTTGGAAGCAGCTTACAGAAATAAAGAAAGGTAGAAA 2288  
 QY 2473 CAGGAGGACCCAGAAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGCAATTCCTCTAGA 2532  
 DB 2289 CAGGAGGACCCAGAAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGCAATTCCTCTAGA 2348  
 QY 2533 AACCTCAACAAAGTAGAGAACTTGGCTTAGAATAAATCTGGAAACAAATATGCAATATACAT 2592

Db 2349 AACCTCAACAGTAGAACTTGCCTAGACAATAAAGTGAATAATACAT 2408  
QY 2593 GAACTTTTTCATGGCATATGATGTTTCAATGGTGGGAAATTCAGCTGAGTTCCA 2652  
Db 2409 GAACTTTTTCATGGCATATGATGTTTCAATGGTGGGAAATTCAGCTGAGTTCCA 2468  
QY 2653 CCAATTATAAATTAATCCATGATAGTAACTTTCCTAATAGGCTTTTTCCTC 2702  
Db 2469 CCAATTATAAATTAATCCATGATAGTAACTTTCCTAATAGGCTTTTTCCTC 2518

RESULT 7

US-10-067-632-53  
; Sequence 53, Application US/10067632  
; Publication No. US20030166849A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey S.  
; Kolodkin, Alex L.  
; Matthes, David  
; Bentley, David R.  
; O'Connor, Timothy  
; TITLE OF INVENTION: The Semaphorin Gene Family  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/067,632  
; FILING DATE: 04-Feb-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/060,610  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/835,268  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: B94-002-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2601 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16..2331  
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Query Match 92.6%; Score 2508.4; DB 16; Length 2601;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 193 CTGCAGCATGGCTGGTGAATGATGTTCTCTCTGGGAGTATTACTTACAGC 252  
Db 9 CTGCAGCATGGCTGGTGAATGATGTTCTCTCTGGGAGTATTACTTACAGC 68

QY 253 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTGCAAGGCTGAAATTTATCTCAAAAGA 312  
Db 69 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTGCAAGGCTGAAATTTATCTCAAAAGA 128  
QY 313 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372  
Db 129 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188  
QY 373 TACCTTCCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCAATATT 432  
Db 189 TACCTTCCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCAATATT 248  
QY 433 TTTCAATTCGACCTGGTTTAAATATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACAC 492  
Db 249 TTTCAATTCGACCTGGTTTAAATATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACAC 308  
QY 493 CAGAAGAGATGAATCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCAT 552  
Db 309 CAGAAGAGATGAATCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCAT 368  
QY 553 CAGGTACTTAAGGCATATATCAAGCTCACTTTGTACGCTGTGGAACGGGGGCTTTTCA 612  
Db 369 CAGGTACTTAAGGCATATATCAAGCTCACTTTGTACGCTGTGGAACGGGGGCTTTTCA 428  
QY 613 TCCAAATTTGACCTACTATTGAAATTTGGACATCATCTGAGGACATATATTTTAAAGCTGA 672  
Db 429 TCCAAATTTGACCTACTATTGAAATTTGGACATCATCTGAGGACATATATTTTAAAGCTGA 488  
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Db 549 ATCCCTTTTAAATAGATGAGAAATTTATCTCTGGAACCTGAGTGAATTTTATGGGGCGAGA 608  
QY 793 CTTTGTCTATCTTCGGAACCTTTGGGACACACACCACCAATCAGGACAGAGCATGATTC 852  
Db 609 CTTTGTCTATCTTCGGAACCTTTGGGACACACACCACCAATCAGGACAGAGCATGATTC 668  
QY 853 CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCACCTCATCTCAGAGAGTGAACAATCC 912  
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QY 913 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGAGAACCTCTGG 972  
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QY 973 AAAAGCTACTCAACGCTAGATAGGTTCAGATATGCAAGAAATGACCTTTGGAGGGCACAGAAG 1032  
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QY 1033 TCTGTGTAATTAATGGAACAACATTCCTCAAGCTGCTGTGATTTGCTCAGTGGCCAGGTCC 1092  
Db 849 TCTGTGTAATTAATGGAACAACATTCCTCAAGCTGCTGTGATTTGCTCAGTGGCCAGGTCC 908  
QY 1093 AAATGGCAATTCGACACTCACTTTTGTGATGAATCAGAGTGTATTCCTTAATGAATTTTAAAGA 1152  
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1333 AGGAACTTCTCCAGCAAAACATTTGGTGGTTTGAATCTCAAGAGGACCTTCTGTATGA 1392  
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 2289 CAGGAGGACCCACGAAATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCAATTAACCTCTAGA 2348  
 2533 AACCTCAAAACAAAGTGAAGAACTTGCCTAGACAAATACTGGAAGAAACAAATGCAATATACAT 2592  
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 2593 GAACCTTTTTCATGTCATTTATGTCATGATGTTTACAATGGTGGAAATTCAGCTGAGTTCCA 2652  
 2409 GAACCTTTTTCATGTCATTTATGTCATGATGTTTACAATGGTGGAAATTCAGCTGAGTTCCA 2468  
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 2469 CCAATTAATAAATAAATCCATGAGTAACTTTCTCTAATAGGCTTTTTTTTTC 2518

RESULT 8  
 US-10-723-860-6714  
 ; Sequence 6714, Application US/10723860  
 ; Publication No. US20040253606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aziz, Natasha  
 ; APPLICANT: Ginsburg, Wendy M.  
 ; APPLICANT: Zlotnik, Albert  
 ; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
 ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
 ; FILE REFERENCE: 05882.0193.NPUS01  
 ; CURRENT APPLICATION NUMBER: US/10723,860  
 ; CURRENT FILING DATE: 2003-11-26  
 ; PRIOR APPLICATION NUMBER: 60/429,739  
 ; PRIOR FILING DATE: 2002-11-26  
 ; NUMBER OF SEQ ID NOS: 8393  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 6714  
 ; LENGTH: 3023  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-723-860-6714

Query: Match 92.6%; Score 2508.4; DB 18; Length 3023;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 9 CTGCAGCATGGCTGGTTAACTAGGATTTGCTCTTTCTGGGAGTATTACTTACAGC 68  
 253 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTCAGGCTGAAATATCTTACAAAGA 312  
 69 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTCAGGCTGAAATATCTTACAAAGA 128  
 313 AATGTTGGAATCCAACTATGTCATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372  
 129 AATGTTGGAATCCAACTATGTCATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188  
 373 TACCTTCTCTTTGGATGAGGAACGGATAGGCTGTATGTTGGAGCAAGGATCACATATT 432  
 189 TACCTTCTCTTTGGATGAGGAACGGATAGGCTGTATGTTGGAGCAAGGATCACATATT 248  
 433 TTCATTTCGACCTGGTTTAAATATCAAGATTTTCAAAAGATTTGTTGGCCAGTATCTTACAC 492  
 249 TTCATTTCGACCTGGTTTAAATATCAAGATTTTCAAAAGATTTGTTGGCCAGTATCTTACAC 308  
 493 CAGAAGAGATGAATCAAGTGGGCTCGAAAGACATCTCTGAAAGAAATGTGCTAAATTTCAAT 552  
 309 CAGAAGAGATGAATCAAGTGGGCTCGAAAGACATCTCTGAAAGAAATGTGCTAAATTTCAAT 368  
 553 CAAGGTACTTAAAGGATATTAATCAGACTCATTGTACGCTGTGGACCGGGGCTTTTCA 612



369	DB	CAAGGTACTTAAAGGCATATAATCAGACTCATTCTGTAGCCCTGTGGAAACGGGGCGCTTTTCA	428
613	QY	TCCAAATTTGCACCTACATATTGAAATTTGGACATCATCTCTGAGGACAATAATTTTTTAAGCTGGGA	672
429	DB	TCCAAATTTGCACCTACATATTGAAATTTGGACATCATCTCTGAGGACAATAATTTTTTAAGCTGGGA	488
673	QY	GAACTCACATTTTTGAAAAACGGCCGTGGGAGAGTCCCATATGACCCTTAAGCTGCTGACAGC	732
489	DB	GAACTCACATTTTTGAAAAACGGCCGTGGGAGAGTCCCATATGACCCTTAAGCTGCTGACAGC	548
733	QY	ATCCCTTTTAATAGATGAGAAATTTATACTCTGTGAAATCTGCAGCTGATTTTTATGGGGCCAGA	792
549	DB	ATCCCTTTTAATAGATGAGAAATTTATACTCTGTGAAATCTGCAGCTGATTTTTATGGGGCCAGA	608
793	QY	CTTTTGTCTATCTTCCGAACCTTTGGGCAACCAACCCAAATCAGGACAGAGCATGATTC	852
609	DB	CTTTTGTCTATCTTCCGAACCTTTGGGCAACCAACCCAAATCAGGACAGAGCATGATTC	668
853	QY	CAGGTGGCTCAATGATCAAAAGTTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAAATCC	912
569	DB	CAGGTGGCTCAATGATCAAAAGTTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAAATCC	728
913	QY	TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTCG	972
729	DB	TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTCG	788
973	QY	AAAAGCTACTCACGCTAGATAGTGCAGATATGCAAGAATGACTTTTGGAGGGCACAGAAG	1032
789	DB	AAAAGCTACTCACGCTAGATAGTGCAGATATGCAAGAATGACTTTTGGAGGGCACAGAAG	848
1033	QY	TCTGGTGAATAAAATGGGCAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCACAGTCC	1092
849	DB	TCTGGTGAATAAAATGGGCAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCACAGTCC	908
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909	DB	AAATGGGCAATTCGACACTCATTTTGTATGAACTGCAGGATGTATTCCTAATGAACCTTTAAAGA	968
1153	QY	TCCTTAAAAATCCAGCTGTGTATGAGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATC	1212
969	DB	TCCTTAAAAATCCAGCTGTGTATGAGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATC	1028
1213	QY	AGCCGTGTGTATGTATAGCATAGTGTATGTAGAGAGGTGTCTTGTTCCATATGCCCCA	1272
1029	DB	AGCCGTGTGTATGTATAGCATAGTGTATGTAGAGAGGTGTCTTGTTCCATATGCCCCA	1088
1273	QY	CAGGGATGGACCCAACTATCAATGGGTGCCCTTATCAAGGAAGAGTGCCTTATCCAGCGGC	1332
1089	DB	CAGGGATGGACCCAACTATCAATGGGTGCCCTTATCAAGGAAGAGTGCCTTATCCAGCGGC	1148
1333	QY	AGGAACTTGTCCCAGCAAAAACATTTGGTGGTGTTTTGACTCTACAAAGGACCTTCTCTGATGA	1392
1149	DB	AGGAACTTGTCCCAGCAAAAACATTTGGTGGTGTTTTGACTCTACAAAGGACCTTCTCTGATGA	1208
1393	QY	TGTTTAAACCTTTTCAGAAAGTCAATCAGCCATGTACAAATCCAGTGTTCCTATGAACAA	1452
1209	DB	TGTTTAAACCTTTTCAGAAAGTCAATCAGCCATGTACAAATCCAGTGTTCCTATGAACAA	1268
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1269	DB	TCGCCCAATAGTGAATCAAAACGGATGAAATTTATCAATTTACAAATTTGCTGTAGACCG	1328
1513	QY	AGTGGATGCAGAGATCGCAGTATGATGTATGTTTTATCGGAACAGATGTTTGGGACCGT	1572
1329	DB	AGTGGATGCAGAGATCGCAGTATGATGTATGTTTTATCGGAACAGATGTTTGGGACCGT	1388
1573	QY	TCTTTAAAGTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTTTAAAGAGAGTTCCTGTGGA	1632
1389	DB	TCTTTAAAGTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTTTAAAGAGAGTTCCTGTGGA	1448
1633	QY	AGAAATGACAGTTTTTTCGGAAACCGACTGCTATTTTACGAAATCGAGGATTTTCCACTAAGCA	1692
1449	DB	AGAAATGACAGTTTTTTCGGAAACCGACTGCTATTTTACGAAATCGAGGATTTTCCACTAAGCA	1508

QY	1693	GCAACAACTATATATATGGTTCACACGGCTGGGGTTGCCAGCTCCCTTTACACGGTGTGA	1752
DB	1509	GCAACAACTATATATGGTTCACACGGCTGGGGTTGCCAGCTCCCTTTACACGGTGTGA	1568
QY	1753	TATTTACGGGAAAGCGTGTGCTGAGTGTTCGCTCGCCCGAGACCTTTACTGTGCTCGGA	1812
DB	1569	TATTTACGGGAAAGCGTGTGCTGAGTGTTCGCTCGCCCGAGACCTTTACTGTGCTCGGA	1628
QY	1813	TGGTTCTGCATGTTCTCGCTATTTTCCCATGCAAGAGAGACGCAACAGACGACAAATAT	1872
DB	1629	TGGTTCTGCATGTTCTCGCTATTTTCCCATGCAAGAGAGACGCAACAGACGACAAATAT	1688
QY	1873	AAGAAATGGAGACCCACTGACTCACTCTTCAGACTTACACATGATAATCACCATGCGCA	1932
DB	1689	AAGAAATGGAGACCCACTGACTCACTCTTCAGACTTACACATGATAATCACCATGCGCA	1748
QY	1933	CAGCCCTGAAGAGAGAAATCATCTATGGGTAGAGAAATAGTAGACATTTTTTGAATGCGAG	1992
DB	1749	CAGCCCTGAAGAGAGAAATCATCTATGGGTAGAGAAATAGTAGACATTTTTTGAATGCGAG	1808
QY	1993	TCCGAAGTCGACAGACGGCTGGTCTATTTGGCAATTCACAGAGCGAAATCAAGAGCGAAA	2052
DB	1809	TCCGAAGTCGACAGACGGCTGGTCTATTTGGCAATTCACAGAGCGAAATCAAGAGCGAAA	1868
QY	2053	AGAAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGGCTTCTGCTACGTAG	2112
DB	1869	AGAAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGGCTTCTGCTACGTAG	1928
QY	2113	TCTACACAGAAAGATTCAGGCAATTAACCTTCGCATCGGTCGGAACATGGGTTCAATACA	2172
DB	1929	TCTACACAGAAAGATTCAGGCAATTAACCTTCGCATCGGTCGGAACATGGGTTCAATACA	1988
QY	2173	AACCTTTCTTAAAGGTAAACCTTGGAGTCAATTGACACAGAGCATTTTGGAGAACTTCTTCA	2232
DB	1989	AACCTTTCTTAAAGGTAAACCTTGGAGTCAATTGACACAGAGCATTTTGGAGAACTTCTTCA	2048
QY	2233	TAAAGATGATGATGGAGATGGCTCTAAGACCAAGAGAAATGTCCAAATAGCATGACACCTAG	2292
DB	2049	TAAAGATGATGATGGAGATGGCTCTAAGACCAAGAGAAATGTCCAAATAGCATGACACCTAG	2108
QY	2293	CCAGAAAGTCTGGTACAGAGACTTCATGACAGTCTCATCAACCCCAATCTCAACACGAT	2352
DB	2109	CCAGAAAGTCTGGTACAGAGACTTCATGACAGTCTCATCAACCCCAATCTCAACACGAT	2168
QY	2353	GGATGAGTCTGTGCAACAGTTTGGAAAAAGGGACCGAAACACAGTCGCGCAAGGCCAGG	2412
DB	2169	GGATGAGTCTGTGCAACAGTTTGGAAAAAGGGACCGAAACACAGTCGCGCAAGGCCAGG	2228
QY	2413	ACATACCCCGAGGAAACAGTAAACAAATGGAAAGCACTTACAGAAAAATAGAAAGGTAGAAA	2472
DB	2229	ACATACCCCGAGGAAACAGTAAACAAATGGAAAGCACTTACAGAAAAATAGAAAGGTAGAAA	2288
QY	2473	CAGGAGACCCACGAAATTCAGAGGGCACCCAGGAGTGTCTGAGCTGCATTAACCTCTAGA	2532
DB	2289	CAGGAGACCCACGAAATTCAGAGGGCACCCAGGAGTGTCTGAGCTGCATTAACCTCTAGA	2348
QY	2533	AACCTCAAAACAGTAGAAACTTCCTAGACAAATPAACCTGGAAAAACAAATGCAATATACAT	2592
DB	2349	AACCTCAAAACAGTAGAAACTTCCTAGACAAATPAACCTGGAAAAACAAATGCAATATACAT	2408
QY	2593	GAACTTTTTTCATGGCAATATGTGGATGTTTCAATGTTGGGAAATTCAGCTCAGTTTCCA	2652
DB	2409	GAACTTTTTTCATGGCAATATGTGGATGTTTCAATGTTGGGAAATTCAGCTCAGTTTCCA	2468
QY	2653	CCAATTATAAATAAATCCATGATGTAACCTTCTTAATAGCTTTTTTTC	2702
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; Publication No. US20030232411A1
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE THEREOF
; FILE REFERENCE: Q59878
; CURRENT APPLICATION NUMBER: US/10/404,438
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/582,419A
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: PCT/JP98/05952
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: P. Hei. 9-358811
; PRIOR FILING DATE: 1997-12-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-404-438-2

Query Match      26.5%; Score 718.6; DB 17; Length 2331;
Best Local Similarity 61.9%; Pred. No. 1.2e-202;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

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QY 329 AATGTGATCACTTTCATGGCTTGGCCACAGCTCCAGTATATCATCACTTCTTTGGAT 388
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QY 389 GAGGAACGAGTAGGCTGTATGTGGAGCAAAAGGATCAATATTTTCATTCGACCTGGTT 448
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QY 449 AA---TATCAAGGATTTTCAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGAA 505
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QY 506 TCCAGTGGGCTGGAAAGACATCTGAAAGATGTGCTAAATTTTCATCAGTACTTAAG 565
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QY 566 GCATATAATCAGACTCACCTTGTAGGCTGTGGAACGGGGCTTTTCATCCAAATTTGCACC 625
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DB 949 GGGGAGATATCTTCTTGTGAGCTTCAAGATATTTATTTACTCCCAAGAGATGAA 1008

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DB 1069 GTTGTGTATAGCATGCTGATCAGAGCAGTTTTTAATGGTCCATATGCTCATAG 1128

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QY 1634 GAAATGACAGATTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTTCCACTAAGCAG 1693
DB 1486 GAGTTGAGATATTTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGGAAGCAG 1545

QY 1694 CAACAACTATATATTTGGTTTCAACGGCTGGGTTGCCAGTCCCTTTTACACCGGTGAT 1753
DB 1546 CAACAAATTTGATTTGTTTCCGAGATGGAATTTAGTTTCAGCTCTCTCTTGCACAGATGCGAC 1605

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QY 1814 GGTTCCTGATGTTCTGCTATTTTCCCACTGCAAGAGAGACGCAAGAGCAAGATATA 1873
DB 1666 GGAATGATGCTCTGATATGCTCTACTTCTAAAGAGAGAGCTAGACGCCAAGATGTA 1725

QY 1874 AGAAATGGAGACCCCACTGACTCATCTGTTTCAGATTTTACACATGATTAATCACCATGGCCAC 1933
DB 1726 AAATATGGGACCCCAATCACCCAGTGTGGGACATCGAAGACAGCATTTAGTCATG---AA 1782

QY 1934 AGCCCTGAAGAGAGAAATCATCTATGTTGTAGAAATAGTAGCACAATTTTGGAAATGCACT 1993
DB 1783 ACTGCTGATGAAGAGGATGATTTTGGCAATTTAACTCAACCTTCTTGGAAATGATA 1842

QY 1994 CGGAAGTCCGAGAGAGCGCTGCTGCTATTTGGCAATTTTCCAGAGGCGGAAATGAAGAGCGAAA 2053
DB 1843 CCTAAATCCCAACAAGCAACTATTTAAATGGTATATCCAGAGGTGAGGAGATGAGCATCGA 1902

QY 2054 GAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCGCTTCTGCTACGTAGT 2113

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Qy 2114 CTACACAGAGAATTACCGAATTAACCTGCGCATGCGGTGGAAACATGGGTTTCAACAA 2173
Db 1963 TTGCAGAGAAGGATTTCTGGGATGTATTACTGCAAAAGCCGAGGACACACTTTTCATCCAC 2022
Qy 2174 ACTCTTCTTAAGTAACCTGGAAGTCATTGACACAGAGCAATTTGGAAGCACTTCTTCAT 2233
Db 2023 ACCATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2082
Qy 2234 AAAGATGATGATG 2246
Db 2083 GCAGAGCATGAGG 2095

RESULT 10
US-09-946-374-309
; Sequence 309, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
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; PRIOR APPLICATION NUMBER: 60/101743
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215	ACTTTGAAGCAAAATATTTCCAGACTCAAGCTAACCTTACAANGACTTGTCTTTCAAAT	274		
329	AATGTGATCACATTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTCTTTTGGAT	388		
275	AGCTGTATTTCCCTTTTGGGTTTCATCAGAAGGAGCTGGATTTTCAAACTCTTCTCTTGAAT	334		
389	GAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATTTTTCATTCGCAGCTCGTT	448		
335	GAGGAAGAGGAGGAGGCTGCTCTTGGGAGCCAAAGACCAATCTTTTCTACTCAGTCTCGTT	394		
449	AA---TATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGAA	505		
395	GACTTAAACAAAAATTTTAAAGAGATTTATTTGGCTGCTGCAAGGAACGGGTGGAATTA	454		
506	TCAAAGTGGCTGGAAAAGACATCTGAAAGAAATGTGCTAATTTTCATCAAGGTACTTTAAG	565		
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515	CCCTATAACAAACTCACATATATGTGTGGAACTGGAGCATTTTCACATATATGTGGG	574		
626	TACATTGAAATGGACATCATCTCGAGGACAATATTTTAAAGCTGGAGAACTCAATTTT	685		
575	TATATTGATCTTGGAGTCTCAAGGAGGATATTTATTTCAAACCTAGACACACATAAATTG	634		
686	GAAACGGCGGTGGGAAGAGTCCATATGACCTTAAGCTGTGTGACAGCATCTCCTTTTAAATA	745		
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746	GATGAGAAATATATCTCTGGAACTGACGCTGATTTTATGGGGCGAGACTTTGTCTATCTTC	805		
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806	CGAACTCTTGGGC-----ACACACCAAAATCAGGACAGAGCAGCATGATTCACGG	856		
755	CGATCCCTTGGCCCTACTCATGACCCACTACATCAGAACTGACATTTTCAGAGCACTAC	814		
857	TGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGCAATCTTGAA	916		
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977	GCTACTCAGCTAGGAATAGGTGAGATATGCAAGAAATGATCTTGGAGGGGACAGAAAGTCTG	1036		
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1037	GTGAAATAATGACAAACATCTCTCAAAGCTCGTCTGATTTGCTCAGTGGCCAGGTCCTAAAT	1096		
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1217	GTGTGTATGATAGCATCAGTGTATGTGAAAGGGTGTTCCTTGTGTCATATGCCACAGG	1276		
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;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 26.5%; Score 718.6; DB 13; Length 3871;

Best Local Similarity 61.9%; Pred. No. 1.6e-202;  
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DB 275 AGCTGTATTCCTTTTGGGTTTCATCAGAAGGACTGGATTTTCAAACTCTTCTCTTAGAT 334  
QY 389 GAGGAACGAGTAGGCTGTATCTTTGGAGCAAGGATCATATTTTCATTCGACCTGGTT 448  
DB 335 GAGGAAGAGGCAGGCTGCTCTTTGGAGCCAAAGACCACATCTTCTTACTCATGCTGGTT 394  
QY 449 AA---TATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAAGAGAGATGAA 505  
DB 395 GACTTAACAAAATTTTAAGAGATTTATTGGCTGCTGCGCAAGAGCGGTGGATTA 454  
QY 506 TCGAAGTGGGCTGGAAAAGACATCTCTGAAGAATGTGCTTAATTTTCATCAAGGTACTTAAG 565

Db 455 TGTAAATAGCTGGAAAGATGCAATACAGAAATGCAAAATTCATCAGAGTACTTCAG 514  
 QY 566 GCATATAATCAGACTCATTGTAGCGCTGTGGAAACGGGGCTTTTCAATCAATTTTCACCC 625  
 Db 515 CCCTATAACAAACTCACATATATGTGTGGAACTGGAGCAATTCATCAATATATGGG 574  
 QY 626 TACATTTGAAATTTGACATCATCTCGAGGACAAATATTTTAAAGCTGGAGAACTCACATTTT 685  
 Db 575 TATATTGATCTTGGAGCTTACAAGGAGGATATATATTCAAATAGACACACATATTTG 634  
 QY 686 GAAACCGCGCTGGGAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAAATA 745  
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 QY 746 GATGGAGAAATATACCTCTGGAAGTGCAGCTGATTTTATGGGGGAGACTTTGCTATCTTC 805  
 Db 695 GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTTCTTGGCAAGATATGCTGATTTCACT 754  
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 Db 875 GATGATAAATATATTTCTTTCTGTTGAACTCATCTCAAGAGGCGATGCTCCGATATA 934  
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 QY 1037 GTGAATAATGACAACTTCCTCAAGCTCGTGTGATTTGCTGATGCTGCGAGGTCCAAT 1096  
 Db 995 ATAAACAAGTGGACGACTTTCTTAGGCGCAGACTGATTTGCTCAATTTCTGGAAGTGT 1054  
 QY 1097 GGCATTGACACTCATTTTCATGAATGACAGGATGATTTCTTAATGAATTTAAAGATCT 1156  
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 QY 1337 ACTGTGCCAGCAAAACATTTG---GTGGTTTGAATCTTACAAAGGACCTTCTCTGATGAT 1393  
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 QY 1394 GTTATAACCTTTGCAAGAGTATCCAGCCATGTCATCAATCCAGTGTTCCTATGAACAT 1453  
 Db 1355 GTCATCAGTTTCATAAGCGGCACCTCTGTGATGTATAAGTCCGTATATCCAGTTCACAGGA 1414  
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 Db 1475 GTCAATGGCAGAGATGGCCAGTACGATGATGATGTTTCTTGGAAACAGACATTTGGAATGTC 1534  
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 QY 1634 GAAATGACAGTTTTCGGGAACCGACTGCTATTTCAGCAATGGAGCTTTTCCACTAAGCAG 1693  
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 QY 1994 CGAAGTCGACAGAGCGCTGCTCTATTGGCAATTTCCAGAGCGGAAATGAAGAGCGAATA 2053  
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RESULT 12

US-10-174-590-347  
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 ; Publication No. US20030008352A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
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 ; APPLICANT: Pan, James  
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 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: ACIDS ENCODING THE SMO  
 ; FILE REFERENCE: P3430R1C42  
 ; CURRENT APPLICATION NUMBER: US/10/174,590  
 ; CURRENT FILING DATE: 2002-06-18  
 ; Prior application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 347  
 ; LENGTH: 3871  
 ; TYPE: DNA



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US-10-174-590-347			
Query Match		26.5%; Score 718.6; DB 14; Length 3871;	
Best Local Similarity		61.9%; Pred. No. 1.6e-202;	
Matches 1233; Conservative		0; Mismatches 739; Indels 21; Gaps 5;	
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QY	329	AATGTGATCACTTTCAATGCTTGGCCACAGCTCCAGTTATCATACCTTCTCTTTGGAT	388
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QY	389	GAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGATCACATATTTTCATTCGACCTGGTT	448
DB	335	GAGGAAGAGGCGAGCTGCTTTGGGAGCCAAAGACCAATCTTCTACTCAGCTCTGTT	394
QY	449	AA---TATCAAGATTTTCAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGAA	505
DB	395	GACTTAAACAAAATTTTAAGAGATTTATTTGGCTGCTGCAAGGAACGGGTGGAATTA	454
QY	506	TGCAAGTGGGCTGGAAGACATCTCTGAAGATGTCTAAATTTTCATCAAGTACTTAA	565
DB	455	TGTAATTAAGTGGGAAGATGCAATACAGAATGTGCAAAATTTTCATCAGAGTACTTCAG	514
QY	566	GCATATAATCAGACTCACTTTGTACGCTGTGGAACGGGGCTTTTTCATCCAATTTTGCACC	625
DB	515	CCCTATAACAAACTACATATATGTGTGGAACTGGAGCATTTTCATCCATATGTGGG	574
QY	626	TACATTTGAATTTGGAATCATCTGAGGACAAATATTTTAAAGCTGGAGAACTCACATTTT	685
DB	575	TATATTTGATCTTGGAGTCTACAAAGGAGGATATATATTCAAAATAGACACACATAATTTG	634
QY	686	GAAACGGGCGTGGGAAGTCCATATGACCTTAAGCTGCTGACACATCCCTTTTAATA	745
DB	635	GAGTCTGGCAGACTGAAATGTCTTTCGATCTCAGCAGCCTTTTCTTCAGTAATGACA	694
QY	746	GATGGAGAATTAATCTCTGAACTGCGAGCTGATTTTATGGGCGAGACTTTGCTATCTTC	805
DB	695	GATGAGTACTCTCTCTGGAACAGCTTCTGATTTCTTGGCAAGATACCTGATTCAT	754
QY	806	CGAATCTTTGGGC-----ACCAACCCCAATCAGACAGAGCAGATGATCCAGG	856
DB	755	CGATCCCTTTGGGCTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTAC	814
QY	857	TGGCTCAATGATCCAAAGTTCATAGTGGCCCACTCATCTCAGAGAGTCAATCTGAA	916
DB	815	TGGCTCAATGGAGCAAAATTTTATTTGAACTTTCTTCATACCAAGACCTTCAATCCAGAT	874
QY	917	GATGACAAAGTATACCTTTCTTCCGTGAAATGCAATAGATGAGAACTCTGGA	976
DB	875	GATGATAAATATATTTCTTCTTCTGTAATCATCTCAAGAGGCAAGTACCTCCGATAAA	934
QY	977	GCTACTCAGCTAGAAATAGTTCAGATATGCAAGAAATGACTTTGGAGGGCAGAGAAGTCTG	1036
DB	935	ACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGTAGGAGGACAAACGACGCTG	994
QY	1037	GTGAATAATGGAACATCTCTCAAGCTGCTGATTTGCTCAGTGGCAGGTCCAAAT	1096
DB	995	ATAAACAGTGGAGCACTTTTCTTAAGGCGCAGACTGAITTTGCTCAATTTCTGGAAGTAT	1054
QY	1097	GGCATTGACACTCATTTTGTATGAACTGCAAGATGATTTCTTAATGAATTTTAAAGATCCT	1156
DB	1055	GGGGCAGATACCTTCTTGTATGAGCTTCAAGATATTTATTTACTTCCCAACAGAGATGAA	1114
QY	1157	AAAAATCCAGTTGTATATGAGTGTATGAGCTTCCAGTAAACATTTTCAAGGATCAGCC	1216
DB	1115	AGAAATCTGTATATGAGTCTTTTACTTACAAACAGCTCCATCTTCAAAGGCTCTGCT	1174
QY	1217	GTGTGTATATAGCATAGTATGTGAGAGGGTGTCTTGTGTCATATGCCCCACAGG	1276

RESULT 13  
US-10-176-758-347

DB	1175	GTTTGTGTATAGCATGCTGACATCAGACGAGTTTTTAATGGTCCATATGCTCATAAG	1234
QY	1277	GATGGACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCCTATCCAGGCGCAGGA	1336
DB	1235	GAAAGTGCAGACCACTGTTGGGTGCAGTATGATGGAGAAATTCCTTATCCAGGCGCTGGT	1294
QY	1337	ACTTGTCCCGCAAAACATTTG---GTGGTTTGTACTCTACAAAGACCTTCTCTGATGAT	1393
DB	1295	ACATGTCCAAGCAAAACCTTATGACCCACTGATTTAAGTCCACCGAGATTTTCCAGATGAT	1354
QY	1394	GTTATAACCTTTTGAAGAAGTCAATCCAGCCATGTACAAATCCAGTGTCTCTATGAACAAT	1453
DB	1355	GTATCATGTTTCAAAAGCGGCACCTCTGTGATGTATAGTCCGTATACCCAGTTGCGAGGA	1414
QY	1454	CGCCCAATAGTATGATCAAAACGGATGTAAATTAATCAATTTTACACAAATTTGCTGTAGACCGA	1513
DB	1415	GGACCAACCTTCAAGAGATCAATGTGGATTTACAGACTGACACAGATAGTGGTGGATCAT	1474
QY	1514	GTGGATGCAAGAGATGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGTT	1573
DB	1475	GTCAATTTGCAAGAAGATGGCCAGTACGATGTAAATGTTTCTTTGGAAACAGACATTTGGAACCTGTC	1534
QY	1574	CTTAAAGTAGTTTCAATTTCTTAAGGAGCTTGTGTATGATTTTGAAGAGAGTTTCTGTGGAA	1633
DB	1535	CTCAAAAGTTGTGAGCATTTTCAAGGAAAGTGG---AATATGGAAGAGGTAGTGTCTGGAG	1591
QY	1634	GAAATGACAGTTTTTGGGAACCGACTGTCTATTTTACAGCAATGGAGCTTTCCACTAAGCAG	1693
DB	1592	GAGTTGCAGATATTTCAAGCACTCATCAATCACTTTGAACATGGAATTTGCTCTGNAAGCAG	1651
QY	1694	GAACTATATATTTGGTTCAAGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGAT	1753
DB	1652	CAACAATTTGATATTTGGTTCCCGAGATGATTTAGTTTCACTCTCTTGCACAGATGCGAC	1711
QY	1754	ATTTAGGGAAGCGTGTCTGAGTGTCTGCTCGCCGAGAGCCCTTACTGTGCTCTGGGAT	1813
DB	1712	ACTTATGGGAAGCTTTGCCAGACATGTTGTCTTCCAGAGAGCCCTTACTGTGCTGGGAT	1771
QY	1814	GGTTCTGCACTGTCTCGCTATTTTCCACTGCAAAAGAGACGCAAGAGACAGACATATA	1873
DB	1772	GGAAATGCACTGCTCTCGATATGCTCTCTACTTCTTAAAGGAGAGCTAGAGCCCAAGATGA	1831
QY	1874	AGAAATGGAGACCACTGACTCACTGTTCAGACTTACACCATGATTAATCACCATGGCCAC	1933
DB	1832	AAATATGGCGACCAATCAACCAGTGTGCGGACATCGAAGACAGCATTTAGTCTATG---AA	1888
QY	1934	AGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACACATTTTGGAAATGCAAT	1993
DB	1889	ACTGCTGATGAAAGGTGATTTTGGCATTTGAATTTTAACTCAACCTTTCTGGAATGTATA	1948
QY	1994	CCGAAGTCCGAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGCAAAATGAAGAGCGAAAA	2053
DB	1949	CCTAATCCCAACAGCACTATTAAATGGTATATCCAGAGTTCAGGGATGAGCATCGA	2008
QY	2054	GAAAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCCCTTCTGTACCTAGT	2113
DB	2009	GAGGAGTTGAAGCCCGATGAAAGAAATCATCAAAACGGAATATGGGCTACTGATTCGAAGT	2068
QY	2114	CTACAACAGAGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAATGGGTTTCATACAA	2173
DB	2069	TTGCAGAAAGAGATTTCTGGGATGTTTACTCTCAAGCCCGAGGAGCACACTTTTCATCCAC	2128
QY	2174	ACTCTTTTAAAGTAAACCTCGAAGTTCATTGTGACAGAGCATTTTGAAGAACTTCTTTTCAT	2233
DB	2129	ACCATAGTGAAGTGAATTTGAAATGTCATTGAGATGAACAGATGGAATATCCAGAGG	2188
QY	2234	AAAGATGATGATG 2246	
DB	2189	GCAGAGCATGAGG 2201	

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: Sequence 347, Application US/10176758
: Publication No. US20030008353A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C104
: CURRENT APPLICATION NUMBER: US/10/176,758
: CURRENT FILING DATE: 2002-06-21
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 347
: LENGTH: 3871
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-176-758-347

```

Query Match	26.5%	Score 718.6	DB 14	Length 3871	
Best Local Similarity	61.9%	Pred. No. 1.6e-202			
Matches 1233	Conservative	0	Mismatches 739	Indels 21	Gaps 5
QY	269	AATGGGAGAACATGTGCCAAGGCTCAAAATATCCTACAAAGAAATGTTGGAAATCCAAC	328		
DB	215	ACTTTGAAGCAAAATATATCCAAGACTCAAGCTAACCTTACAAGACTTGTGCTTTCAAAT	274		
QY	329	AATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTCTCTTTTCGAT	388		
DB	275	AGCTGTATTCCTTTTGGTTCATCAGAAGGACTGGATTTTCAAATCTTCTCTTAGAT	334		
QY	389	GAGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATATTTCAATTCGACCTGGTT	448		
DB	335	GAGGAAAGAGCGAGGCTGCTCTTTGGGAGCCAAAGACCACATCTTTCTACTCAGTCTGGTT	394		
QY	449	AA---TATCAAGGATTTTCAAAGATTTGTGGCCAGTATCTTACACCAGAGAGATGAA	505		
DB	395	GACTTAACAAAATTTTAAAGAGATTTATTTGGCCCTGCTGCAAGGAACGGGTGGAAATTA	454		
QY	506	TGCAAGTGGCTTGGAAAAGACATCCTGAAAAGATGTGCTAAATTTTCATCAAGGTACTTTAAG	565		
DB	455	TGTAATTTAGCTGGGAAAGATGCCAATACAGATGTCAAAATTTTCATCAGAGTACTTCAG	514		
QY	566	GCATATAATCAGACTCACTTGTAGCCCTGTGGAAACGGGGGCTTTTCAATCAATTTGCACC	625		
DB	515	CCCTATAACAAAACCTCACATATATGTGTGGAACTGGAGCAATTTATCCAATATGTGGG	574		
QY	626	TACATTGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGGAGACTCACATTTT	685		
DB	575	TATATTTGATCTTGAGTCTCAAGAGGAGATTTATATTTCAAACCTVAGACACACATAATTTG	634		
QY	686	GAAACCGCCGTGGGAAGAGTCCATATGACCCCTAAAGCTGCTGACAGCATCCCTTTTAAATA	745		
DB	635	GAGTCTGGCAGACTGAAATGTCTCTTCGATCTCTCAGCAGCCTTTTGTCTCAGTAATGACA	694		
QY	746	GATGGAGAAATTACTCTGGAACCTGCAGCTGATTTTATGGGGGAGAGCTTTGTCTATCTTC	805		
DB	695	GATGAGTACTCTTACTCTGGAAACAGCTTCTGATTTTCCCTTGGCAAAAGATATCTGCATTCAC	754		
QY	806	CGAATCTTTGGGC-----ACCACCCCAATCAGGACAGCAGCATGATTTCCAGG	856		
DB	755	CGATCCCTTTGGGCTACTCATGACCCACTCATCATAGAACTGACATTTTCAGAGCACTAC	814		
QY	857	TGCTCAATGATCCAAGTTTCATTAGTGCCCACTCATCTCAGAGAGTGCATTCCTGAA	916		

815	DB	TGGCTCAATGGAGCAAAATTTATTGGAACTTTCTTTCATACAGACACCTCAAAATCCAGAT	874
917	QY	GATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGAGAACACTCTGGAAA	976
875	DB	GATGATAAAATATATTTCTTTCTGTTGAATCATCTCAAGNAGCAGTAGTCTCCGATATA	934
977	QY	GCTACTCAGCGTAGAATAGGTCAGATATGCAAGAATGACTTTGAGGGCACAGAGTCTG	1036
935	DB	ACCATCTCTTCTCCAGTTGGAAAGATTGTGAAGAATGATGTAGGAGGACCAACGCGAGCTG	994
1037	QY	GTGAATAAATGGACAAATCTCTCAAGCTCGTCTGATTTTGCTCAGTGCAGGTCCTCAAT	1096
995	DB	ATAAACAGTGGACGACTTTTCTTAAGCCAGACTGATTTGCTCAATCTCTGGAAGTGAT	1054
1097	QY	GGCAATGACACTCAATTTTGATGAACTCGACGATGATTTCTTAATGAACCTTTAAAGATCCT	1156
1055	DB	GGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTACTCCCAACAAGAGATGAA	1114
1157	QY	AAAAATCCAGTTGATATGGAGTGTTTACGACTTCAGTAAACATTTTCAAGGAGTACGCC	1216
1115	DB	AGAAATCCTGTAGTATAGGAGTCTTTACTACAAACGAGCTCCATCTTTCAAAGGCTCTGCT	1174
1217	QY	GTGTGTATGTATAGCATGAGTGTCAGAAAGGCTGTCTTGCTCCATATGCCACAGG	1276
1175	DB	GTTTGTGTATAGCATGGCTGACATCAGAGCAGTTTAAATGGTCCATATGCTCATAG	1234
1277	QY	GATGGACCAACTATCAATGGTGCTTTTCAAGGAAGAGTGCCCTATCAACGGCCAGGA	1336
1235	DB	GAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAATCCTTATCACGGCCTGGT	1294
1337	QY	ACTTGTCCACAGCAAAACATTTG--GTGGTTTTGACTCTCAAAAGGACCTTCCTGATGAT	1393
1295	DB	ACATGTCACAGCAAAACCTATGACCCACTGATTAAGTCCACCGAGATTTTCCAGATGAT	1354
1394	QY	GTTATAACCTTTGCAAGAAGTCATCCAGCCATGTACAATCCAGTGTTCCTATGAACAAT	1453
1355	DB	GTCAATCAGTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGAGGA	1414
1454	QY	CGCCCAATAGTGATCAAAAACGAGTGAATAATTATCAATTTACAAATTTGTCGTAGACCGA	1513
1415	DB	GGACCAACGTTCAAGAGATCAATGTGGATTCAGACTGACAGATAGTGGTGGATCAT	1474
1514	QY	GTGGATGCAGAAGTGGACATGATGTATGTTTATCGGAACAGATGTGGGACCGTT	1573
1475	DB	GTCAATGCAGAAGTGGCAGTACGATGTAATGTTCTTGGAAACAGACATTGGAACTGTC	1534
1574	QY	CTTAAAGTAGTTTCAATTCCTAAGGAGACTTGATATGATTTAGAAGGTTCTCTGGAA	1633
1535	DB	CTCAAAGTTTCAGCATTTCAAAGGAAAAGTGG--AATATGAAGAGGTAGTGTGGAG	1591
1634	QY	GAATGACAGCTTTTGGGAACCGACTGCTATTATTCAGCAATGGAGCTTTCCACTAAGCAG	1693
1592	DB	GAGTTGCAGATATTCAGCACTCATCAATCATCTTGAAATGATCTCTGTAAGCAG	1651
1694	QY	CAACAACATATATTTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGAT	1753
1652	DB	CAACAAATGTACATTTGGTTTCCGAGATGGAATTAGTTTCACTCTCTTTCACAGATGCGAC	1711
1754	QY	ATTTACGGGAAACGTGTGCTGAGTGTGCTCGCCGAGACCTTTACTGTGCTTGGGAT	1813
1712	DB	ACTTATGGGAAAGCTTTGCGCAGACTGTTGTTTGCAGAGACCCCTACTGTGCTGGGAT	1771
1814	QY	GGTCTGCAATGTTCTCGCTATTTTCCACTGCAAAAGAGACGCAACAAGACAAAGATATA	1873
1772	DB	GGAAATGCATGCTCTCGATATGCTCTACTTCTTAAAGGAGAGCTAGAGCCCAAGATGA	1831
1874	QY	AGAAATGGAGACCACTGACTACTGTCAGACTTACACCATGATTAATCACCATTGCCAC	1933
1832	DB	AAATATGGGACCCCAATCACCCAGTCTGGGACATCGAAGACAGCATTAGTCAATG--AA	1888
1934	QY	AGCCCTGAAGAGAGAAATCATCTATGGTGTAGAAATAGTAGCAATTTTTTGGAAATGCAGT	1993
1889	DB	ACTGCTGATGAAAGGTGATTTTTGGCATTTGAATTTAACTCAACCTTTCTGGAATGTATA	1948

Qy	1994	CCGAACTCGCAGACAGCGCTGGTCTATTGGCAATTCAGAGGCGAAATGAAGAGCGAAAA	2053
Db	1949	CCTAAATCCCCAACGAACAACATTAAATGGTATATCCAGAGGTGAGGGGATGAGCATCGA	2008
Qy	2054	GAAGAGATCAGAGTGAGTGCATCATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAGT	2113
Db	2009	GAGGAGTTGAGCCCGATGAAGAATCATCAAAAACGGAATATGGGCTACTGATTCGAAGT	2068
Qy	2114	CTACAAACAGAAAGGATTCAGGCCAAATTACTCTGCCATCGGTGGAAACATGGTTTCATACAA	2173
Db	2069	TTGCAGAAGAAGGATTCCTGGATGTATTACTGCAAGCCNAGGACACATTTTCATCCAC	2128
Qy	2174	ACTCTTCTTAAGGTAAACCTGGAAGTCATTGACACAGAGCATTGGGAAGAACTTCTTCAT	2233
Db	2129	ACCATAGTAGCTGACTTTTGAATGTATTGAGAATGAACAGATGGGAAAAATCCAGAGG	2188
Qy	2234	AAAGATGATGATG 2246	
Db	2189	GCAGAGCATGAGG 2201	

```

RESULT 14
US-10-175-737-347
; Sequence 347, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-347

```

Query Match	26.5%	Score 718.6	DB 14	Length 3871
Best Local Similarity	61.9%	Pred. No. 1.6e-202		
Matches 1233	Conservative 0	Mismatches 739	Indels 21	Gaps 5
Qy	269	AATGGGAAGACAAATGTGCCAAGGCTGAAATATTCCTACAAAGAAATGTGTGGAAATCCAAC	328	
Db	215	ACTTTGAAGCAAAATATTCDAAGACTCAAGCTAACCTTACAAGACTTGTCTTCAAAT	274	
Qy	329	AATGTGATCATCTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTCCTTTTGGAT	388	
Db	275	AGCTGTATTCCTTTTGGTTCATCAGAAGGACTGGATTTTCAAACCTCTTCTCTTAGAT	334	
Qy	389	GAGGAACGGAGTAGCGCTGTATGTGGAGCAAAAGGATCACATATTTTCATTCGACCTCGTT	448	
Db	335	GAGGAAGAAGCAGCGCTGCTCTTGGAGCCAAAGACCAATCTTTCTACAGTCTCGTT	394	
Qy	449	AA---TATCAAGGATTTTCAAAGATTTGTGTGGCCAGTATCTTACACCAGAAAGAGATGAA	505	
Db	395	GACTTAAACAAAAATTTTAAAGAGATTTATTGGCCCTGCTGCAAAAGGAACGGGTGGAATTA	454	
Qy	506	TGCAAGTGGGTGAAAAGACATCTGAAAGAAATGTCTAATTTTCATCAAGGTACTTTAAG	565	

Db	455	TGTAATTA	TACTGGG	AAAGATGCC	AATACAG	AATGTGCA	AAATTTTC	ATCAGAGT	ACTTTCAG	514
Qy	566	GCATATA	TAATCAG	ACTCACTT	GTAGCCT	GTGGAAC	CGGGGCTT	TTTCATCC	AAATTTGC	625
Db	515	CCCTATA	AAAAAACT	CACATAT	TGTGTG	TGGAAC	TGGAGCA	TTTTCATC	CAATATGT	574
Qy	626	TACATTG	AAATTTGG	ACATCATC	CTGAGG	ACAATAT	TTTTTAAG	CTGGAG	ACTCACAT	685
Db	575	TATATTG	ATCTTGG	AGTCTCA	AGGAGGA	TATTATAT	TTCAA	CTTAGC	ACACATAA	634
Qy	686	GA AAAA	CGCCGTGG	GAAGAGT	CCATATG	ACCCCTAA	GCCTGTG	ACAG	CATCCCTTTT	745
Db	635	GAGTCTG	GCAGACTG	AAATGCTC	TTTCGATC	CTCAGC	AGCCTTTT	GCTTCAG	TAAATGCA	694
Qy	746	GATGGAA	ATTATATCT	CTGAACTG	CAGCTG	ATTTTAT	TGGGGG	CGAGACTT	TGCTATCT	805
Db	695	GATGAGT	ACCTCTACT	CTGGAAC	AGCTTCTG	ATTTCTCT	TGGCAA	AGATAC	TGCAATCA	754
Qy	806	CGAACTC	TTGGGC-----	ACCAC	CCCCAATC	AGGACAG	CAGCAG	CATGAT	TCCAGG	856
Db	755	CGATCC	CTTGGG	CTACTCA	TAGCAC	CCACTAT	CATCAG	AACTG	CATTTCC	814
Qy	857	TGGCTCA	ATCATCC	AAAGTTCA	TTAGTGC	CCACTCAT	CTCAG	AGAGT	GACAACTC	916
Db	815	TGGCTCA	TGAGG	AAATTTAT	TGNACTTT	CTTCAT	CAGC	ACCTAC	ATCCAGAT	874
Qy	917	GATGACA	AAAGTATAT	CTTTTCTT	CCGTG	AAAAATG	CAATAG	ATGG	AGAACACT	976
Db	875	GATGATA	AAAAATAT	TTTCTTCT	TTTGGT	GAAATCAT	CTCA	AGAG	GCAGTAC	934
Qy	977	GCTACTC	ACCTAGA	TATAGT	GCAGAT	ATGCA	AGNATG	ACTTTGG	AGGGCAC	1036
Db	935	ACCATC	CTTCTCG	AGTTGGA	AGGTTT	GTAA	GAATGAT	GTAG	GAGGAC	994
Qy	1037	GTGAATA	AAATGG	CAACAT	TCCTCAA	AGTCGTCTG	ATTTGCTC	CAGTGC	CCAGGTC	1096
Db	995	ATAAAC	AGTGG	AGCACTTTT	CTTTA	GGCCAG	ACTGAT	TTTGCTCA	ATCTCG	1054
Qy	1097	GGCATTTG	ACACTCAT	TTTTTG	ATGA	CTGCAGG	ATGTAT	TCCTAA	TGAACTTT	1156
Db	1055	GGGCGA	GATACTTT	TGATG	AGCTTCA	AGATATTTAT	TTTACT	CCCC	CAACAG	1114
Qy	1157	AAAAATC	CACTTGTAT	TGAGTGT	TTTAC	CACTTCC	AGTAA	CATTTTCA	AGGGATC	1216
Db	1115	AGAAATC	CTGTAGT	ATATGG	AGTCTTT	PACTAC	AAACCA	CGTCCAT	CTTTCAA	1174
Qy	1217	GTGTGTAT	GTATAG	CATGAGT	GTGTG	CAGAA	GGGTGTTC	TGTGCT	CAATATGCC	1276
Db	1175	GTTTGTG	TATAG	CATGGCTG	ACATC	NAG	AGCAGT	TTTTTA	TGTCATATG	1234
Qy	1277	GATGGAC	CCCAACTAT	CAATGG	GTGCTTTAT	CAAG	AGAGATGCC	CTTATCC	ACGGCC	1336
Db	1235	GA AAGT	GCAGAC	CACTCG	TTGGGTG	CAGTATG	ATGGG	AGAAATC	CTTATCCA	1294
Qy	1337	ACTGTCC	CAGCAAA	CAATTTG--	GTGG	TTTTTG	CACTCA	AAAG	ACCTTCC	1393
Db	1295	ACATGT	CCAA	AGCAAA	ACCTAT	GAC	CCCA	CGAG	ATTTTCC	1354
Qy	1394	GTTATAC	CTTTTGC	AAAGTGC	ATCCAG	CCATGTAC	AAATCC	AGTGTTC	CTATG	1453
Db	1355	GTCA	TGATTT	CATAA	AGCG	CACTCTG	TGATGTAT	TAAGTCC	GTATAC	1414
Qy	1454	CGCCCA	TAGTGT	CAAAAC	CGGATG	TAAATAT	CAATTTA	CACAA	ATTGCTG	1513
Db	1415	GGACCA	CGTTCA	AGAGAA	TCATGT	TGGA	TTACAG	ACTG	ACACAG	1474
Qy	1514	GTGATG	CAGAA	TGACAG	TATGAT	TGTTAT	TGTTAT	CGGA	CAGATG	1573
Db	1475	GTCA	TTGC	AGAGA	TGCC	AGTAC	GTATGT	TTCTCG	GAACAG	1534
Qy	1574	CTTAA	AGTGT	TTCA	ATTC	TAA	GGAG	ACTTGG	TATGAT	1633
Db	1535	CTCA	AGTGTG	CAGCAT	TTCAA	AGGA	AAAGTGG---	AA	TATG	1591



; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082797  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/083495  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083496  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083499  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083559  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/084366  
 ; PRIOR FILING DATE: 1998-05-05  
 ; PRIOR APPLICATION NUMBER: 60/084414  
 ; PRIOR FILING DATE: 1998-05-06  
 ; PRIOR APPLICATION NUMBER: 60/084639  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084640  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084643  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085580  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085582  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085700  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/086023  
 ; PRIOR FILING DATE: 1998-05-18  
 ; PRIOR APPLICATION NUMBER: 60/086392  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/086486  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087098  
 ; PRIOR FILING DATE: 1998-05-28  
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 ; PRIOR FILING DATE: 1998-06-09  
 ; PRIOR APPLICATION NUMBER: 60/088722  
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 ; PRIOR FILING DATE: 1998-06-10

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 ; PRIOR APPLICATION NUMBER: 60/089653  
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 ; PRIOR APPLICATION NUMBER: 60/089653

Query Match 26.5%; Score 718.6; DB 14; Length 3871;  
 Best Local Similarity 61.9%; Pred. No. 1.6e-202;  
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGCAAAATGCGCAAGGCTGAAATATCTCTACAAAGAAATGTTGGAATCCAAC 328  
 DB 215 ACTTTGAAGCAAAATATTTCCAAGACTCAAGCTAACCTACAAAGACTTGTGCTTTCAAAAT 274  
 QY 329 AATGTGATCAGCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACACAGAGATGAA 505  
 DB 275 AGCTGATTCCTTTTGGGTTTCATCAGAGAGACTGGATTTTCAAACTCTTCTTAGAT 334  
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 DB 575 TATATTGATCTTGGAGTCTCAAGAGGAGATATTATTCAAACTAGACACACATAATTTG 634  
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 QY 746 GATGAGAAATTAATCTTGGAACTGAGCTGATTTTATGGGGCGAGACTTTTGTATCTTC 805  
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 Db 1055 GGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAGAGATGAA 1114  
 QY 1157 AAAAAATCCAGTTGTATATCGAGTGTATAGCACTTCCAGTAAACATTTTCAAGGGATCAGCC 1216  
 Db 1115 AGAAATCCGTGTAGTATATGGAGCTTTTACTACAAACAGCTCCATCTTCAAAGGCTCTGCT 1174  
 QY 1217 GTGTGTATGTATAGCATGATGTGAGAAGGGTGTCTTGTGCTCATATGCCACAGG 1276  
 Db 1175 GTTTGTGTATAGCATGCTGACATCAGACGAGTTTTTAATGGTCCATATGCTCATAG 1234  
 QY 1277 GATGGACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCACGGCCAGGA 1336  
 Db 1235 GAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAATTCCTTATCCACGGCTGCT 1294  
 QY 1337 ACTTGTCCAGCAAAACATTTG---GTGGTTTTGACTCTACAAAGGACCTTCTCTGATGAT 1393  
 Db 1295 ACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354  
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 QY 1874 AGAAATGGAGACCCACTGACTCAGTGTTCAGACTTACACCATGATAATCAACATGGCCAC 1933  
 Db 1832 AAATATGGCGACCCCAATCAACCAGTGTGGGACATCGAAGACAGCATTAGTCATG---AA 1889

QY 1934 AGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGATAGTAGACACATTTTGGAAATGCAGT 1993  
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 QY 1994 CCGAAGTCCGACAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAA 2053  
 Db 1949 CCTAAATCCCAACAGCAACTATTTAAATGGTATATCCAGAGGTGAGGGATGAGCATCGA 2008  
 QY 2054 GAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGT 2113  
 Db 2009 GAGGAGTTTGAAGCCCGATGAAAAGATCATCAAAACGGAATATGGCTACTGATTCGAACT 2068  
 QY 2114 CTACAAACAGAGGATTCAGGCAATTTACCTCTGCCATCGGTGGACATGGGTTCATCAA 2173  
 Db 2059 TTGCAGAAAGAGGATTTCTGGGATGTATTTACTGCAAAAGCCAGGAGCACATTTTCATCCAC 2128  
 QY 2174 ACTCTTTCTTAAGGTAAACCTCTGAAAGTCAATTTGACACAGAGCATTTTGGAAAGAACTTCTTCAT 2233  
 Db 2129 ACCATAGTGAAGCTGACTTTTGAATGTCTATTGAGATGAACAGATGGAATAATACCCAGAGG 2188  
 QY 2234 AAAGATGATGATG 2246  
 Db 2189 GCAGAGCATGAGG 2201

Search completed: March 10, 2005, 13:26:07  
 Job time : 2348 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 03:07:03 ; Search time 8640 Seconds  
(without alignments)  
11934.734 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 2709

Sequence: 1 aatctttatttcatcgatg.....aggcttttttctctaataacc 2709

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2232.4	82.4	2319	9	AY402636 Homo sapi
2	2052.2	75.8	2289	9	AY402637 Pan trogl
3	1764.6	65.1	2292	9	AY402638 Mus muscu
4	868.4	32.1	997	7	CN646558 ILLUMIGEN
5	723	26.7	723	4	BI870437
6	715.2	26.4	3317	3	AK052671 Mus muscu
7	715.2	26.4	3672	3	AK028900 Mus muscu
8	712	26.3	4248	3	AK031704 Mus muscu
9	701.2	25.9	714	7	CR789306
10	674.8	24.9	679	4	BM711125 UI-E-DX1-
11	667.6	24.6	849	7	CF726328 UI-M-HBO-
12	663.8	24.5	702	4	BM723807 UI-E-EO1-
13	624.8	23.1	777	7	CF742166 UI-M-HBO-
14	622.8	23.0	763	7	CN461035 UI-M-HBO-
15	620.2	22.9	2960	3	AK043634 Mus muscu
16	620.2	22.9	3154	3	AK033597 Mus muscu
17	620.2	22.9	3292	3	AK037034 Mus muscu
18	617	22.8	3287	3	AK048364 Mus muscu
19	615.4	22.7	828	7	CN534641 UI-M-HS0-
20	609.4	22.5	832	7	CN534073 UI-M-HO0-
21	596.4	22.0	2328	9	AY407760 Homo sapi
22	594.6	21.9	729	6	CD349263 UI-M-FY0-
23	590.4	21.8	900	6	CB196368 AGENCOURT
24	588.6	21.7	889	2	BF667677 602121773

25	586.8	21.7	719	7	CK636248	UI-M-HNO-
26	581	21.4	775	5	BU703431	UI-M-FOO-
27	577	21.3	725	5	CN457302	UI-M-HNO-
28	573	21.2	754	7	CN538762	UI-M-HS0-
29	567.4	20.9	699	6	CA327319	UI-M-FY0-
30	549.8	20.3	785	7	CO428820	UI-M-HX0-
31	548.8	20.3	689	7	CN460658	UI-M-HBO-
32	548	20.2	633	7	CN295126	170005326
33	543.8	20.1	604	4	BI183160	UI-M-PN-
34	543	20.0	804	7	CO430718	UI-M-HX0-
35	541.4	20.0	2307	9	AY407762	Mus muscu
36	537.8	19.9	773	5	BU515916	AGENCOURT
37	536.6	19.8	656	7	CF728356	UI-M-HBO-
38	524.2	19.4	3436	3	AK014333	Mus muscu
39	522.4	19.3	3884	3	AK034239	Mus muscu
40	518.4	19.1	804	5	BP730858	BP730858
41	514	19.0	1911	9	AY403382	Mus muscu
42	510	18.8	570	2	BE033028	133242 WA
43	506.8	18.7	510	6	CD216784	EST Y164
44	506	18.7	605	7	CO045601	UI-M-HO0-
45	504.2	18.6	3394	3	AK053632	Mus muscu

## ALIGNMENTS

RESULT 1	AY402636	2319 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY402636				
DEFINITION	Homo sapiens SEMA3A gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY402636				
VERSION	AY402636.1	GI:39758619			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2319)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2319)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..2319				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
gene	<1..>2319				
	/gene="SEMA3A"				
	/locus_tag="HCM1290"				
ORIGIN					
Query Match	82.4%;	Score	2232.4;	DB 9;	Length 2319;
Best Local Similarity	96.9%;	Pred. No.	0;		
Matches	2246;	Conservative	0;	Mismatches	70;
				Indels	3;
				Gaps	1;
QY	200	ATGGCTGGTAACTAGGATTGTCGTTCTTTCTGGGAGTATTACTTACACAGACGA	259		



Db 1 ATGGGCTGGTTAACTAGGATTGTCGTCTTTCTGGGGAGTATTACTTACAGCAAGAGCA 60  
Qy 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAGGCTGAAATTTATCTTACAAAGAAATGTTG 319  
Db 61 AACTATCAGAAATGGGAAGAACAAATGTGCCAGGCTGAAATTTATCTTACAAAGAAATGTTG 120  
Qy 320 GAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTC 379  
Db 121 GAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTC 180  
Qy 380 CTTTTCGATGAGAAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATTTTCATTC 439  
Db 181 CTTTTCGATGAGAAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATTTTCATTC 240  
Qy 440 GACCTGGTTAAATCAAGGATTTTCAAAAGATTGTGTGGAGCAAAAGGATCACATATTTTCATTC 499  
Db 241 GACCTGGTTAAATCAAGGATTTTCAAAAGATTGTGTGGAGCAAAAGGATCACATATTTTCATTC 300  
Qy 500 GATGAATGCAAGTGGGCTGGAAGACATCCCTGAAAGAAATGTCTAATTTTCATCAAGGTA 559  
Db 301 GATGAATGCAAGTGGGCTGGAAGACATCCCTGAAAGAAATGTCTAATTTTCATCAAGGTA 360  
Qy 560 CTTAAGGCATATAATCAGACTCACTTGACGCTGTGGAACCGGGCTTTTCATCCAAAT 619  
Db 361 CTTAAGGCATATAATCAGACTCACTTGACGCTGTGGAACCGGGCTTTTCATCCAAAT 420  
Qy 620 TGCACCTACATTTGAATTTGGACATCATCTCTGAGGACAAATTTTAAAGCTGAGAACTCA 679  
Db 421 TGCACCTACATTTGAATTTGGACATCATCTCTGAGGACAAATTTTAAAGCTGAGAACTCA 480  
Qy 680 CATTTTGAAGAACGGGCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGATCCCTT 739  
Db 481 CATTTTGAAGAACGGGCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGATCCCTT 540  
Qy 740 TTAATAGATGGAATTAATCTCTGGAATGACGCTGATTTTATGGGGGAGACTTTGCT 799  
Db 541 TTAATAGATGGAATTAATCTCTGGAATGACGCTGATTTTATGGGGGAGACTTTGCT 600  
Qy 800 ATCTTCGGAACCTTTGGGACACACCACTTGAAGATGACTTTGGAGGGCAGAGATCTGGTG 859  
Db 601 ATCTTCGGAACCTTTGGGACACACCACTTGAAGATGACTTTGGAGGGCAGAGATCTGGTG 660  
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Qy 1040 AATAAATGACAACTTCCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCTCAATGGC 1099  
Db 841 AATAAATGACAACTTCCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCTCAATGGC 900  
Qy 1100 ATTGACACTCATTTTGTATGAACTGAGAGATGATTCCTTAATGAACTTTAAAGATCCTAAA 1159  
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Qy 1160 AATCAGTTGTATATGGAGTGTATGAGTTCAGCTTCAGGTAACTTTTCAAGGGATCAGCCGTG 1219  
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Qy 1280 GACCCCACTATCAATGGGTGCTTATCAAGAGAGTCCCTATCCAGGGCCAGGAAT 1339  
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Qy 1340 TGTCCCGACAAAACAATTTGGTGGTGTGACTCTACAAAGGACCTTCTCTGATGATGTTATA 1399  
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Qy 1400 ACCTTTGCAAGAAGTCACTCCAGCCATGTACAAATCCAGTGTTCCTTATGAACAAATCGCCCA 1459  
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Qy 1460 ATAGTGATCAAAACCGATGTAAATTTATCAATTTTACACAAATTTGCTGAGACCGTTCCTAAA 1519  
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Qy 1937 CCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGACATTTTGGAAATGCACTCGG 1996  
Db 1741 CCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGACATTTTGGAAATGCACTCGG 1800  
Qy 1997 AAGTCGACAGAGAGCGCTGCTCTATTTGGCAATTCAGAGCGGAAATGAGAGCGGAAAAGAA 2056  
Db 1801 AAGTCGACAGAGAGCGCTGCTCTATTTGGCAATTCAGAGCGGAAATGAGAGCGGAAAAGAA 1860  
Qy 2057 GAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTCTA 2116  
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Qy 2117 CAACAGAGAGGATTCAGGCAATTTACTCTGCCATGCGGTGGAACTGGGTTTCATACAAACT 2176  
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Qy 2237 GATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATCACACCTAGCCAG 2296  
Db 2041 GATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATCACACCTAGCCAG 2100  
Qy 2297 AAGTCTGGTACAGAGACTTTCATGAGCTCATCAACCCCAATCTCAACACGATGGAT 2356  
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 DEFINITION genomic survey sequence.  
 ACCESSION AY402637  
 VERSION AY402637.1 GI:39758620  
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 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 (bases 1 to 2289)  
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 2289)  
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.

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DEFINITION
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genomic survey sequence.
ACCESSION
AY402638
VERSION
AY402638.1 GI:39758621
KEYWORDS
GSS.
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SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2292)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 2292)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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## RESULT 4

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DEFINITION (H8.252451), mRNA sequence.

ACCESSION CN646558  
VERSION CN646558.1 GI:47160001  
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ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 997)  
AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.  
TITLE Large-scale Rhesus Macaque cDNA Sequencing  
JOURNAL Unpublished (2003)  
COMMENT Contact: C. Magnus

ILLUMIGEN Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagnus@illumigen.com  
Sequenced on 2004.03.10. 794 Q20 bases.

PCR Primers  
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 BACKWARD: CACTATAGGCGCAATTGGTA  
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RESULT 5	BI870437	723 bp	mRNA	linear	EST 11-OCT-2001
LOCUS	603395690F1 NIH_MGC_90	723 bp	mRNA	linear	EST 11-OCT-2001
DEFINITION	603395690F1 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:5405519 5', mRNA sequence.	723 bp	mRNA	linear	EST 11-OCT-2001
ACCESSION	BI870437	723 bp	mRNA	linear	EST 11-OCT-2001
VERSION	BI870437.1	723 bp	mRNA	linear	EST 11-OCT-2001
KEYWORDS	EST.	723 bp	mRNA	linear	EST 11-OCT-2001
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ORGANISM	Homo sapiens	723 bp	mRNA	linear	EST 11-OCT-2001
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	723 bp	mRNA	linear	EST 11-OCT-2001
AUTHORS	NIH-MGC	723 bp	mRNA	linear	EST 11-OCT-2001
TITLE	NIH-MGC	723 bp	mRNA	linear	EST 11-OCT-2001
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	723 bp	mRNA	linear	EST 11-OCT-2001
COMMENT	Unpublished (1999)	723 bp	mRNA	linear	EST 11-OCT-2001
	Contact: Robert Strausberg, Ph.D.	723 bp	mRNA	linear	EST 11-OCT-2001
	Email: cgabbs-r@mail.nih.gov	723 bp	mRNA	linear	EST 11-OCT-2001
	Tissue Procurement: ATCC	723 bp	mRNA	linear	EST 11-OCT-2001
	CDNA Library Preparation: Life Technologies, Inc.	723 bp	mRNA	linear	EST 11-OCT-2001
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	723 bp	mRNA	linear	EST 11-OCT-2001
	DNA Sequencing by: Incyte Genomics, Inc.	723 bp	mRNA	linear	EST 11-OCT-2001
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	http://image.llnl.gov	723 bp	mRNA	linear	EST 11-OCT-2001
	Plate: LLNL12034	723 bp	mRNA	linear	EST 11-OCT-2001
	High quality sequence stop: 723.	723 bp	mRNA	linear	EST 11-OCT-2001

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Note: this is a NIH MGC Library."

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## ORIGIN

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Best Local Similarity 100.0%; Pred.No. 2.3e-196;
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DEFINITION		Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630019P03 product:SEMAPHORIN 3D PRECURSOR homolog [Homo sapiens], full insert sequence.
ACCESSION		AK052671
VERSION		AK052671.1 GI:26342870
KEYWORDS		HTC; CAP trapper.
SOURCE		Mus musculus (house mouse)
ORGANISM		Mus musculus
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS		1
TITLE		Carninci, P. and Hayashizaki, Y.
JOURNAL		High-efficiency full-length cDNA cloning
MEDLINE		Meth. Enzymol. 303, 19-44 (1999)
PUBMED		99279253
AUTHORS		2
TITLE		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.



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ORIGIN

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ACCESSION AK028900  
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 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5

THE PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3672)

ADACHI, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/

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VERSION AK031704.1  
KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159

REFERENCE 3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Kono, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 4248)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/

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CDS

FEATURES  
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COMMENT

JOURNAL

REFERENCE

JOURNAL

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 2060 ATCAGAGTGTATGATATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTATACAA 2119  
 2067 TTGAACCTGTAAGAGGATCATCAAACTGATATGGGCTACTGATTCGAGTGTGAG 2126  
 2120 CAGAAGGATTCAGGCAATTTACCTCTGCAATGGGTGGAACTGGTGTATACAAACTCTT 2179  
 2127 AAGAGGATTCGGGATGTTTACTTGAAGAGCAGAGGAGCAGCTTTTATCCACCAATA 2186

2180 CTTAAGAGTAACCTGGAAGTCAATTCACACAGAGCACTTTTGAAGA 2223  
 2187 GTGAAGCTGCTTGAATGCTCATTGAGATGACAGATGGAAGA 2230

CR789306 714 bp mRNA linear EST 01-OCT-2004  
 DKFZp45900365\_r1 459 (synonym: pcorl) Pongo pygmaeus cDNA clone  
 DKFZp45900365 5', mRNA sequence.

CR789306  
 CR789306.1 GI:53708188  
 EST.

Pongo pygmaeus (orangutan)  
 Pongo pygmaeus  
 Pongo pygmaeus  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 1 (bases 1 to 714)  
 Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,  
 Fobo, G., Han, M. and Wiemann, S.  
 Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)  
 Unpublished (2004)  
 Contact: MIPS  
 MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,  
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen  
 (Hilden/Germany) within the cDNA sequencing consortium of the  
 Human Genome Project. This clone (DKFZp45900365) is available at  
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
 Berlin, Germany. Please contact RZPD for ordering:  
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp45900365  
 Further information about the clone and the sequencing project is  
 available at http://mips.gsf.de/projects/cdna/.

Location/Qualifiers  
 1..714  
 /organism="Pongo pygmaeus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9600"  
 /clone="DKFZp45900365"  
 /tissue\_type="cortex"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="459 (synonym: pcorl)"  
 /note="Vector: pSport1\_Sfi; Site\_1: SfiIb; Site\_2: SfiIb"

FEATURES  
 source

Query Match 25.9%; Score 701.2; DB 7; Length 714;  
 Best Local Similarity 98.9%; Pred. No. 4.5e-190;  
 Matches 706; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 848 GATTCAGGTGGCTCAATGATCCAAAGTTCATTAGTGCCTCCTCATCTCAGAGGTGAC 907  
 1 GATTCAGGTGGCTCAATGATCCAAAGTTCATTAGTGCCTCCTCATCTCAGAGGTGAC 60

QY 908 AATCTGAGATGACAAAGTATCTTTTCTTCGTTGAAATGCAATAGATGGAGAACAC 967  
 61 AATCTGAGATGACAAAGTATCTTTTCTTCGTTGAAATGCAATAGATGGAGAACAC 120

QY 968 TCTGAAAGACTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTGGAGGGCAC 1027  
 121 TCTGAAAGACTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTGGAGGGCAC 180

QY 1028 AGAAGTCTGGTGAATATGACAACTTCCTCAAGCTCGTCTGATTTGCTCAGTGCCA 1087  
 181 AGAAGTCTGGTGAATATGACAACTTCCTCAAGCTCGTCTGATTTGCTCAGTGCCA 240

QY 1088 GGTCCAAATGCACTTGCACCTCATTTTGTATGCACTGAGGATGATTTCTTAATGAACCTTT 1147  
 241 GGTCCAAATGCACTTGCACCTCATTTTGTATGCACTGAGGATGATTTCTTAATGAACCTTT 300

QY 1148 AAGATCCTAAATCCAGTTGTTATGAGAGTGTTCAGATTCAGTAAACATTTTCAAG 1207

|||||  
301 AAGATGCTTAAATCAATGTATATGAGGTGTTTACGACTTCCAGTAACATTTTCAAG 360  
1208 GGATCAGCGGTGTATATAGCATGAGTGTGAGAGGGTGTCTTGGTCCATAT 1267  
361 GGATCAGCGGTGTATATAGCATGAGTGTGAGAGGGTGTCTTGGTCCATAT 420  
1268 GCCCAGGAGTGGACCCCACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTATCCA 1327  
421 GCCCAGGAGTGGACCCCACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTATCCA 480  
1328 CGGCCAGGAACTTGTCCAGCAAAACATTTGGTGGTTTGACTCTCAAGAGGACCTTCT 1387  
481 CGGCCAGGAACTTGTCCAGCAAAACATTTGGTGGTTTGACTCTCAAGAGGACCTTCT 540  
1388 GATGATGTTATACCTTTTGCAGAGTGCATCCAGCCATGTCAATCCAGTGTTCCTATG 1447  
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1448 ACAATCGCCCAATAGTATCAAAACGGATGTAAATATCAATTTACAAATTTGCGTA 1507  
601 ACAATCGCCCAATAGTATCAAAACGGATGTAAATATCAATTTACAAATTTGCGTA 660  
1508 GACCGAGTGGATGCAGAGATGCACAGTATGTTATCTTATCGGACAGAT 1561  
661 GACCGAGTGGATGCAGAGATGCACAGTATGTTATCTTATCGGACAGAT 714

RESULT 10  
BM711125  
LOCUS  
DEFINITION  
UI-E-DX1-agv-i-12-0-UI.r1 UI-E-DX1 Homo sapiens cDNA clone  
UI-E-DX1-agv-i-12-0-UI 5', mRNA sequence.  
BM711125  
BM711125.1 GI:19024383  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 679)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1. .679  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/issue\_type="fetal eyes"  
/dev\_stage="fetal"  
/lab\_host="PH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-DX1"  
/note="Organ: eye; Vector: p7T73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;

FEATURES  
source  
Location/Qualifiers  
1. .679  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-DX1-agv-i-12-0-UI"  
/issue\_type="fetal eyes"  
/dev\_stage="fetal"  
/lab\_host="PH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-DX1"  
/note="Organ: eye; Vector: p7T73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;

UI-E-DX1 is a normalized cDNA library containing the following tissue(s): fetal eyes. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCAAGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match 24.9%; Score 674.8; DB 4; Length 679;  
Best Local Similarity 99.6%; Pred. No. 1.8e-182;  
Matches 676; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1964 GAGAAATAGTAGCACATTTTGGAAATGCAGTCCGAAAGTCCGAGAGCGCTGGTCTATTGG 2023  
DB 1 GAGAAATAGTAGCACATTTTGGAAATGCAGTCCGAAAGTCCGAGAGCGCTGGTCTATTGG 60  
QY 2024 CAATTCAGAGCGGAAATGAAGCGGAAAGAGATCAGAGTGGATCATATCATC 2083  
DB 61 CAATTCAGAGCGGAAATGAAGCGGAAAGAGATCAGAGTGGATCATATCATC 120  
QY 2084 AGGACAGATCAAGGCTTCTGCTAGTCTTACAAAGAGGATTCAGGCAATACCTC 2143  
DB 121 AGGACAGATCAAGGCTTCTGCTAGTCTTACAAAGAGGATTCAGGCAATACCTC 180  
QY 2144 TGCCATTCGGGTGGAACATGGGTTTCATACAAACTCTTTAAAGGTAAACCTTGGAGTCA 2203  
DB 181 TGCCATTCGGGTGGAACATGGGTTTCATACAAACTCTTTAAAGGTAAACCTTGGAGTCA 240  
QY 2204 GACACAGAGCATTTGGAAGAACTTCTTCAAAAGATGATGGAGATGGCTCTAAGACC 2263  
DB 241 GACACAGAGCATTTGGAAGAACTTCTTCAAAAGATGATGGAGATGGCTCTAAGACC 300  
QY 2264 AAGAAATGTCCAAATAGCATGACACCTAGCCAGAGAGTCTGTTACAGAGACTTTCATGCAG 2323  
DB 301 AAGAAATGTCCAAATAGCATGACACCTAGCCAGAGAGTCTGTTACAGAGACTTTCATGCAG 360  
QY 2324 CTCATCAACCCCACTCAACAGCATGGATGAGTCTGTGAACAAGTCTTGGAAAGG 2383  
DB 361 CTCATCAACCCCACTCAACAGCATGGATGAGTCTGTGAACAAGTCTTGGAAAGG 420  
QY 2384 GACCGAAACAAACGTCGGCAAGGCGGACATACCCAGGGAACAGTAACAAATGGAAG 2443  
DB 421 GACCGAAACAAACGTCGGCAAGGCGGACATACCCAGGGAACAGTAACAAATGGAAG 480  
QY 2444 CACTTACAGAAATAAGAAAGTGAACACGAGGACCCACGAATTTTCAGAGGGGACCC 2503  
DB 481 CACTTACAGAAATAAGAAAGTGAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
QY 2504 AGGAGTGTCTGAGTGCATTTACTCTAGAAACCTCAAAACAGTAGAGAACTTGGCTAGACA 2563  
DB 541 AGGAGTGTCTGAGTGCATTTACTCTAGAAACCTCAAAACAGTAGAGAACTTGGCTAGACA 600  
QY 2564 ATAACTGGAAACAAATATGCAATATACATGAATCTTTTTCATGGGCAATATGATGGATGTT 2623  
DB 601 ATAACTGGAAACAAATATGCAATATACATGAATCTTTTTCATGGGCAATATGATGGATGTT 660  
QY 2624 ACAATGGTGGGAAATTCAG 2642  
DB 661 ACAATGGTGGGAAATTCAG 679

## RESULT 11

CF726328  
LOCUS  
DEFINITION  
UI-M-HB0-ckh-a-17-0-UI.r1 NIH\_BMAP\_HB0 Mus musculus cDNA clone  
CF726328  
EST 09-OCT-2003  
linear  
musculus cDNA clone

IMAGE:30547504 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF726328 1 GI:37600496  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 849)  
N1H-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-f@mail.nih.gov](mailto:cgapbs-f@mail.nih.gov)  
Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

FEATURES  
source

Seq primer: pYX-5.  
Location/Qualifiers  
1..849  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30547504"  
/tissue\_type="whole eye"  
/dev\_stage="embryo 12.5,13.5,14.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="N1H BMAP HB0"  
/note="Organ: Eye; Vector: pYX- Asc; Site: 1: EcoR I;  
Site: 2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is TTTATGAAGT. This library was created for the University  
of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 24.6%; Score 667.6; DB 7; Length 849;  
Best Local Similarity 88.2%; Pred. No. 2.3e-180;  
Matches 746; Conservative 0; Mismatches 98; Indels 2; Gaps 2;  
QY 241 ATTACTTACGACGAGCAAACTATCAGATGGGAAGACAATGTGCCAAGCTGAAT 300  
DB 1 ATTACTTACGACGAGCAAACTATCAGAAACGGAAGACAATGTGCCAAGCTGAAT 60  
QY 301 ATCTCAAGAAGAAATGTGGATCCCAACATGTGATCACTTCAATGGCTGGCCACAG 360  
DB 61 ATCGTCAAGAAGAAATGTGGATCCCAACATGTGATCACTTCAATGGCTGGCCACAG 120  
QY 361 CTCCAGTTATCATACCTCTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAA 420  
DB 121 CTCCAGTTACCAACCTCTCTCTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAA 180  
QY 421 GGATCATATTTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGGCC 480  
DB 181 AGATCATATATTTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGGCC 240  
QY 481 AGTATCTTACCAAGAGAGATGAATGCAAGTGGGCTGGAAGACATCTCTCAAGAAATG 540  
DB 241 AGTATCTTACCAAGAGAGATGAATGCAAGTGGGCTGGAAGATATCTCTGAAGAAATG 300

QY 541 TGTCTAATTTTCATCAAGGTACTTTAAGGCATATATAATCAGACTCACTTTGTAGCCCTGTGGAA 600  
DB 301 TGCCCAATTTTCATCAAGGTCTCTGGAGCTTATATAATCAGACTCACTTTGTATGCTGTGGAA 360  
QY 601 GGGGGCTTTTCATCCAAATTTGCACCTACATTTGAAATTTGGACATCATCTCTGAGGACAATAT 660  
DB 361 TGGGGCTTTTCATCCAAATTTGCACCTACATTTGAAATTTGGACATCATCTCTGAGGACAATAT 420  
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QY 721 GCTGCTGACAGCATCCCTTTTAAATAGATGGAGAATTTATCTCTGGAATCTGCAGCTGATTT 780  
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QY 781 TATGGGGCGAGACTTTTGTCTATCTTCCGAATCTCTGGGCAACCAACCAATCAGGACAGA 840  
DB 541 CATGGGACGGGACTTTGGCTATCTTCAGAAACACTGGGGCAACCATCACCCCATCAGGACGA 600  
QY 841 GCAGCATGATTCACAGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCACCTCATCTCAGA 900  
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QY 961 AGAACACTCTTGAAAAGTACTCACGCTAGATAGGTAGATATGATATGCAAGAAATGCAATAGATGG 1020  
DB 721 AGAACACTCTTGAAAAGTACTCACGCTAGATAGGTAGATATGATATGCAAGAAATGCAATAGATGG 779  
QY 1021 AGGGCAGCAGAGTCTGGTGAATAATGACACACATCTCTCAAGCTGCTGTGATTTGCTC 1080  
DB 780 TGGACACAGAGTCTTTGTGAATAATGAC-ACATTTCTANNAGCACGCGCTGATTTGCTC 838  
QY 1081 AGTGCC 1086  
DB 839 TGTGCC 844  
BM723807 702 bp mRNA linear EST 01-MAR-2002  
UI-E-E01-aix-o-04-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone  
UI-E-E01-aix-o-04-0-UI.5', mRNA sequence.  
BM723807 GI:19045138  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research







```

Db      62  TACAGCCAGACAACTATGCAACGGAAGAAACAAATGTGCCAAGACTGAAATATTCGTA 121
Qy      307  CAAGAAGATCTGGATCCACATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAG 366
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Db      182  TTACACACCTCTCTCTGGATGAGAAACGAGTGGCTGTATGTTGGAGCAAGGATCA 241
Qy      427  CATATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATC 486
Db      242  TATATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATC 301
Qy      487  TTACACAGAGATGCAATGCAAGTGGCTGGAAGAGACATCTCTCAAAAGATTTGTCTAA 546
Db      302  TTACACAGAGATGCAATGCAAGTGGCTGGAAGAGATCTCTCAAAAGATTTGTCTAA 361
Qy      547  TTTTCATCAAGGTACTTAAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAAACGGGGC 606
Db      362  TTTTCATCAAGGTACTTAAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAAACGGGGC 421
Qy      607  TTTTCATCAAGGTACTTAAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAAACGGGGC 666
Db      422  TTTTCATCAAGGTACTTAAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAAACGGGGC 481
Qy      667  GCTGGAGAGACTCATTTTGAAGCGCTGGAAGAGTCCATATGACCTCAAGCTGCT 726
Db      482  GCTGGAGAGACTCATTTTGAAGCGCTGGAAGAGTCCATATGACCTCAAGCTGCT 541
Qy      727  GACAGCATCCCTTTTAAATAGATGGAATATATCTCTGGAACCTGCAAGCTGATTTATGG 786
Db      542  GACTGCTCTCTTCTAATAGACGCTGATGTTACTCTGGAAGCTGTCGGACTTCATGG 601
Qy      787  GCGAGACTTGTCTCTGGAAGCTCTGGGACACACACCCCAATCAGAGAGAGAGCA 846
Db      602  ACGGAGCTTGTCTCTGGAAGCTCTGGGACACACACCCCAATCAGAGAGAGAGCA 661
Qy      847  TGATTCAGGTGCTCAATGATCCAAAGTTTCAATAGTCCCACTCTATCTCAGAGAGTCA 906
Db      662  TGATTCAGGTGCTCAATGATCCAAAGTTTCAATAGTCCCACTCTATCTCAGAGAGTCA 721
Qy      907  CAATCTGAGATGACAAAGTATA-CTTTTCTTCGTTGAAATGCAATAGATGA 961
Db      722  CACCCCTGAGATGACAAAGTATATTTTCTTCGAGAAATGCAATAGATGA 777

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RESULT 14

CN461035  
LOCUS  
DEFINITION  
UI-M-HB0-cpa-g-18-0-UI.r1 NIH-BMAP\_HB0 Mus musculus cDNA clone  
IMAGE:30649793 5', mRNA sequence.

CN461035  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 763)

NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mouseefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)  
Seq primer: pYX-5.  
Location/Qualifiers  
1..763  
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/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30649793"  
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/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP HB0"  
/note="Organ: Eye; Vector: pYX- Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTTTGAAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."  
ORIGIN

Query Match 23.0%; Score 622.8; DB 7; Length 763;  
Best Local Similarity 88.5%; Pred. No. 1.8e-167;  
Matches 675; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
Qy 480 CAGTATCTTACACCAAGAGATGATGCAATGGGCTGGAAGAGATATCTCTGGAAGAT 539  
Db 1 CAGTATCTTACCAAGAGAGATGATGCAATGGGCTGGAAGAGATATCTCTGGAAGAT 60  
Qy 540 GTGCTAAATTTTCAAGGCTACTTAAAGCATATATAATCAGACTCACTTGTACGGCTCTGGA 599  
Db 61 GTGCCAATTTTCAAGGCTCTTGGAGGCTTATATCAGACTCACTTGTATGCTGTGGA 120  
Qy 600 CGGGGGCTTTTCAATCCAAATTTGACCTACATTTGAAATTTGACATCATCTCTGAGGACAATA 659  
Db 121 CTGGGGCTTTTCCATCCAAATCTGCACCTATATTGAAGTTGGACATCATCTCTGAGGACAACA 180  
Qy 660 TTTTAAAGCTGAGAACTCACATTTTGAAGCGGCTGGAAGAGTCCATATGACCCCTA 719  
Db 181 TTTTAAAGCTGAGAACTCACATTTTGAAGCGGCTGGAAGAGTCCATATGACCCCTA 240  
Qy 720 AGCTGCTGACAGCATCCCTTTTAAATAGATGGAAGATATATACTCTGGAAGTCTGAGCTGATT 779  
Db 241 AACTACTGACTGCTCTCTTCTAATAGACGGTGGAGTGTACTCTGGAAGTCTGCGGACT 300  
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Db 301 TCATGGGACGGGACTTCGCTATCTTTCAGAACACTGCGGACCATCACCCCATCAGACGG 360  
Qy 840 AGCAGCATGATTTCAGAGTGGCTCAATGATCAAAAGTTCATTAGTCCCACTCATCTCTCAG 899  
Db 361 AGCAGCATGATTTCAGAGTGGCTCAATGATCAAAAGTTCATTAGTCCCACTCATCTCTCAG 420  
Qy 900 AGAGTGACAATCTTGAAGATGACAAGATATATCTTTTCTCCGTGGAATGCAATAGATG 959  
Db 421 AGAGTGACAATCTTGAAGATGACAAGATATATTTTCTCCGTGGAATGCAATAGATG 480  
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VERSION  
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SOURCE  
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
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TITLE  
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PUBMED  
REFERENCE  
AUTHORS  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kusunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
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4

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

6 (bases 1 to 2960)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
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Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
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Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasumishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submision  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
CDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

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(without alignments)  
5732.363 Million cell updates/sec

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Searched: 1391452 seqs, 329044822 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4201	85.8	771	14	US-10-262-538-10	Sequence 10, Appl
3	4201	85.8	771	14	US-10-067-632-54	Sequence 54, Appl
4	4201	85.8	771	14	US-10-247-671-164	Sequence 164, App
5	3568	72.9	655	14	US-10-320-769-3	Sequence 3, Appl
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ALIGNMENTS

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; Publication No. US20030087250A1  
; GENERAL INFORMATION:  
; APPLICANT: John MONAHAN  
; APPLICANT: Manjula GANNAVAPURU  
; APPLICANT: Sebastian HOERSCH  
; APPLICANT: Shubhangi KAMATKAR  
; APPLICANT: Steve G. KOVATS  
; APPLICANT: Rachel E. MEYERS  
; APPLICANT: Michael MORRISSEY  
; APPLICANT: Peter OLANDT  
; APPLICANT: Ami SEN  
; APPLICANT: Peter VEIBY  
; APPLICANT: Gordon B. MILLS  
; APPLICANT: Robert C. BAST, Jr.  
; APPLICANT: Karen LU  
; APPLICANT: Rosemarie SCHMANDT  
; APPLICANT: Xumei ZHAO  
; APPLICANT: Karen GLATT  
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

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; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
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; SEQ ID NO 284
; LENGTH: 771
; TYPE: PRT
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US-10-097-340-284

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Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 14 Gaps: 0

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US-09-774-490-1 (1-2709) x US-10-097-340-284 (1-771)

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QY 200 AFGGCTGGTTAACTAGGATTCCTCTTTCTGGGAGTATTACTTACAGCAAGACA 259
DB 1 MetGlyTrpLeuThrArgileValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGATGGGAAGACAACTGCGCAAGGCTGAATATCTTACAAAGAAATGTG 319
DB 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGlnMetLeu 40
QY 320 GAATCCAAACATGTGATCACTTTCAATGGCTGGCCCAACAGCTCCAGTTATCATACCTTC 379
DB 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439
DB 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisPheSerPhe 80
QY 440 GACCTGGTTAATATCAAGATTTTCAAAGATTGTGCGCCAGTATCTTACACCAAGA 499
DB 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATCAAGTGGCTGGAAAGACATCTGAAAGAAATGTGCTAAATTTTCATCAAGTA 559
DB 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAGACTCATTTGACGCTGTGGAACGGGGCTTTTCATCCAAT 619
DB 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTAATGGACATCATCTCGAGGACATATTTTAACTGGAGACTCA 679
DB 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTGAAAACGGCCGTGGGAAGAGTCCATATGACCCCTAAAGCTGCTGACAGCATCCCTT 739
DB 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAATATTACTCTGGAACTCGCAGCTGATTTTATGGGCGGAGACTTTGCT 799

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DB 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACACTTTGGGCACACACCCCAATCAGGACAGACATGATTTCCAGGTGG 859
DB 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATGATCCAAAGTTCATTAGTCCACCTCATCTCAGAGAGTGAACAATCCTCAAGAT 919
DB 221 LeuAsnAspProLysPheIleSerAlaHisIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTCTTCGCGTGAATAATGCAATAGATGGAGAACACTCTGGAAGCT 979
DB 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTGCAGATATGCAAGAAATGACTTTGGAGGCGACAGAGTCTGTG 1039
DB 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCTCAATGCG 1099
DB 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGATGAATCTGCAGGATGTATTCTTAATGAACTTTAAAGATCCTAAA 1159
DB 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGATATGGAGTGTTCAGACTTCCAGTAACATTTTCAAGGGATCAGCCGTG 1219
DB 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGATACATGAGTGTGAGAGGCTGTCTTGTGTCATATGCCACAGGGAT 1279
DB 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCCACTAATGGTGCCTTTATCAAGGAAGAGTCCCTATCCAGGCCCGAGAACT 1339
DB 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCCAGCAAAACATTTGGTGGTTTGACTCTACAAAGGACCTTCTCGATGATGTTATA 1399
DB 381 CysProSerTyrThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGGCAAGAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAAATCGCCA 1459
DB 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGGATGTAAATTTATCAATTTTACAAATTTGCTGAGACCGAGTGGAT 1519
DB 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAAGTGCAGAGTATGATGTTATGTTTATCGGAACAGATGTTGGACCGTCTTTAAA 1579
DB 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639
DB 461 ValValSerIleProLysGluThrTyrTrpAspLeuGluValLeuLeuGluGluMet 480
QY 1640 ACAGTTTTCGGGAACCGAGCTGTATTTTCAGCAATGAGAGCTTTTCCACTAAGCAGACAA 1699
DB 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
QY 1700 CTATATATTTGGTTCACCGCTGGGTTGCCAGCTCCCTTTTACACCGGTGGATATTATAC 1759
DB 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAGAGCTGTGCTGAGTGTGTGCTCGCCGAGACCTTACTGTGCTGGGATGGTTCT 1819
DB 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTGCTATTTTCCACTGCAAGAGAGCGCAAGACGCAAGATATTAAGAAAT 1879

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Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560  
QY 1880 GGAGACCCACTGACTCACTGTTCCAGACTTACACCATGATAATCACCATGGCCACACGCCCT 1939  
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580  
QY 1940 GAAGAGAGATCATCATGTTGTTAGAGATAGTAGCACATTTTGAATGCAGTCCGAAG 1999  
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
QY 2000 TCCAGAGAGCGCTGCTATTGCGCAATCCAGAGCGGAAATGAAGAGCGGAAAGAGAG 2059  
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGlnGluArgLysGluGlu 620  
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCGCTTCTGCTAGCTAGTACAA 2119  
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640  
QY 2120 CAGAAGATTGAGGCAATTACCTCTGCCATGCGGTGGAACATGGTTTCATAAACTCTT 2179  
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660  
QY 2180 CTTAAGGTACCTGGAAGTCATTGACACAGAGCATTTGGAAGAACTTCTTCATAAGAT 2239  
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGlnGluLeuHisLysAsp 680  
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACTGACCCAGAAG 2299  
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700  
QY 2300 GTCTGTACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359  
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
QY 2360 TTCCTGTGAACAAGTTTGGAAAAGGACCGAAAACACGTCGGCAAAAGGCGCAGACATACC 2419  
Db 721 PheCysGlnGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740  
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACCTTACAGAAAAATAAGAAAGGTAGAAACAGGAG 2479  
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760  
QY 2480 ACCACGAATTTGAGAGGCGCACCCAGAGTGTC 2512  
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2

US-10-262-538-10  
; Sequence 10, Application US/10262538  
; Publication No. US20030113324A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37564  
; CURRENT APPLICATION NUMBER: US/10/262,538  
; CURRENT FILING DATE: 2002-09-30  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 771  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-262-538-10

Alignment Scores:  
Pred. No.: 0 Length: 771  
Score: 4201.00 Matches: 771  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 85.80% Indels: 0  
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-262-538-10 (1-771)

QY 200 ATGGGCTGGTTAACTAGGATTCCTGTCTCTTTCTGGGAGTATTACTTACACAAAGACA 259  
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QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGCTGAAATTTATCTTACAAAGAAATGTG 319  
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40  
QY 320 GAATCCAAACAATGTGATCACTTTCAATGGCTTTGGCCAAACAGCTCCAGTTATCATACCTTC 379  
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QY 380 CTTTTCGATGAGAACCGAGTAGGCTGTATGTTGGAGCAAAAGATCACATATTTTTCATTTC 439  
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QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGTGGCAGTATCTTACACCACAAGA 499  
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100  
QY 500 GATGAATGCAAGTGGCTGGAAGACATCTCGAAAGAAATGTGCTAAATTTTCATCAAGGTA 559  
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120  
QY 560 CTTAAGGCATATAATCAGACTCACTGTACGCTGTGGAAACGGGGCTTTTTCATCCAATT 619  
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140  
QY 620 TGCACCTACATTTGAAATTTGGACATCATCTGTAGGACATATTTTAAAGTGGAGAACTCA 679  
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
QY 680 CATTTTGAAAACGGCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTT 739  
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Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
QY 980 ACTCAGCTAGAAATAGGTAGATATGCAAGATAGCTTTGGAGGGCAGACAGATCTGGTG 1039  
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
QY 1040 AATAAATGACAACATCTCCCTCAAGCTGCTGATTGCTCAGTGCAGGTCCAAATCGC 1099  
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QY 1100 ATTGACACTCATTTTGTGAAGTGGAGATGTATTCTTAATGAACCTTTAAAGATCTCTAAA 1159  
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QY 1160 AATCAGCTGTATATGAGAGTGTTTAGACTTCCAGTAAACATTTTCAAGGGATCAGCCGTG 1219  
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Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360





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QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGCTGAAATTTATCTTACAAAGAAATGTTG 319  
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QY 320 GAATCCAAACAAATGTGATCACTTTCAATGCTTGGCCCAACAGCTCCAGTTTATCATACCTTC 379  
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QY 380 CTTTTCGATGAGAAACCGAGTAGCTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439  
Db 61 LeuLeuAspGluLysArgSerArgLeuTyrlValGlyAlaLysAspHisIlePheSerPhe 80  
QY 440 GACCTGGTTAATATCAAGATTTTCAAAAGATGTGTGCCAGTATCTTACACCAAGAAGA 499  
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrlhisArgArg 100  
QY 500 GATGAATGCAAGTGGCTCGAAAGACATCCTCGAAAGAAATGTCTAATTTTCATCAAGGTA 559  
Db 101 AspGluCysLeuTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120  
QY 560 CTTAAGGCATATAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCATCCAATT 619  
Db 121 LeuLysAlaTyrlAsnGlnThrHisLeuTyrlAlaCysGlyThrGlyAlaPheHisProlIle 140  
QY 620 TGCACCTACATTTCAAAATTCGACATCATCCTCGAGGACAAATATTTTAAAGTGGAGAACTCA 679  
Db 141 CysThrTyrlleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
QY 680 CATTTTGAACACGGCCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGTGACAGATCCCTT 739  
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrlAspProLysLeuLeuThrAlaSerLeu 180  
QY 740 TTAATAGATGGAAATTAATCTCTGAACTGTGAGCTGATTTTATGGGGAGACTTGGCT 799  
Db 181 LeuIleAspGlyGluLeuTyrlSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
QY 800 ATCTCCGAACTCTTGGGCACACCAACCAATCAGACAGAGCAGCATGATTTCCAGGTGG 859  
Db 201 IlePheArgThrLeuGlyHisHisHisProlIleArgThrGluGlnHisAspSerArgTrp 220  
QY 860 CTCATGATCCAAAGTTCAATAGTGCACCTCATCTCAGAGAGTGACAAATCCTGAAGAT 919  
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240  
QY 920 GACAAAGTATCTTTTCTCCGTGAAATGCAATAGATGGAGACACTCTCGAAAGCT 979  
Db 241 AspLysValTyrlPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
QY 980 ACTCAGCTAGAAATAGGTGAGATATCAAGAAATGACTTTGGAGGGCACAGAAAGTCTGGTG 1039  
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280  
QY 1040 AATAATGACAAACATTCCTCAAGCTCTGTGATTTGCTCAGTGCAGGTCCAAATGGC 1099  
Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
QY 1100 ATGACACTCATTTTCACTGACAGGATGTATTCCTAATGACTTAAAGATCCTAAA 1159  
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QY 1160 AATCCAGTTGTATAGAGTGTGTACGACTTCAGTAAACATTTTCAAGGGATCAGCCGTG 1219  
Db 321 AsnProValValTyrlGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
QY 1220 TGTATGTATAGCATGATGTGAGAGGGTGTCTTGGTCCATATATCCCAACAGGGAT 1279  
Db 341 CysMetTyrlSerMetSerAspValArgValPheLeuGlyProTyrlAlaHisArgAsp 360  
QY 1280 GGACCCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTATCCAGGGCCAGGAAT 1339  
Db 361 GlyProAsnTyrlGlnTrpValProTyrlGlnGlyArgValProTyrlProArgProGlyThr 380

QY 1340 TGTCCAGACAAACATTTGGTGGTTTGTGACTCTCAAAAGGACCTTCTCTGATGATGTTATA 1399  
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400  
QY 1400 ACCTTTGCAAGAGTCATCCAGCCATGTACATCCAGTGTCTTCTCATGACAACTGCCCA 1459  
Db 401 ThrPheAlaArgSerHisProAlaMetTyrlAsnProValPheProMetAsnAsnArgPro 420  
QY 1460 ATAGTGATCAAAACCGATGTAATATCAATTTTACAAATTTGTCTAGACCGAGTGGAT 1519  
Db 421 IleValIleLysThrAspValAsnTyrlGlnPheThrGlnIleValValAspArgValAsp 440  
QY 1520 GCAGAAGATGGACAGTATGATGTTTATTCGGAACAGATGTTGGGACCGTCTCTAAA 1579  
Db 441 AlaGluAspGlyGlnTyrlAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTTAGAGAGGTCTCTCGTGAAGAAATG 1639  
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QY 1880 GGAGACCCACTGACTCCTGTTTACAGCTTACACCATGATTAATCACCATGGCCACAGCCCT 1939  
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580  
QY 1940 GAAGAGAGATCATCTATGCTAGAGATAGTAGACACATTTTGGATGCGAGTCCGAG 1999  
Db 581 GluGluArgIleIleTyrlGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
QY 2000 TCGCAGAGAGCTGCTGCTATTGGCAATTCAGAGCGCAATGAAAGAGCGAAAGAGAG 2059  
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QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGTCTACAA 2119  
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QY 2120 CAGAAGGATTCAGGCAATTTACCTGCTCCATGCGGTGGAAACATGCGGTTCATACAACTCT 2179  
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QY 2180 CTTAAGGTAACCTCGAAGTCAATTCACACAGAGCATTTGGAAAGAACTTCTTCAAAAGAT 2239  
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680  
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QY 2300 GTCTGGTACAGAGATCTCATGCGCTCATCAACACCCCAATCTCAACACGATGATGAG 2359  
Db 701 ValTrpTyrlArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720  
QY 2360 TTCTCTGACAAAGTTTGGAAAGGACCGAAACACGTCGCGCAAGGCCAGGACATACC 2419  
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740

QY 2420 CCAGGGAACAGTAACAAATGGAGCACTTACAGAAAAATAAGAAAGGTAGAACAGGAGG 2479  
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnLysArg 760  
 QY 2480 ACCAGCAATTTGAGAGGGCACCCAGGAGTGC 2512  
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

## RESULT 4

US-10-247-671-164  
 ; Sequence 164, Application US/10247671  
 ; Publication No. US20030194721A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mikita, Thomas  
 ; APPLICANT: Shiffman, Dov  
 ; APPLICANT: Porter, Gordon, J.  
 ; APPLICANT: Kaser, Matthew R.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS  
 ; FILE REFERENCE: PA-0050 US  
 ; CURRENT APPLICATION NUMBER: US/10/247,671  
 ; PRIOR FILING DATE: 2002-09-18  
 ; PRIOR APPLICATION NUMBER: 50/323,784  
 ; PRIOR FILING DATE: 2001-09-19  
 ; NUMBER OF SEQ ID NOS: 186  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 164  
 ; LENGTH: 771  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CD1  
 US-10-247-671-164

## Alignment Scores:

Pred. No.: 0 Length: 771  
 Score: 4201.00 Matches: 771  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 85.80% Indels: 0  
 DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-247-671-164 (1-771)

QY 200 ATGGGCTGTTAACTAGGATTCCTCTTTCTGGGAGTATTACTTACAGCAAGACGA 259  
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaGala 20  
 QY 260 AACTATCAGATGGGAAGAACAAATGTGCCAGGCTGAAATTCCTACAAAGAAATGTG 319  
 Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40  
 QY 320 GAATCCACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTC 379  
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60  
 QY 380 CTTTGGGATGAGCAACGGAGTGGCTGTATGTGGAGCAAGACACATATTTTCATTC 439  
 Db 61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80  
 QY 440 GACCTGGTTAATATCAAGATTTTCAAGATGTGTGGCCAGTATCTTACACCAAGAAGA 499  
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 QY 560 CTTAAGGCATATAATCAGACTCACATGTACGCTGTGGAAACGGGGCTTTTTCATCCAATT 619  
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 QY 620 TCCACCTACATTTGAAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGAGAACTCA 679

Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160  
 QY 680 CATTTTGAAAACGGCCGTGGGAAGAGTCCATATAGACCTTAAGCTCTGACAGCATCCCTT 739  
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180  
 QY 740 TTAATAGATGGAGTAATATTACTCTGGAACCTGCAGCTGATTTTATGGGGGAGACTTTC 799  
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200  
 QY 800 ATCTTCCGAACCTCTTGGGCACCCACCAATCAGACAGACAGCATGATTCAGAGTGG 859  
 Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220  
 QY 860 CTCATATGATCCAAAGTTCATTAGTCCCACTCATCTCAGAGAGTGACAAATCCTCAAGAT 919  
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240  
 QY 920 GACAAAGTATATCTTTCTTCGTAAGTGCATAGATGGAGACACTCTGGAAAGCT 979  
 Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260  
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 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280  
 QY 1040 AATAAATGGACAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAATGCG 1099  
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300  
 QY 1100 ATTGACACTCATTTTGTAGTAACTGAGGATGATTTCTTAATGAATTTTAAAGATCCCTAAA 1159  
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320  
 QY 1160 AATCCAGTTGTATATGGAGTCTTTACGACTTCCAGTAACATTTTCAAGGGATCAGCCGTG 1219  
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340  
 QY 1220 TGTATGATACATGAGTGTGAGAGGGTGTCTTGTGCTCCATATGCCACAGGGAT 1279  
 Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360  
 QY 1280 GGACCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCACGCCAGGAACT 1339  
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
 QY 1340 TGTCCCAAGCAAAACATTTGGTGGTTTGACTCTCAAGAGACCTTCTCTGATGATGTTATA 1399  
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400  
 QY 1400 ACCTTTGCAGAAAGTCAATCCAGCCATGTACAAATCCAGTGTTCCTATGAAACAATCGCCCA 1459  
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420  
 QY 1460 ATAGTGATCAAAACCGATGTAATTTATCAATTTACAAATTTGTCTAGACCGAGTGTGAT 1519  
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440  
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 QY 1640 ACAGTTTTTCCGGGAACCGACTGCTTATTTTCAGCAATGGAGCTTTTCTACTAACAGCAACA 1699  
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Db 501 LeuTyrlleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAACGGTGTCTCAGTGTTCCTCGCCCGAGACCCCTTACTGTGCTTTGGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaAaGAspProTyrCysAlaIrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGACAGAGCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGAGCCCACTGACTCAGTGTTCAGACTTACACCATGATAATCACCATGCCACACCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTACACATTTTTTGGAAATGCATCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAenSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCGTGTCTTATTTGGCAATTCAGAGCGGAAATGCAAGAGCGAAAGAGAG 2059
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Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
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Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAGTTTGGAAAGGACCGGAAACAAACACGCTCGGCAAGGCCAGACATACC 2419
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QY 2420 CCAGGCAACAGTAACAATGAGACACTTACAGAAATAGAAAGTAAAGCAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCCAGCAATTTGAGAGGCGCACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

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RESULT 5

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US-10-320-769-3
; Sequence 3, Application US/10320769
; Publication No. US20030158402A1
; GENERAL INFORMATION:
; APPLICANT: FREEMAN, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPAF,
; CURRENT APPLICATION NUMBER: US/10/320,769
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/08/556,422
; PRIOR FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

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; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-769-3

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Score: 3568.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.88% Indels: 0
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-320-769-3 (1-655)
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Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAATGGGAAGAACAAATGTGCAAGGCTGAAATATCTTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAACTGATGATCATTCTCAATGCTTGGCCACAGCTCCAGTTTATCATATCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGGATGAGCAACGGAGTAGGCTGTATGTTGGAGCAAGAGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATPATCAAGGATTTTCAAAGATGTTGTGCGCAGTATCTTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGATGCAAGTGGCTGGAAAGACATCTCTGAAAGATGCTTAATTTTCATCAAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCAATATAAATCAGACTCACCTTGTACGCTGTGGAACGGGGCTTTTTCATCAAAT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TCCACTACATTTGAATTTGACATCATCTCTGAGGACAAATATTTTAAAGCTGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGCTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAAATTAATCTCTGAACTGCACTGAGCTGATTTTATGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyLysLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTTTGGGCAACCAACCAATCAGSACAGACAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATGATCCAAAGTTTCAATAGTGGCCACCTCATCTCAGAGAGTGACATCTCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTTCTTCCTGAAATGCAATAGATGGAGAACACTCTCGAAAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGAAATAGGTCAGATATGCAAGAAATGACTTTTGGAGGGCACAAGAGTCTGGT 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGAACAACATTCCTCAAGCTGCTGATTTGCTCAGTGCCAGGTCCTCAAAATGGC 1099

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Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuLeuIleCysSerValProGlyProAsnGly 300  
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 QY 1280 GGCACCAACTATCAATGGGTGCTTATCAAGNAGAGTCCCTATCCAGCCGACGAATC 1339  
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380  
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 QY 1520 GCAGAGATGGACAGTATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTCTAAA 1579  
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460  
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 Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480  
 QY 1640 ACAGTTTTTCGGAAACCGACTGCTATTTCAGCAATGGAGCTTTCACATAAGCAGCAACA 1699  
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500  
 QY 1700 CTATATATTGTTCAACGCTGGGTGCCAGTCCCTTTACACCGGTGTGATTTTAC 1759  
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520  
 QY 1760 GCGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCCCTTACTGCTGCTGGATGTTCT 1819  
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 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580  
 QY 1940 GAAGAGAGATCATCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1999  
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600  
 QY 2000 TCCAGAGAGCGCTGGTCTATTGGCAATTTCCAGAGCGCAAAATGAAGAGCAAAAGAAG 2059  
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGlu 620  
 QY 2060 ATCAGATGGATCATATCATCATCAGCAGATCAAGGCTTCTCTAGTACGTCTCAAA 2119  
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 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655

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 ; Sequence 310, Application US/09946374  
 ; Publication No. US20030073129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas P.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1C1  
 ; CURRENT APPLICATION NUMBER: US/09/946,374  
 ; CURRENT FILING DATE: 2001-09-04  
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; PRIOR APPLICATION NUMBER: 60/102484
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; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

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Alignment Scores:
Pred. No.:      2,43e-201      Length:      777
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Percent Similarity: 73.67%    Conservative: 141
Best Local Similarity: 54.92%  Mismatches:  177
Query Match:     45.86%      Indels:      21
DB:              10          Gaps:         9

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US-09-774-490-1 (1-2709) x US-09-946-374-310 (1-777)

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Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuLeuSerAsnSerCys 58
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 335 ATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTATCATACCTCTCTTTGGATGAGGAA 394

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[illegible]

Db	419	SerPheileuLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro	438
QY	1460	ATAGTGATCAAAACGGATGTAAATATCAATTTACACAAATTCGTGTAGACCGAGTGGAT	1519
Db	439	ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle	458
QY	1520	GCAGAAGATGACAGTAGTATGTTATGTTATTCGGAACACAGATGTGGACCGTCTCTTAAA	1579
Db	459	AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478
QY	1580	GTAGTTTCAATTCCTAAGGACACTTGATGATTTAGAAGAGGTCTCTGCGAAGAAATG	1639
Db	479	ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluLeu	497
QY	1640	ACAGTTTTCCGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTCCACTAAGCAGCAACA	1699
Db	498	GlnIlePheLysHisSerSerIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln	517
QY	1700	CTATATATTGGTTCACACGGCTGGGGTTGCCAGCTCCCTTTTACACCGTGTGATATTAC	1759
Db	518	LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr	537
QY	1760	GGGAAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTGGGATGGTTCT	1819
Db	538	GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn	557
QY	1820	GCATGTTCTCGCTATTTTCCCACTGCAAGACGACGACAGCACAAGATATAAGAAAT	1879
Db	558	AlaCysSerArgTyrAlaProThrSerLysArgArgAlaArgGlnAspValLysTyr	577
QY	1880	GGACACCCACTCACTGCTTCAGACTTACACCATGATAATCACCAGTGCACACGCCCT	1939
Db	578	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596
QY	1940	GAAGAGAGAATCATCTATGCTGTAGAGATAGTAGACATTTTTTGGAAATGCAGTCCGAAG	1999
Db	597	AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616
QY	2000	TCGCAGAGAGCGTGGTCTATTGGCAATTCACAGGCGGAAATGACAGCGCAAAAGAGAG	2059
Db	617	SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu	636
QY	2060	ATCAGAGTGATGATCATCATCATCAGACAGATCAAGGCTTCTGCTAGCTAGTCTACAA	2119
Db	637	LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln	656
QY	2120	CAGAAGATTTCAGCAATTACCTCTCGCATGCGGTGGAAATCATGGTTCATACAACTCTT	2179
Db	657	LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle	676
QY	2180	CTTAAGGTAACTCGGAAGTCATTGACACAGACATTTGGAGAACTTCTTCATAAAGAT	2239
Db	677	ValLysLeuThrLeuAsnValIleGluAenGluGlnMetGluAsnThrGlnArgAlaGlu	696
QY	2240	GATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGATGATGACACTGACCCAGAAG	2299
Db	697	HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg	710
QY	2300	GTCTGGTACAGACATTCATGCACTCATCAACCCCACTTCACACGATGGATGAG	2359
Db	711	LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln	729
QY	2360	TTCTGTGAACAAGTTTGGAAAGGCCAGCAACAAACAGTCGCGCAAGGCCAGGCATACC	2419
Db	730	TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly-----	747
QY	2420	CCAGGGAAACAGTAAACAAATGGAGCACTTACAAGAAATAAGAAAGGTGAACAGGAGG	2479
Db	748	-----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg	763
QY	2480	ACCCAC---GAATTTGAGGGGCCACCCAGAGTGTC	2512
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RESULT 7  
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; Publication No. US20020127584A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C1  
; CURRENT APPLICATION NUMBER: US/10/052,586  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
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; PRIOR FILING DATE: 1998-06-02



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/ PRIOR FILING DATE: 1998-06-17
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Alignment Scores:

Pred. No.:	2,436-201	Length:	777
Score:	2245.50	Matches:	413
Percent Similarity:	73.67%	Conservative:	141
Best Local Similarity:	54.92%	Mismatches:	177
Query Match:	45.86%	Indels:	21
DB:	13	Gaps:	9

US-09-774-490-1 (1-2709) x US-10-052-586-348 (1-777)

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QY 275 AAGACAATGCCAGGCTGAATATCTCAAGAGAAATGTGTGAATCCAAACAATGTG 334
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Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrlLysAspLeuLeuSerAsnSerCys 58
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 335 ATCACTTCAATGGCTTGCCCAACAGCTCCAGTTATCATCTCTCTTTGGATGAGGAA 394
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Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
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QY 395 CGGAGTAGCTGTATGTTGGAGCAAGATCAATATTTTCATTCGACTGCTGTTAATATC 454
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Db 79 ArgGlyArgLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
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QY 455 ---AAGGATTTTCAAAAGATTGTGGCCAGTATCTTACACGAGAGAGATGAATGCAAG 511
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Db 99 AsnLysAsnPhelLysIleTyrlProAlaAlaLysGluArgValGluLeuLysCys 118
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QY 512 TGGGCTGGAAGACACATCTGAAAGATGTGCTAATTTTCATCAAGGTACTTTAAGCATAT 571
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Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelIleArgValGluGlnPro 138
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QY 572 ATCAGACTCATTGTAGCCCTGTGGAAGGGGGCTTTTCATCCAAATTTGCACCTACATT 631
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Db 139 AsnLysThrHisIleTyrlValCysGlyThrGlyAlaPheHisProIleCysGlyTyr 158
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QY 632 GAAATTTGGACATCATCTGAGGACAATATTTTAACTGGGAGAACTCACATTTTGAAC 691
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QY 692 GGCCTGGGAAGAGTCCATATGACCTAAGCTGCTGACAGCATCCCTTTTAAATAGATGA 751
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QY 812 CTGGG-----CACCAACCCCAATCAGGACAGAGCAGCATGATTCAGGTGGGCTC 862
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QY 923 AAAGTATATCTTTCTTCGCGTGAATAATCAATAGATGGAGAACACTCTGGAAGACTACT 982
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QY 1400 ACCTTTGCAAGAAGTTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAATGCGCCA 1459
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Db 219 LeuGlyProThrHisAspHisThrIleArgThrAspIleSerGlyHisTyrTrpLeu 238  
QY 863 AATGATCCAAAGTTCAATTAGTGCACCTCATCTCAGAGAGTGACAAATCCTCAAGATGAC 922  
Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258  
QY 923 AAGTATACCTTTCTTCGCGTGAATGCAATAGATGGAGAACACTCTCGGAAAGCTACT 982  
Db 259 LysIleTyrPhePheArgGluSerSerGlnGlySerThrSerAspLysThrIle 278  
QY 983 CAGCTAGATAGGTGAGATGCAATGCAAGTGTTCGAGGCGCAGAGTCTGGTGAAT 1042  
Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298  
QY 1043 AATGACACCAATTCCTCAAGCTCGTCTGATTGCTCAGTGCCAGGTCCAAATGGCATT 1102  
Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318  
QY 1103 GACACTCATTTGATGAAGTCAAGATGATTCCTTAATGAACCTTAAAGATCCTAAAT 1162  
Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338  
QY 1163 CAGTTGTATATGGAGTGTTCAGCACTCCAGTCAACATTTTCAAGGATCACCGTGT 1222  
Db 339 ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358  
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Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378  
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QY 1400 ACCTTTGCAAGAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAAATGCCCA 1459  
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QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGTTCTGCTGGAAGAAATG 1639  
Db 479 ValValSerIleSerLysGluLysTrp--AsnMetGluGluValValLeuGluGluLeu 497  
QY 1640 ACAGTTTTCGGAACCGACTCTATTTCAGCAATGAGCTTTCACCTAAGCAGCAACAA 1699  
Db 498 GlnIlePheLysHisSerIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517  
QY 1700 CTATATATTGGTTCACCGCTGGGTGTCGCCAGCTCCCTTTACACCGGTGTGATTTTAC 1759  
Db 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuLeuHisArgCysAspThrTyr 537  
QY 1760 GGGAAAGCGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGCTGCTGGAGTGTCT 1819  
Db 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557  
QY 1820 GCATGTTCTCGTATTTTCCCACTCGAAGAGACCGCACAGACGACAGATATAGAAAT 1879

Db 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaAlaArgGlnAspValLysTyr 577  
QY 1880 GGAGACCCACTGACTCAGCTGTTTACAGCTTACACCATGATATACCATCGGCCACAGCCCT 1939  
Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596  
QY 1940 GAAGAGAGAATCATCTATGGTGTAGAGAAATAGTAGACATTTTGGAAATCGAGTCCGAAG 1999  
Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616  
QY 2000 TCGCAGAGAGCGCTGCTCTATTGGCAATTCAGAGCGGCAATGAAGAGCGAAAGAGAG 2059  
Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636  
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTACAA 2119  
Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656  
QY 2120 CAGAAGGATTCAGGCAATTTACCTCTGCTCGGTGGAACATGGCTTCATACAACTCTT 2179  
Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676  
QY 2180 CTTAAGGTAACTCGGAAGTCAATGACACAGAGCAATTTGGAGAACTTCTTCATAAAGAT 2239  
Db 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696  
QY 2240 GATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAG 2299  
Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710  
QY 2300 GTCTGGTACAGAGACTTCATGCTCAGCTCATCAACACCACTTCACACGATGGATGAG 2359  
Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729  
QY 2360 TTCTGTGACAACTTTGGAAGAGGACCGCAACAAACGTCGCAAGCCAGGACATACC 2419  
Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly----- 747  
QY 2420 CCAGGGAACAGTAACAATGAAGCAGCTTCAAGAAATAAGAAAGGTAGAAACAGGAGG 2479  
Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763  
QY 2480 ACCCAC---GAATTTGAGAGGCGCCACCGAGGAGTGTCT 2512  
Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 9  
US-10-176-758-348  
; Sequence 348, Application US/10176758  
; Publication No. US20030008353A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430P1C104  
; CURRENT APPLICATION NUMBER: US/10/176,758  
; CURRENT FILING DATE: 2002-06-21  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 348  
; LENGTH: 777  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-176-758-348

## Alignment Scores:

Pred. No.: 2,43e-201 Length: 777  
 Score: 2245.50 Matches: 413  
 Percent Similarity: 73.67% Conservative: 141  
 Best Local Similarity: 54.92% Mismatches: 177  
 Query Match: 45.86% Indels: 21  
 DB: 14 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-176-758-348 (1-777)

QY 275 AGRACAAATGTCAGGCTGGAATATCTCAAGAAGATGTTGGAATCCAAATGTC 334  
 Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58  
 QY 335 ATCACTTTCAATGGCTTGCCACAGCTCCAGTTATCATACCTTCCTTTGGATGAGAA 394  
 Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78  
 QY 395 CGGAGTAGGCTGTATGTTGGAGCAAGAGTACATATTTTCATTCGACCTGGTTAATATC 454  
 Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98  
 QY 455 ---AAGGATTTCAAGATTGTGGCCAGTATCTTACACAGAGAGATGAATGCAG 511  
 Db 99 AsnLysAsnPhelLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118  
 QY 512 TGGGCTGGAAGAGACATCTGAAAGATGCTGTAATTTTCATCAAGTACTTAAGGCATAT 571  
 Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelIleArgValLeuGlnProTyr 138  
 QY 572 AATCAAGCTCAGTGTACGCTGTGGACGGGGCTTTTCATCCAAATTTGCACCTACATT 631  
 Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158  
 QY 632 GAAATTTGACATCCTCAGACAAATATTTTAACTGGAGAACTCATTGTTGAAAC 691  
 Db 159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178  
 QY 692 GCGGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGACATCCCTTTTAATAGTGA 751  
 Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198  
 QY 752 GAAATATCTCTGGAATCGAGCTGATTTTATGGGCGAGAGCTTGTCTATCTTCGCACT 811  
 Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218  
 QY 812 CTTGGG-----CACACACCCCAATCAGACAGACAGATGATTCAGGTGGCTC 862  
 Db 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238  
 QY 863 AATGATCCAAAGTTCATTAGTCCCACTCATCTCAGAGATGACATCTCAAGATGAC 922  
 Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAspAsp 258  
 QY 923 AAGATATCTTTTCTTCGCTGAAATGCAATGATGAGAGAACACTCTCGAAAGTACT 982  
 Db 259 LysIleTyrPhePhePheArgGluSerSerGlnGlySerThrSerAspLysThrIle 278  
 QY 983 CAGCTAGAAATAGTCAGATATGCAAGATGACTTTGGAGGGCAGAGAGTCTGGTGAAT 1042  
 Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298  
 QY 1043 AATGACACATCTCTCAAGCTGCTGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1102  
 Db 299 LysTrpThrPheLeuLysAlaArgLeuIleCysSerIleProIleSerAspGlyAla 318  
 QY 1103 GACACTCATTTTGCATGAACTGAGAGTATGATTCCTTAATGAACTTTAAAGATCTTAAAT 1162  
 Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338  
 QY 1163 CCAGTTGTATATGGAGTGTATACGACTTCAGTAAACATTTTCAAGGGATCAGCCGCTGT 1222

Db 339 ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358  
 QY 1223 ATGTATAGCATGATGATGAGAGGGTGTCTTGGTCCATATGCCCCACAGAGATGGA 1282  
 Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378  
 QY 1283 CCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCAGCCGCGCAGAACTTGT 1342  
 Db 379 AlaAspHisArgTyrValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398  
 QY 1343 CCCACAAAACATTTGGTGGT---TTTGACTCTCAAAAGGACCTCTCTCATGATGATTATA 1399  
 Db 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle 418  
 QY 1400 ACCTTTTCAAGGAAGTCCATCCAGCCATGACCAATCCAGTGTCTTCCCTATGAACCAATCCCCA 1459  
 Db 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438  
 QY 1460 ATAGTGATCAAAACCGATGTAATATCAATTTTACAAATTTGCTAGACCGAGTGGAT 1519  
 Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458  
 QY 1520 GCAGAGATGGACATGATGATGTTTATCGGAACAGATGTTGGGACCGTCTTCTTAA 1579  
 Db 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478  
 QY 1580 GTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTAGAAGAGGTCTCTGCGAAGAAATG 1639  
 Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluLeu 497  
 QY 1640 ACAGTTTTTTCGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCCACTAAGCAGCAACAA 1699  
 Db 498 GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517  
 QY 1700 CTATATATTGTTCAACGCTGGGTGCGGCTGCGGCTCCCTTTTACCGGTGTATATTTAC 1759  
 Db 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537  
 QY 1760 GCGAAGGCTGTGCTGAGTGTGCTGCGCCGAGAGCCCTTACTGCTTGGATGCTTCT 1819  
 Db 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557  
 QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGACAGCAGCAGATATAAGAAAT 1879  
 Db 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr 577  
 QY 1880 CGAGACCCACTGACTCAGTCTGTTTACACTTACCATGATTAATCACCATGCGCCACAGCCCT 1939  
 Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596  
 QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGAAATAGACACATTTTGGAAATGCGATCCGAAG 1999  
 Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616  
 QY 2000 TCCAGAGAGCGCTGCTCTATTGGCAATTCAGAGCGGCAATTAAGAGCGAAAGAGAG 2059  
 Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636  
 QY 2060 ATCAGATGGATCATCATATCATCAGACAGATCAAGGCTTCTGCTAGTCTACAA 2119  
 Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656  
 QY 2120 CAGAAGGATTTCAGGCAATTTACCTCTGCCATGCGGTGGAACATGGGTTTCATAAACTCTT 2179  
 Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676  
 QY 2180 CTTAAGGTAACCTCGAAGTCTTACACAGAGCATTTTGGAAAGAACTTCTTCATAAAGAT 2239  
 Db 677 ValLysLeuThrLeuAsnValIleGluAsnGlnMetGluAsnThrGlnArgAlaGlu 696  
 QY 2240 GATGATGGAGTGGCTCTTAAGACCAAGAAATGTCATAGCATGACACCTAGCCAGAGAG 2299

Db 697 HisGluGluGlyGlnVallys-----AspLeuLeuAlaGluSerArg 710  
 QY 2300 GTCGTGACAGACTTCATGAGCTCATCAACCAACCCCAATCTCAACAGATGATGAG 2359  
 Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729  
 QY 2360 TTCGTGAACAAGTTTGGAAAGGACCGAAACACAGTCGGCAAGGCCAGACATACC 2419  
 Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747  
 QY 2420 CCAGGGAACAGTAACAATGGAAGCAGCTTACAGAAAATAAGAAAGGTGAACAAGAGG 2479  
 Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763  
 QY 2480 ACCCAC---GAATTTGAGAGGGCACCACCGAGGTGTC 2512  
 Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

## RESULT 10

US-10-175-737-348  
 ; Sequence 348, Application US/10175737  
 ; Publication No. US20030013153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430301C50  
 ; CURRENT APPLICATION NUMBER: US/10/175,737  
 ; PRIOR FILING DATE: 2002-06-19  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 348  
 ; LENGTH: 777  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-175-737-348

## Alignment Scores:

Pred. No.: 2,43e-201 Length: 777  
 Score: 2245.50 Matches: 413  
 Percent Similarity: 73.67% Conservative: 141  
 Best Local Similarity: 54.92% Mismatches: 177  
 Query Match: 45.86% Indels: 21  
 DB: 14 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-175-737-348 (1-777)

QY 275 AAGAACAAATGCGCAGGCTGAATATCTCAAGAAATGTTGGAATCCAACAATGTG 334  
 Db 39 LysGlnAsnIleProArgLeuLysLeuThrLysAspPheGlnThrLeuLeuAspGlu 58  
 QY 335 ATCACTTTCAATGGGCTTGCCCAACAGCTCCAGTTATCATACCTCTCTTTGGATCAGGAA 394  
 Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuAspGlu 78  
 QY 395 CGAGTAGGCTGTATGTTGGACAAAGATCATATTTTCATTCGACTGGTTAATATC 454  
 Db 79 ArgGlyArgLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98  
 QY 455 ---AAGGATTTCAAAAGATTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAG 511  
 Db 99 AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118

QY 512 TGGCGTGGAAAGACATCTCTGAAGAATGTGCTAATTTTCATCAAGGTACTTAAAGCATAT 571  
 Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138  
 QY 572 AATCACTCACTTGTAGCCCTGTGGAACGGGGCTTTTCATCCCAATTTGCACCTACATT 631  
 Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158  
 QY 632 GAAATTGACATCATCTCTGAGGACAATATTTTAAGCTGGGAACTCATATTTGAAAAAC 691  
 Db 159 AspLeuGlyValTyrLysGluAspIlePheLysLeuAspThrHisAsnLeuGluSer 178  
 QY 692 GSCCTCGGAAGAGTCCATATACACCTAAGCTGTGCACAGCATCCCTTTTATATAGATGA 751  
 Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198  
 QY 752 GAATTATATCTCTGGAACCTGCAGCTGATTTTATGGGGCGAGACTTTTGCTATCTTCGAACT 811  
 Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218  
 QY 812 CTTGGG-----CACCAACCCCAATCAGGACAGCAGCATGATTCAGGTGGCTC 862  
 Db 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238  
 QY 863 AATGATCCAAAGTTCATTAGTGCCACCTCATCTCAGAGAGTGACAATCTCGAAGATGAC 922  
 Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258  
 QY 923 AAGTATATCTTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTGGAAAACTACT 982  
 Db 259 LysIleTyrPhePhePheArgGluSerSerGlnGlyGlySerThrSerAspLysThrIle 278  
 QY 983 CACGCTAGATAGTGCAGATATGCAGATATGCAGATTCAGGAGGCACAGAGCTGTGTGAT 1042  
 Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298  
 QY 1043 AAATGGACAACATTCCTCAAGCTCGTCTGATTGTGCTCAGTGCCAGGTCCCAATGGCATT 1102  
 Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318  
 QY 1103 GACACTCAATTTGATGAACCTGAGATGTATTCCTAATGAACCTTTAAGAGCTCTTAAAT 1162  
 Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338  
 QY 1163 CCAGTTGTATATGAGTGTTCACGACTTCACAGTAACTTTTCAAGGGATCAGCCGTGTGT 1222  
 Db 339 ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358  
 QY 1223 ATGTATAGCATGATGTGAGAGGGTGTTCCTTGTGTCATATGCCACAGGATGGA 1282  
 Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378  
 QY 1283 CCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCACGGCCAGGAACTTGT 1342  
 Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398  
 QY 1343 CCCAGCAAAACATTTGGTGGT---TTTGACTCTCAAGAGGACCTTCCTGATGATGTTATA 1399  
 Db 399 ProSerLysThrThrAspProLeuIleLysSerThrArgAspPheProAspAspValIle 418  
 QY 1400 ACCTTTGCAAGAAGTCCATCCAGCCATGTACAAATCCAGTGTTCCTTATGAACAATCGCCA 1459  
 Db 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438  
 QY 1460 ATAGTGATCAAAACGGATGTAATTTCAATTTACAAATTTGCTGTAGACGGAGTGAT 1519  
 Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458  
 QY 1520 GCAGAAAGTGCACAGTATGATGTTATGTTATCGAACACAGATGTTGGACCGCTTCTTAAA 1579  
 Db 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478  
 QY 1580 GTAGTTTCAATTCCTTAAGAGACTTGGTGTATGATTTTAGAAGAGGTTCCTCGGAAGAAATG 1639

```

Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValValLysGluGluLeu 497
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1640 ACAGTTCCTGGGAAACCGAGCTGCTATTTCAGCAATGGAGCTTTCACCTAAGCAGCAACAA 1699
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
498 GlnIlePheLysHisSerSerIleLeuLeuAsnMetGluLeuSerLeuLysGlnGln 517
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1700 CTATATATTGGTTCACACGGCTGGGTGCCCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1760 GGGAAAGCGTGTGCTCAGTGTTCCTCCGCGCCAGACCTTACTGTGCTTGGATGTTCT 1819
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1820 GCATGTTCTCGCTATTTCCTCACTGCAAGACGCGCACAAAGCAGCAAGATATAAGAAAT 1879
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
558 AlaCysSerArgTyrAlaProThrSerLysArgArgAlaArgGlnAspValLysTyr 577
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1880 GGAGACCCACTCACTACTGTTTCAGACTTACACCATGATGATCAATCCAGCCAGCCCT 1939
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1940 GAAGAGAGATCATCTATGCTAGAGATAGTAGACATTTTGGAAATGCACTCCGAG 1999
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2000 TCGCAGAGCGCTGCTATTTCGCAATTCAGAGCGCGAAATTCAGAGCGAAAGAAAGAG 2059
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspLysHisArgGluGlu 636
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2060 ATCAGAGTGATGATCATATCATCATCAGGACAGATCAAGGCTTCTGCTAGTACTACAA 2119
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2120 CAGAGGATTCAGGCAATACCTCTGCAATGCGGTGGAGACATGGTTTCATCAAACTCTT 2179
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2180 CTTAAGTAAACCTGGAAGTCAATGCACAGACAGCATTTTGGAAAGACTTCTTCATAAAG 2239
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2240 GATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAG 2299
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2300 GTCTGTACAGAGACTTCATGAGCTCATCAACCCCACTCAACACGATGGATGAG 2359
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2360 TTCTGTGAACAAGTTTGGAAAGGACCGCAAAACAGTCGCAAGCGCCAGCATACAC 2419
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
730 TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly----- 747
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2420 CCAGGGAACAGTAACAAATGGAAGCAGCTTCAAGAAATATAAGAAAGGTAGAAACAGGAG 2479
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2480 ACCAC---GAATTGAGAGGGACCCAGAGTGTCT 2512
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

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RESULT 11
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; Sequence 348, Application US/10174581
; Publication NO. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
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; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653

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Alignment Scores:

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Score:	2245.50	Matches:	413
Percent Similarity:	73.67%	Conservative:	141
Best Local Similarity:	54.92%	Mismatches:	177
Query Match:	45.86%	Indels:	21
DB:	14	Gaps:	9

US-09-774-490-1 (1-2709) x US-10-174-581-348 (1-777)

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Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrlsAspLeuLeuLeuLeuSerAsnSerCys 58
Qy 335 ATCACTTTCAATGGCTTGGCCACACAGCTCCAGTATTATCATCTTCTTTTGGATGAGGAA 394
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Qy 395 CGGAGTAGGCTGTATGTTGGAGCAAGATACATATTTTCATTCGACCTGGTTAATATC 454
Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisilePheLeuLeuSerLeuValAspLeu 98
Qy 455 ---AAGGATTTTCAAAAGATTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAG 511
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512 TGGCGTGGAAAGACATCTCTGAAAGAAATGCTGCTAATTTTCATCAAGGTACTTAAGGCATAT 571  
Db |||||  
119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138  
Qy |||||  
572 AATCAGACTCAGTTGACGCTGTGGAACGGGGCTTTTCATCCAAATTTGCACCTACATT 631  
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139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158  
Qy |||||  
632 GAAATTGGACATCCTCTCAGGACAAATATTTTAAAGCTGGAGAACTCACATTTTGAAC 691  
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159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178  
Qy |||||  
692 GCGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGCACAGCATCCCTTTTAAATAGTGA 751  
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179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198  
Qy |||||  
752 GAATATATCTCTGGAAGTGCAGCTGATTTTATGGGGCGAGACTTTCATCTCTCCGAAGCT 811  
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199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218  
Qy |||||  
812 CTTGGG-----CACCAACCAATCAGGACAGACAGCATGATTCAGGTGGCTC 862  
Db |||||  
219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238  
Qy |||||  
863 AATGATCCAAAGTTCAATAGTCCACCTCATCTCAGAGAGTGACAAATCTGAAGATGAC 922  
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239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258  
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299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318  
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538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557  
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1820 GCATGTCTCTCGCTATTTTCCCACTGCAAGAGACGCCACAAGACGACGACGACGACGAC 1879  
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558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgArgGlnAspValLysTyr 577  
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Db |||||  
578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596  
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; Sequence 348, Application US/10176483  
; Publication No. US20030017541A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

; APPLICANT:	Gurney,Austin L.
; APPLICANT:	Pan,JAMES
; APPLICANT:	Smith,Victoria
; APPLICANT:	Watanabe,Colin K.
; APPLICANT:	Wood,William I.
; APPLICANT:	Zhang,Zemin
; TITLE OF INVENTION:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE:	F3430RIC68
; CURRENT APPLICATION NUMBER:	US/10/176,483
; PRIORITY FILING DATE:	2002-06-20
; Prior application removed - See File Wrapper or Palm	
; NUMBER OF SEQ ID NOS:	612
; SEQ ID NO	348
; LENGTH:	777
; TYPE:	PRT
; ORGANISM:	Homo Sapien
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Score:	2245.50
Percent Similarity:	73.6%
Best Local Similarity:	54.92%
Query Match:	45.86%
DB:	14
Length:	777
Matches:	413
Conservative:	141
Mismatches:	177
Indels:	21
Gaps:	9
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Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGlu	78
QY 395 CGGAGTAGCGCTGATGTTGGACCAAGAAGATCACATATTTTCATTCGCAGCTGGTGAATATC	454
Db 79 ArgGlyArgLeuLeuLeuGlyAlaValAspHisIlePheLeuLeuSerLeuValAspLeu	98
QY 455 ---AAGGATTTCAAAGATTGTGGCCAGTATCTTTACACCAGAAGAGATGAATCAAG	511
Db 99 AsnLysAsnPheLysIleTyTrpProAlaIalysGluArgValGluLeuCysLys	118
QY 512 TGGCGTGAAAAAGACATCCTGAAAGAATGTCTAATTTTCATCAAGGTACTTAAGGCATAT	571
Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr	138
QY 572 ATCAGACTCACTTCAGCCCTGTGGAACGGGGCTTTTCATCCAATTTGCACCTACATT	631
Db 139 AsnLysThrHisIleTyValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle	158
QY 632 GAAATGGACATCACTCTGAGGACAATATTTTTAAGCTGGAGAACTCACATTTTGAAMAC	691
Db 159 AspLeuGlyValTyLysGluAspIleilePheLysLeuAspThrHisAsnLeuGluSer	178
QY 692 GGCGGTGGGAAGAGTCATATGACCTCAAGCTGCTGACAGCATCCCTTTTAATAGATGGA	751
Db 179 GlyArgLeuLysCysProPheAspProGlnInProPheAlaSerValMetThrAspGlu	198
QY 752 GAATATATCTCTGGAACCTGACGCTGATTTATGGGCGAGACTTTCGTATCTTCCCAGCT	811
Db 199 TyrLeuTySerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer	218
QY 812 CTTGGG-----CACCACACCCCAATCAGGACAGCAGCATGATTCAGCGTGGCT	862
Db 219 LeuGlyProThrHisAspHisIstyriIleargThrAspIleSerGluHisTyTrpLeu	238
QY 863 AATGATCCAAGTTCAATTAGTGCCCACTCATCTCAGAGAGTGACAATCTCTGAAGATGAC	922
Db 239 AsnGlyAlaLysPheIleGlyThr-PhePheIleProAspThrTyrAsnProAspAsp	258

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Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
QY 2060 ATCAAGAGTGATCATATCATCAGACAGATCAAGGCTTCTGCTAGCTAGTCTACAA 2119
Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
QY 2120 CAGAGGATTCAGGCAATTAACCTTCGCCATGCGGTGGGAACATGGGTTCATACAAACTCTT 2179
Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle. 676
QY 2180 CTTAAGTAACTCGAAGCTGATGACACAGAGCATTTGGAAGAACTTCTTCATAAGAT 2239
Db 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGAGATGGCTCTAAGACCAAGAAAGATGCTCAATAGACACACCTAGCCAGAAAG 2299
Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY 2300 GTCTGTGATCAGAGCTTCATGAGCTCATCAACCCCACTCAACAGATGATGAG 2359
Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGAACAAGTTTGGAAAGGACCGAACAACACGTCCGCAAGGCCAGACATACC 2419
Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAAAGAAATAAGAAAGGTAGAAACAGGAG 2479
Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysArgAsnArgArg 763
QY 2480 ACCCAC---GAATTGAGAGGCCACCCAGGAGTGTC 2512
Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

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## RESULT 13

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US-10-176-749-348
; Sequence 348, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-348

```

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Alignment Scores:
Pred. No.: 2,436-201 Length: 777
Score: 2245.50 Matches: 413
Percent Similarity: 73.67% Conservative: 141
Best Local Similarity: 54.92% Mismatches: 177
Query Match: 45.86% Indels: 21
DB: 14 Gaps: 9

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US-09-774-490-1 (1-2709) x US-10-176-749-348 (1-777)

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QY 275 AGAACAAATGTGCCAAGGCTGAATATTCCTACAAAGAAATGTTGGAATCCCAACATGTG 334
Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY 335 ATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTCTCTTTGGATGAGGAA 394
Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
QY 395 CGAGTAGGCTGTATGTTGGAGCAAGAGTACATATTTTCATTCGACTGGTGAATATC 454
Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY 455 ---AAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAG 511
Db 99 AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118
QY 512 TGGGCTGGAAAGACATCTGAAAGAAATGTGCTAAATTTTCATCAAGTACTTAAAGGCATAT 571
Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY 572 AATCAGACTCACTTGTAGCCCTGTGGAACGGGGGCTTTTCATCCAAATTTGCACCTACAT 631
Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY 632 GAAATTGGACATCTCTGAGACAAATATTTTAAAGCTGGAGAACTCACATTTTGAAGAAC 691
Db 159 AspLeuGlyValTyrLysGluAspIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY 692 GCCCTGGAGAGTCCATATGACCCCTAAGCTGTGACAGACATCCCTTTTAATAGATGGA 751
Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY 752 GAAATATATCTCTGGAACCTGCAGCTGATTTTATGGGCGAGACTTTCGTATCTTCCCAACT 811
Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY 812 CTTGGG-----CACACACCAATCAGACAGACAGCATGATTCAGAGTGCGCTC 862
Db 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY 863 AATGATCCAAAGTTCATTAGTCCACCTCATCTCAGAGAGTGACATCTCCTCAAGATGAC 922
Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY 923 AAAAGTATATCTTTTCTCCGTGAAAATGCAATAGATGGAGAACACTCTCGAAAAGCTACT 982
Db 259 LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
QY 983 CACGCTAGAATAGTGCAGATATGCAAGAAATGATTTGGAGGCGCACAGAAAGTCTGGTGAAT 1042
Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
QY 1043 AAATGGACAACTTCTCAAGCTCGTCTGATTTGCTAGTCCAGTCCAGTCCAAATGGCATT 1102
Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerGlyAla 318
QY 1103 GACACTCATTTTGTAGTGAAGTGCAGATGTATTCTTAATGAAGTCTTAAAGATCTCAAAAT 1162
Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY 1163 CCAGTTGTATGAGAGTGTTCACGACTTCCAGTAAACATTTTCAAGGATCAGCCGGTGT 1222
Db 339 ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
QY 1223 ATGTATAGCATGATGATGTGAGAGGTTCTCTTGTCTCATATGCCACAGGGATGGA 1282
Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
QY 1283 CCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCACGGCCAGGAACTGT 1342
Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398

```

Qy	1343	CCGAGCAAAACATTTTGGTGGT---TTTGACTCTACAAAGGACCGTTCCTGATGATGTTATA	1399
Db	399	ProSerLysThrTyrrArgAspProLeuIleLysSerThrArgAspPheProAspAspValIle	418
Qy	1400	ACCTTTTCCAAGAAGTCATCCAGCCATGACAAATCCAGTCTTCCTATGACAAATCGCCCA	1459
Db	419	SerPheIleLysArgHisSerValMetTyrrLysSerValTyrrProValAlaGlyGlyPro	438
Qy	1460	ATAGTGTACAAACCGGATGTAAATTTACAAATTTACACAAATTTGCTGTAGACCCGAGTGGAT	1519
Db	439	ThrPheLysArgIleAenValAspTyrrArgLeuThrGlnIleValValAspHisValIle	458
Qy	1520	GCAGAAATGGACAGTATGATGTTATGTTATTCGGAACAGATGTTGGACCGTTCCTTAAA	1579
Db	459	AlaGluAspGlyGlnTyrrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478
Qy	1580	GTAGTTTCAATTCCTAAGGAGACTGCTGATGATTAGAACAGGTTCTGCTGGAAGAAATG	1639
Db	479	ValValSerIleSerLysGluLysTrp--AsnMetGluGluValValLeuGluGluLeu	497
Qy	1640	ACAGTTTTCGGNAACCGACTGCTATTTCACGAATAGGAGCTTTCACATAAGCAGCAACAA	1699
Db	498	GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln	517
Qy	1700	CTATATATTGGTTCACACGGCTGGGGTGGCCAGCTCCCTTTTACACCGGTCTGATATTAC	1759
Db	518	LeuTyrrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyrr	537
Qy	1760	GGGAAACGGTGCTGAGTGTCCTCGCCGAGACCTTACTGTCTGGGATGGTTCT	1819
Db	538	GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrrCysAlaTrpAspGlyAsn	557
Qy	1820	GCATGTTCTCGCTATTTTCCACTGCAAGAGAGCGCACAGACGACGAAGATATAAGAAAT	1879
Db	558	AlaCysSerArgTyrrAlaProThrSerLysArgAlaArgGlnAspValLysTyrr	577
Qy	1880	GGAGACCCACTGACTCTACTGTTCCAGACTACCCATGATTAATCACCATGCCACAGCCCT	1939
Db	578	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596
Qy	1940	GAGAGAGATCATCATGCTGTAGAAATAGTAGACATTTTGGATCGATCGGAG	1999
Db	597	AspLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616
Qy	2000	TCGCAGAGCGGTGGTCTATTGGCAATTCACAGAGCGAAATCAAGAGCGAAAGAGAG	2059
Db	617	SerGlnGlnAlaThrIleLysTyrrTyrrIleGlnArgSerGlyAspGluHisArgGluGlu	636
Qy	2060	ATCAGAGTGATGATCATATCATCATCAGACAGATCAAGCGCTTCTGCTACGTACTACAA	2119
Db	637	LeuLysProAspGluArgIleIleLysThrGluTyrrGlyLeuLeuIleArgSerLeuGln	656
Qy	2120	CAGAAGGATTTCAGCAATTACCTCTGCGATCGGTGGAAACATGGTTTCATACAACTCTT	2179
Db	657	LysLysAspSerGlyMetTyrrTyrrCysLysLeuAlaGlnGluHisThrPheIleHisThrIle	676
Qy	2180	CTTAAGTAAACCTGGAGTTCATGTGACACAGACATTTGGAAGAACTTCTTCATAAGAT	2239
Db	677	ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu	696
Qy	2240	GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCTCAATAGCATGACACCTACCCAGAAG	2299
Db	697	HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg	710
Qy	2300	GTCTGGTACAGACTTTCATGCGACTCATCAACCCCAATCTCAACAGCATGGATGATG	2359
Db	711	LeuArgTyrrLysAspTyrrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln	729
Qy	2360	TTCTGTGCAACAGTTTGGAAAAGGGACCGGAAACACAGCTCGGCAAGGCCAGACATACC	2419
Db	730	TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly-----	747
Qy	2420	CCAGGNAACAGTAAACAAATGGAAGCACTTACAGAAAAATAAGAAAGTGAACAAACGAGG	2479

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Db      748 -----ProLyseTriplyshisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY      2480 ACCCAC---GAATTTGAGGGGCCACCCAGGAGTGTC 2512
Db      764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 14
US-10-914-348
; Sequence 348, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; PRIORITY FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-348

Alignment Scores:
Pred. No.:      2,43e-201      Length:      777
Score:          2245.50      Matches:      413
Percent Similarity: 73.67%      Conservative: 141
Best Local Similarity: 54.92%      Mismatches: 177
Query Match:      45.86%      Indels:      21
DB:              14      Gaps:      9

US-09-774-490-1 (1-2709) x US-10-176-914-348 (1-777)

QY      275 AAGAACATGTGCCAAGCTCAATATTCCTACAAGAAATGTTGGAATCCACAAATGTG 334
Db      39  LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY      335 ATCACTTTCAATGGCTTGCCGACACAGCTCCAGTATTATACATCTCTCTTTGGATCAGAA 394
Db      59  IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
QY      395 CGGAGTAGCGTGATGTTGGAGCAAGATCACATATTTTCATTCGACGTGTTAATATC 454
Db      79  ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY      455 ---AAGGATTTTCAAAGATGTGTGGCCAGTACTTTACACAGAGAGATGAATGCAAG 511
Db      99  AsnLysAsnPheLysLysIleTyrTyrProAlaIalysGluArgValGluLeuCysLys 118
QY      512 TGGCTCGAAAGAAGATCCTCGAAAGAATGTGCTTAATTCATCAAGGTACTTAAGGCATAT 571
Db      119  LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY      572 AATCAGACTCACTGTGACCTGTGGACGGGGCTTTTCATCAATTTGCACCTACATT 631
Db      139  AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY      632 GAAATTTGACATCATCTCGAGGACAATATTTTAAAGCTGGGAAGCTCAATTTTGAAGAAC 691
Db      159  AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGlySer 178

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Qy	692	GGCGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGACATCCCTTTTAAATAGATGGA	751
Db	179	GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu	198
Qy	752	GAATTATCTCGAACTGCAGCTGATTATGGCGGAGACACTTTCGTATCTCCGAACT	811
Db	199	TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer	218
Qy	812	CTTGGG-----CACCACCACCCCAATCAGGACAGACAGCATGATTCACAGTGGCTC	862
Db	219	LeuGlyProThrHisAspHisHisTyrIleArgThrAspIleSerGluHisTyrTrpLeu	238
Qy	863	AATGATCCAAGTTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAATCTCTGAAGATGAC	922
Db	239	AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAspAsp	258
Qy	923	AAAGTATATCTTCTTCCTCGTGAATAATGCAATAGATGGAGAACACTCTGGAAAGCTACT	982
Db	259	LysIleTyrPhePhePheArgGluSerSerGlnGlySerThrSerAspLysThrIle	278
Qy	983	CACCTAGAATAGTTCAGATATGCAACAATGACATTCGGAGGGCACAAATCTCGTGAAT	1042
Db	279	LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn	298
Qy	1043	AAATGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGGCCAGTCCAAATGGCAT	1102
Db	299	LysTrpThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla	318
Qy	1103	GACACTCATTTTGATGAACCTGCAGGATGATTCTCTAATGAACCTTTAAAGATCCTAA	1162
Db	319	AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn	338
Qy	1163	CCAGTCTATATGAGAGTTTACGACTTCAGATAACATTTTCAAGGATCAGCGCTGT	1222
Db	339	ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys	358
Qy	1223	ATGTATAGCATGAGTGTGAGAAAGGCTGTTCTCGTCCATATGCCACAGGATGGA	1282
Db	359	ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer	378
Qy	1283	CCNACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCACGGCCAGGACTTGT	1342
Db	379	AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys	398
Qy	1343	CCAGCAAAACATTTGGTGT---TTTGACTCTACAAGAGACCTTCCTGATGATTTATA	1399
Db	399	ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle	418
Qy	1400	ACCTTTTGCAGAAAGTCTATCCAGCCATGTACAATCCAGTGTTCCTATGACAACATCG	1459
Db	419	SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro	438
Qy	1460	ATAGTGATCAAAACGGATGTAATATCAATTCACAATAATGTCGTAGACCGAGTGGAT	1519
Db	439	ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle	458
Qy	1520	GCAGAAATGCACATATGATTGTTATCTTATCGGAACAGATGTTGGACCGTCTTAAA	1579
Db	459	AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478
Qy	1580	GTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTATTAGAAGAGGTTCCTGGAAGAATG	1639
Db	479	ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu	497
Qy	1640	ACAGTTTTTCGGGAACCGACTGCTATTTCACGAATGGAGCTTTCCACTAAGCAGCAACAA	1699
Db	498	GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln	517
Qy	1700	CTATATATTGGTTCACACGGCTGGGGTGGCCAGACTCCCTTTTACACCGGTGTGATATTAC	1759
Db	518	LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr	537

RESULT 15

US-10-176-915-348

00-10-170-312-310  
; Sequence 348, Application US/10176915

; Publication No. US20030017544A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audre

APPLICANT: Godowski, Paul

**APPLICANT:** Gurney, Austin

**APPLICANT: Pan, James**

APPLICANT: Smith, Victor

APPLICANT: Watanabe, Coli

; APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: D342081C110

FILE REFERENCE: P3430R1C110  
CURRENT ADDICTION NUMBER: HC/10/175 015

; CURRENT APPLICATION NUMBER: US/1  
 : CURRENT FILING DATE: 2002-06-21

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; ; Prior Application removed - See File Wrapper or Palm
; ; NUMBER OF SEQ ID NOS: 612
; ; SEQ ID NO 348
; ; LENGTH: 777
; ; TYPE: PRT
; ; ORGANISM: Homo Sapien
US-10-176-915-348

```

**Alignment Scores:**

Pred. No.:	2,436-201	Length:	777
Score:	2245.50	Matches:	413
Percent Similarity:	73.67%	Conservative:	141
Best Local Similarity:	54.92%	Mismatches:	177
Query Match:	45.86%	Indels:	21
DB:	14	Gaps:	9

US-09-774-490-1 (1-2709) x US-10-176-915-348 (1-7777)

275	AGAACAAATGTC	CAAGGCTGAAAT	TCTCTCA	CAAGAAATGTT	GGAAATCCCA	CAATGTG	334				
39	LysGln	AsnIle	ProArg	LeuLeu	ThrTyr	IysAspLeu	LeuSerAsnSerCys	58			
335	ATCACTTTC	CAATGGCTG	CCCAACAGCT	TCCAGTTAT	CATACCTTCTCTTT	TGGATCAGGAA	394				
59	IlePro	PheLeu	GlySerSer	GluClyLeu	AspPheGln	ThrLeuLeuLeu	AspGluGlu	78			
395	CGGAGT	TAGGCTG	TATGTTGG	CAAGAGAT	CACATATATTTT	CATTCGACCTGGT	TAAATCT	454			
79	ArgGly	ArgLeu	LeuLeu	GlyAla	AlaAspHis	PheLeuLeuSer	LeuValAspLeu	98			
455	---	AAGGATTT	CAAAAGAT	TGTGTGG	CCAGTATCTT	CACCAAGAGAGAT	GAATGCAAG	511			
99	AsnLys	AsnPhe	LeuLys	IleTyrTrp	ProAla	AlaLysGlu	ArgValGluLeu	CysLys	118		
512	TGGGCT	TGGAAAGAC	ATCCTCA	AGAAATGTG	CTAATTTT	CATCAAGGTACT	TAAAGCATAT	571			
119	Leu	IleGly	LysAsp	AlaAsn	ThrGlu	CysAlaAsn	PheIleArgVal	LeuGlnPro	Tyr	138	
572	AATCA	GACTCA	CTTGT	TACGCTGT	GGAACGGGG	CGCTTTT	CATCCAA	TTTGC	ACCTACAT	631	
139	AsnLys	ThrHis	IleTyrVal	CysGlyThr	GlyAla	PheHis	ProIleCys	GlyTyr	Ile	158	
632	GAAAT	TGGACAT	CACTCT	CGAGACA	CAATATTTT	TAAAGCTGG	GAGAACT	CA	CATTTT	GAAAC	691
159	AspLeu	GlyVal	TyrLys	GluAsp	IlePhe	LysLeu	AspThrHis	AsnLeu	GluSer	178	
692	GGCCGT	TGGGAAG	AGTCC	ATATGAC	CTTAAGCTG	TGCACAGCAT	CCCTTTT	ATATAGAT	GGA	751	
179	GlyArg	LeuLys	CysPro	PheAsp	ProGln	GlnPro	PheAla	SerVal	MetThr	AspGlu	198
752	GAA	TATAT	ACTCT	GTGGA	ACTCG	ATGATTTT	TATGGG	CGAGACTTT	GCTATCT	TCCGA	811
199	TyrLeu	TyrSer	GlyThr	AlaSer	AspPhe	LeuGly	AspThrAla	PheThr	ArgSer	218	
812	CTTGG	-----	CACCAC	CCCCAT	CAGACAG	CAGCAGCAT	GA	TCCAGGTGG	CGTC	862	
219	LeuGly	ProThr	HisAsp	HisTyr	IleArg	ThrAsp	IleSerGlu	HisTyr	TrpLeu	238	
863	AATGAT	CAAAAG	TTCAT	TAGTGCC	CACTCATCT	CAGAGAT	CACAATCCT	CAAGATGAC	922		
239	AsnGly	AlaLys	PheIle	GlyThr	PhePhe	IlePro	AspThrTyr	AsnPro	AspAsp	258	
923	AAAGTAT	ATCTTTCT	CCGTG	AAAAAT	GCATAT	GATGG	GAAACACTCT	CTGG	AAAAAGCT	ACT	982
259	Lys	IleTyrPhe	PhePhe	ArgGlu	SerSer	GlnGlySer	ThrSer	AspLys	ThrIle	278	
983	CACGCT	TAGAAT	TAGGT	CAGATAT	GCAAGAT	GACTTTT	TGGGGG	CACAGA	AGTCTGT	GTAAT	1042
279	LeuSer	ArgVal	GlyArg	ValCys	LysAsn	AspVal	GlyGln	ArgSer	LeuIle	Asn	298
1043	AAAT	GGACAA	CATCT	CAAGCT	CGTCT	GATTGT	GTCTAGT	CGCAGGT	CCAAAT	GGCAT	1102
299	Lys	TrpThr	ThrPhe	LeuLys	AlaArg	LeuIle</					

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QY 2180 CTTAGGTTAACCTGGAAGTCTTACACAGAGCATTTTGGAAAGAACTTCTTCATAAAGAT 2239
Db 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAG 2299
Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY 2300 GTCTGGTACAGAGACTTCATGAGTCTCATCAACACCCCAATCTCAACACGATGGATGAG 2359
Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGAACAAGTTTGGAAAGGGACCGAAACAAACACGTCGGCAAGGCCAGGACATACC 2419
Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY 2420 CCAGGGACAGTAACAAATGGAAGCACCTTACAGAAATAAGAAAGGTAGAAACAGAGG 2479
Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY 2480 ACCCAC---GAATTTGAGAGGCGACCCAGGAGTGTC 2512
Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

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Search completed: March 8, 2005, 21:39:35  
Job time : 398 secs



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